

Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 1 ANAFIXLRPGSLRXKXKXOCSEFXAXRIFRDAKRTKLFWTSY 44
 ||||| ||||| | | |||| | ||||| ||||| |||||
 Db 1 anafllelrpgslereckeqcsfeareilfkdaertklfwlsy 44

RESULT 4

AAB84871
 ID AAB84871 standard; Protein: 401 AA.

AC AAB84871;

DT 31-JUL-2001 (first entry)

DE Mutant blood coagulant factor VII (FVII-39).

KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
 mutant; mutein.

XX Homo sapiens.

OS Synthetic.

Key Location/Qualifiers

FT MISC-difference 235..239 /note= "Wild-type Val-Pro-Gly-Thr-Thr substituted by
 Asp-Arg-Lys-Thr-Leu"

FT MISC-difference 311..317 /note= "Wild-type Leu-Gln-Ser-Arg-Lys-Val-Gly-Asp
 -Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"

PN JP2001061479-A.

PD 13-MAR-2001.

PF 24-AUG-1999; 99JP-0237610.

PR 24-AUG-1999; 99JP-0237610.

PA (KAGA) 2H KAGAKU & KESSEI RYOHO KENKYUSHO.

DR WPI; 2001-310677/33.

DR N-PSDB; AAH19464.

PT Mutant of blood coagulant factor VII, used for substitution therapy in
 the treatment of hemophilia

PS Claim 16; Page 23-24; 29pp; Japanese.

CC The present invention relates to mutants of blood coagulant factor VII
 (FVII) or activated blood coagulant factor VII (FVIIa). The present
 CC sequence is one such mutant FVII: VII-39. The mutants can be used as an
 CC agent for the substitution therapy of haemophilia inhibitor patients.

SO Sequence 401 AA;

Query Match 89.6%; Score 172; DB 22; Length 401;
 Best Local Similarity 77.3%; Pred. No. 4e-21;
 Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 1 ANAFIXLRPGSLRXKXKXOCSEFXAXRIFRDAKRTKLFWTSY 44
 ||||| ||||| | | |||| | ||||| ||||| |||||
 Db 1 anafllelrpgslereckeqcsfeareilfkdaertklfwlsy 44

RESULT 5

AAR35764
 ID AAR35764 standard; Protein: 406 AA.

AC AAR35764;

DT 24-SEP-1993 (first entry)

XX Factor VII (VII).

DE PC, protein C; IX; Factor IX; X; Factor X; PT; prothrombin; VII;

KW Factor VII; CT; Chymotrypsinogen; SP; serine protease; binding;
 KW exosite; catalytic activity.

XX Homo sapiens.

Key Location/Qualifiers

FT Region 1..152 /note= "Factor VII light chain"

FT Region 153..406 /note= "Factor VII heavy chain"

FT Peptide 374..388 /note= "exosite 1"

FT Peptide 290..310 /note= "exosite 2"

FT Peptide 290..310 /note= "pref. PC polypeptide; claim 2, page 136"

FT Peptide 374..388 /note= "pref. PC polypeptide; claim 2, page 136"

FT Peptide 289..304 /note= "pref. PC polypeptide; claim 2, page 137"

FT Peptide 290..304 /note= "pref. PC polypeptide; claim 4, page 137"

FT Peptide 245..266 /note= "claim 9, page 138-139 describes an antibody
 that reacts with Factor VII; fragments
 289-304, 290-304, 290-310, 374-388 and
 400-414 but not with fragment 245-266"

PN W09309804-A.

PD 27-MAY-1993.

PF 18-NOV-1992; 92WO-US10242.

PR 18-NOV-1991; 91US-0793989.

PA (SCRI) SCRIPPS RES INST.

DR WPI; 1993-182244/22.

DR Griffiin JH, Masters RM;

PT Serine protease derived-polypeptide(s) and anti-peptide
 PT antibodies - for inhibiting coagulation and assaying for the
 PT presence of serine protease in fluid samples

PS Disclosure; Page 133-135; 149pp; English.

CC The PC polypeptides indicated in the Features Table inhibit
 CC coagulation (they prevent binding of serine protease to natural
 CC substrates), esp. when admin. to give an intravascular blood

CC concn. of 0.1-100 (pref. 0.5-10) microm.

CC NB: Sequences corresp. to SEQ ID NO 6, 7, 8 and 9 are described
 CC in the specification but have not yet been added to the SEQUENCE
 CC LISTING.

SO Sequence 406 AA;

Query Match 89.6%; Score 172; DB 14; Length 406;
 Best Local Similarity 77.3%; Pred. No. 4e-21;
 Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 1 ANAFIXLRPGSLRXKXKXOCSEFXAXRIFRDAKRTKLFWTSY 44
 ||||| ||||| | | |||| | ||||| ||||| |||||
 Db 1 anafllelrpgslereckeqcsfeareilfkdaertklfwlsy 44

RESULT 6

XX	OS	XX	Location/Qualifiers
KW	cardiant; hepatostrophic; cerebroprotective; haemophilia; liver disease;	XX	
KW	myocardial infarction; thrombotic stroke; deep-vein thrombosis.	XX	
XX	Homo sapiens.	XX	
XX	Key	XX	Location/Qualifiers
FT	Misc-difference	FT	/label= glu, OTHER
FT	Misc-difference	FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference	FT	7
FT	Misc-difference	FT	/label= glu, OTHER
FT	Misc-difference	FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference	FT	14
FT	Misc-difference	FT	/label= glu, OTHER
FT	Misc-difference	FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference	FT	16
FT	Misc-difference	FT	/label= glu, OTHER
FT	Misc-difference	FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference	FT	19
FT	Misc-difference	FT	/label= glu, OTHER
FT	Misc-difference	FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference	FT	20
FT	Misc-difference	FT	/label= glu, OTHER
FT	Misc-difference	FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference	FT	25
FT	Misc-difference	FT	/label= glu, OTHER
FT	Misc-difference	FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference	FT	26
FT	Misc-difference	FT	/label= glu, OTHER
FT	Misc-difference	FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference	FT	29
FT	Misc-difference	FT	/label= glu, OTHER
FT	Misc-difference	FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference	FT	35
FT	Misc-difference	FT	/label= glu, OTHER
FT	Misc-difference	FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference	FT	52
FT	Misc-difference	FT	/note= "O-glycosylated"
FT	Misc-difference	FT	60
FT	Misc-difference	FT	/note= "O-glycosylated"
FT	Misc-difference	FT	145
FT	Misc-difference	FT	/note= "N-glycosylated"
FT	Misc-difference	FT	152..153
FT	Misc-difference	FT	"proteolytic cleavage site converting FVII zymogen
FT	Misc-difference	FT	to an activated form, comprising two chains
FT	Misc-difference	FT	linked by a single disulphide bridge"
FT	Misc-difference	FT	322
FT	Misc-difference	FT	/note= "N-glycosylated"
XX	WO200158935-A2.	XX	
XX	16-AUG-2001.	XX	
XX	12-FEB-2001; 2001WO-DK00094.	XX	
XX	11-FEB-2000; 2000DK-0000218.	XX	
XX	18-OCT-2000; 2000DK-0001558.	XX	
XX	(MAXY-) MAXYGEN APS.	XX	
XX	Andersen KV, Pedersen AH, Bornaaes C;	XX	
XX	WPI: 2001-581807/65.	XX	
XX	N-PSDB; AA199982.	XX	
XX	New conjugate, useful for treating Factor VIIa related diseases or	XX	
XX	disorders such as haemophilia, liver disease, myocardial infarction and	XX	
XX	deep-vein thrombosis, comprises non-polypeptide group covalently	XX	
XX	attached to polypeptide group -	XX	
XX	Claim 1; Page 81-83; 89pp: English.	XX	
XX	The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)	XX	

[illegible]

Best Local Similarity 100.0%; Pred. No. 4e-21;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANAFLLXLRPGSLXRXCKXXQCSEFXARXIFKDXARTKLEWISY 44
|||||
Db 1 anafllxlrpgslxrxckxxqcsfxarxifkdxartkclfwlsy 44

RESULT 11

AAM52182

ID AAM52182 standard; Protein: 406 AA.

XX AAM52182;

XX 07-FEB-2002 (first entry)

XX Human FVII mutant K143N/N145F.

KW Factor VII: FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
KW cardiant; hepatotrophic; cerebroprotective; haemophilia; liver disease;
KW myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;
mutain.

XX Homo sapiens.
OS Synthetic.

FH Location/Qualifiers

FT Misc-difference 6 /label= Glu, OTHER

FT /note= "OTHER = gamma carboxyglutamic acid"

FT Misc-difference 7 /label= Glu, OTHER

FT /note= "OTHER = gamma carboxyglutamic acid"

FT Misc-difference 14 /label= Glu, OTHER

FT /note= "OTHER = gamma carboxyglutamic acid"

FT Misc-difference 16 /label= Glu, OTHER

FT /note= "OTHER = gamma carboxyglutamic acid"

FT Misc-difference 19 /label= Glu, OTHER

FT /note= "OTHER = gamma carboxyglutamic acid"

FT Misc-difference 26 /label= Glu, OTHER

FT /note= "OTHER = gamma carboxyglutamic acid"

FT Misc-difference 29 /label= Glu, OTHER

FT /note= "OTHER = gamma carboxyglutamic acid"

FT Misc-difference 35 /label= Glu, OTHER

FT /note= "OTHER = gamma carboxyglutamic acid"

FT Modified-site 52 /note= "O-glycosylated"

FT Modified-site 60 /note= "O-glycosylated"

FT Misc-difference 143 /note= "W1d-type Lys substituted by Asn"

FT Misc-difference 145 /note= "W1d-type Asn substituted by Thr"

FT Cleavage-site 152..153 /note= "proteolytic cleavage site converting FVII zymogen to an activated form, comprising two chains linked by a single disulphide bridge"

FT Modified-site 322 /note= "N-glycosylated"

FT WO200158935-A2.

XX 16-AUG-2001.
PD

XX 12-FEB-2001; 2001WO-DK00094.
XX

XX 11-FEB-2000; 2000DK-0000218.
PR

XX 18-OCT-2000; 2000DK-0001558.
PR

XX (MAXY-) MAXYGEN APS.
PA

XX Andersen KV, Pedersen AH, Bornaes C;
PI

XX WPI; 2001-581807/65.
DR

XX New conjugate, useful for treating Factor VIIa related diseases or
PT disorders such as haemophilia, liver disease, myocardial infarction and
PT deep-vein thrombosis, comprises non-polypeptide group covalently
PT attached to polypeptide group -

PS Example 3; Page -: 89pp; English.
XX

XX The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
CC polypeptide conjugates, comprising at least one non-polypeptide group
CC covalently attached to a polypeptide, where the amino acid sequence of
CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
CC least one amino acid residue containing an attachment group for the
CC non-polypeptide group has been introduced or removed. The FVIIa
CC conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and
CC cerebroprotective activity and are useful for treating FVIIa/FI-related
CC diseases or disorders such as haemophilia, liver disease, myocardial
CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
CC have increased functional in vivo half life and/or increased plasma half
CC life, increased bioavailability and/or reduced sensitivity to proteolytic
CC degradation. Consequently medical treatment using the conjugates has a
CC number of advantages over currently available such as longer duration
CC between injections. The present sequence is that of a human FVII mutant,
CC having an addition in vivo glycosylation site and tested for its
CC amidolytic activity.
CC Note: The present sequence is not shown in the specification but is
CC derived from the human wild-type FVII sequence shown in SEQ ID NO 1
CC (AAM52171).
XX

SO Sequence 406 AA;

Query Match 89.6%; Score 172; DB 22; Length 406;
Best Local Similarity 100.0%; Pred. No. 4e-21;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANAFLLXLRPGSLXRXCKXXQCSEFXARXIFKDXARTKLEWISY 44
|||||
Db 1 anafllxlrpgslxrxckxxqcsfxarxifkdxartkclfwlsy 44

RESULT 12

AAM52183

ID AAM52183 standard; Protein: 406 AA.

XX AAM52183;

XX 07-FEB-2002 (first entry)

XX Human FVII mutant V253N.

XX Factor VII: FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;

KW cardiant; hepatotrophic; cerebroprotective; haemophilia; liver disease;
KW myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;
mutain.

XX Homo sapiens.
OS Synthetic.

FH Location/Qualifiers

XX Key
XX

FT Misc-difference 6 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 7 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 14 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 16 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 19 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 20 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 25 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 26 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 29 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 35 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Modified-site 52 /label= "O-glycosylated"
FT Modified-site 60 /note= "O-glycosylated"
FT Modified-site 145 /note= "O-glycosylated"
FT Cleavage-site 152..153 /note= "N-glycosylated"
FT /note= "proteolytic cleavage site converting FVII zymogen to an activated form, comprising two chains linked by a single disulphide bridge"
FT Misc-difference 253 /note= "Wild-type Val substituted by Asn"
FT Modified-site 322 /note= "N-glycosylated"
XX W0200158935-A2.
XX 16-AUG-2001.
XX 12-FEB-2001; 2001WO-DK0094.
XX 11-FEB-2000; 2000DK-0000218.
XX 18-OCT-2000; 2000DK-0001558.
PA (MAXY-) MAXYGEN APS.
PI Andersen KV, Pedersen AH, Bornaes C;
XX WPI: 2001-581807/65.
XX New conjugate, useful for treating Factor VIIa related diseases or
XX disorders such as haemophilia, liver disease, myocardial infarction and
XX deep-vein thrombosis, comprises non-polypeptide group covalently
XX attached to polypeptide group -
XX Example 3; Page -: 89pp; English.
XX The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
XX polypeptide conjugates, comprising at least one non-polypeptide group
XX covalently attached to a polypeptide, where the amino acid sequence of
XX polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
XX least one amino acid residue containing an attachment group for the
XX non-polypeptide group has been introduced or removed. The FVIIa

CC conjugates have haemostatic, thrombolytic, cardiact, hepatotropic and
CC cerebroprotective activity and are useful for treating FVIIa/TF-related
CC diseases or disorders such as haemophilia, liver disease, myocardial
CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
CC have increased functional in vivo half life and/or increased plasma half
CC life, increased bioavailability and/or reduced sensitivity to proteolytic
CC degradation. Consequently medical treatment using the conjugates has a
CC number of advantages over currently available such as longer duration
CC between injections. The present sequence is that of a human FVII mutant,
CC having an addition in vivo glycosylation site and tested for its
CC amidolytic activity.
CC Note: The present sequence is not shown in the specification but is
CC derived from the human wild-type FVII sequence shown in SEQ ID NO 1
CC (AAM52171).
XX Sequence 406 AA;
SO
Query Match 89.6%; Score 172; DB 22; Length 406;
Best Local Similarity 100.0%; Pred. No. 4e-21;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ANAFLEXLRPGSLXRXCKXQCSFXXARXIFKDAKRLFMISY 44
Db 1 anaflxlrpgslxrxckxqcsfxarxifkdxartrlfwisy 44
RESULT 13
AAM52184
ID AAM52184 standard; Protein: 406 AA.
XX
AC AAM52184;
XX
DT 07-FEB-2002 (first entry)
XX
DE Human FVII mutant R290N/A292T.
XX
KW Factor VII; FVII: Factor VIIa; FVIIa: haemostatic; thrombolytic;
KW cardiact; hepatotropic; cerebroprotective; haemophilia; liver disease;
KW myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;
KW mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 6 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 7 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 14 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 16 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 19 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 20 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 25 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 26 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 29 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"

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FT Misc-difference 35 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Modified-site 52 /note= "O-glycosylated"
FT Modified-site 60 /note= "O-glycosylated"
FT Modified-site 145 /note= "O-glycosylated"
FT Cleavage-site 152..153 /note= "N-glycosylated"
FT /note= "proteolytic cleavage site converting FVII zymogen
FT to an activated form, comprising two chains
FT linked by a single disulphide bridge"
FT Misc-difference 290 /note= "Wild-type Arg substituted by Asn"
FT Misc-difference 292 /note= "Wild-type Ala substituted by Thr"
FT Modified-site 322 /note= "N-glycosylated"
FT WO200158935-A2.
FT 16-AUG-2001.
FT 12-FEB-2001: 2001WO-DK00094.
FT 11-FEB-2000: 2000DK-0000218.
FT 18-OCT-2000: 2000DK-0001558.
FT (MAXY-) MAXYGEN APS.
FT Andersen KV, Pedersen AH, Bornaes C;
FT WPI: 2001-581807/65.
FT New conjugate, useful for treating Factor VIIa related diseases or
FT disorders such as haemophilia, liver disease, myocardial infarction and
FT deep-vein thrombosis, comprises non-polypeptide group covalently
FT attached to polypeptide group -
FT
FT Example 3; Page -: 89pp; English.
FT
FT The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
FT polypeptide conjugates, comprising at least one non-polypeptide group
FT covalently attached to a polypeptide, where the amino acid sequence of
FT polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
FT least one amino acid residue containing an attachment group for the
FT non-polypeptide group has been introduced or removed. The FVIIa
FT conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and
FT cerebroprotective activity and are useful for treating FVIIa/TF-related
FT diseases or disorders such as haemophilia, liver disease, myocardial
FT infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
FT have increased functional in vivo half life and/or increased plasma half
FT life, increased bioavailability and or reduced sensitivity to proteolytic
FT degradation. Consequently medical treatment using the conjugates has a
FT number of advantages over currently available such as longer duration
FT between injections. The present sequence is that of a human FVII mutant,
FT having an addition in vivo glycosylation site and tested for its
FT amidolytic activity.
FT Note: The present sequence is not shown in the specification but is
FT derived from the human wild-type FVII sequence shown in SEQ ID NO 1
FT (AAM52171).
FT
FT Sequence 406 AA:

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RESULT 14
ID AAM52185
XX AAM52185 standard; Protein; 406 AA.
XX
AC AAM52185:
XX
XX 07-FEB-2002 (first entry)
XX
XX Human FVII mutant G291N.
XX
XX Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
XX cardiant; hepatotrophic; cerebroprotective; haemophilia; liver disease;
XX myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;
XX muteln.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Misc-difference 6 /label= Glu, OTHER
XX /note= "OTHER = gamma carboxyglutamic acid"
XX
XX Misc-difference 7 /label= Glu, OTHER
XX /note= "OTHER = gamma carboxyglutamic acid"
XX
XX Misc-difference 14 /label= Glu, OTHER
XX /note= "OTHER = gamma carboxyglutamic acid"
XX
XX Misc-difference 16 /label= Glu, OTHER
XX /note= "OTHER = gamma carboxyglutamic acid"
XX
XX Misc-difference 19 /label= Glu, OTHER
XX /note= "OTHER = gamma carboxyglutamic acid"
XX
XX Misc-difference 20 /label= Glu, OTHER
XX /note= "OTHER = gamma carboxyglutamic acid"
XX
XX Misc-difference 25 /label= Glu, OTHER
XX /note= "OTHER = gamma carboxyglutamic acid"
XX
XX Misc-difference 26 /label= Glu, OTHER
XX /note= "OTHER = gamma carboxyglutamic acid"
XX
XX Misc-difference 29 /label= Glu, OTHER
XX /note= "OTHER = gamma carboxyglutamic acid"
XX
XX Misc-difference 35 /label= Glu, OTHER
XX /note= "OTHER = gamma carboxyglutamic acid"
XX
XX Modified-site 52 /note= "O-glycosylated"
XX
XX Modified-site 60 /note= "O-glycosylated"
XX
XX Modified-site 145 /note= "O-glycosylated"
XX
XX Cleavage-site 152..153 /note= "N-glycosylated"
XX /note= "proteolytic cleavage site converting FVII zymogen
XX to an activated form, comprising two chains
XX linked by a single disulphide bridge"
XX
XX Misc-difference 291 /note= "Wild-type Gly substituted by Asn"
XX Modified-site 322 /note= "N-glycosylated"
XX
XX WO200158935-A2.
XX
XX 16-AUG-2001.
XX
XX 12-FEB-2001: 2001WO-DK00094.
XX
XX 11-FEB-2000: 2000DK-0000218.

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Pt		New conjugate, useful for treating Factor VIIA related diseases or disorders such as haemophilia, liver disease, myocardial infarction and deep-vein thrombosis, comprises non-polypeptide group covalently attached to polypeptide group -
Xx		
Sr		Example 3; Page -: 89pp; English.
Cc		The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
Cc		polypeptide conjugates, comprising at least one non-polypeptide group
Cc		covalently attached to a polypeptide, where the amino acid sequence of
Cc		polypeptide differs from that of the wildtype FVIIa (AAm52171) in that at
Cc		least one amino acid residue containing an attachment group for the
Cc		non-polypeptide group has been introduced or removed. The FVIIa
Cc		conjugates have haemostatic, thrombolytic, cardiac, hepatotropic and cerebroprotective activity and are useful for treating FVIIa/Tf-related
Cc		diseases or disorders such as haemophilia, liver disease, myocardial
Cc		infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
Cc		have increased functional in vivo half life and/or increased plasma half
Cc		life, increased bioavailability and or reduced sensitivity to proteolytic
Cc		degradation. Consequently medical treatment using the conjugates has a
Cc		number of advantages over currently available such as longer duration
Cc		between injections. The present sequence is that of a human FVIII mutant,
Cc		having an addition in vivo glycosylation site and tested for its
Cc		amidolytic activity.
Cc		Note: The present sequence is not shown in the specification but is
Cc		derived from the human wild-type FVIII sequence shown in SEQ ID NO 1
Cc		(AAm52171).
SQ	Sequence	406 AA;
Oy	Query Match	Best Local Similarity 89.6%; Score 172; DB 22; Length 406; Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Dd	1 ANAFLLXLRPGSLAKRXCKXXQCFFAXARXIFKDAKKTKLFWISY 44 1 anaflxlrlpgslakrxckxxqcsffaxarxfkdxarktklftwsly 44	
RRESULT	15	
ID	AAM52186	
AC	AAM52186 standard; Protein: 406 AA.	
DT	07-FEB-2002 (first entry)	
DE	Human FVII mutant R315N/V317T.	
KW	Factor VIII; FVIII; Factor VIIA; FVIIa; hemostatic; thrombolytic;	
KM	cardiac; hepatotrophic; cerebroprotective; haemophilia; liver disease;	
KW	myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;	
mucin.		
OS	Homo sapiens.	
SY	Synthetic.	
Key	Location/Qualifiers	
FH	Misc-difference 6	/label= Glu, OTHER
FT	Misc-difference /note= "OTHER = gamma carboxylutamic acid"	
FT	Misc-difference 7	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxylutamic acid"	

FT	Misc-difference	14	/label= Glu, OTHER
FT		/note= "OTHER = gamma carboxyglutamic acid"	
FT	Misc-difference	16	/label= Glu, OTHER
FT		/note= "OTHER = gamma carboxyglutamic acid"	
FT	Misc-difference	19	/label= Glu, OTHER
FT		/note= "OTHER = gamma carboxyglutamic acid"	
FT	Misc-difference	20	/label= Glu, OTHER
FT		/note= "OTHER = gamma carboxyglutamic acid"	
FT	Misc-difference	25	/label= Glu, OTHER
FT		/note= "OTHER = gamma carboxyglutamic acid"	
FT	Misc-difference	26	/label= Glu, OTHER
FT		/note= "OTHER = gamma carboxyglutamic acid"	
FT	Misc-difference	29	/label= Glu, OTHER
FT		/note= "OTHER = gamma carboxyglutamic acid"	
FT	Misc-difference	35	/label= Glu, OTHER
FT		/note= "OTHER = gamma carboxyglutamic acid"	
FT	Modified-site	52	/note= "O-glycosylated"
FT	Modified-site	60	/note= "O-glycosylated"
FT	Modified-site	145	/note= "N-glycosylated"
FT	Cleavage-site	152..153	"proteolytic cleavage site converting FVII zymogen to an activated form, comprising two chains linked by a single disulphide bridge"
FT	Misc-difference	315	/note= "Wild-type Arg substituted by Asn"
ET	Misc-difference	317	/note= "Wild-type Val substituted by Thr"
ET	Modified-site	322	/note= "N-glycosylated"
PN		WO200158935-A2.	
PD		16-AUG-2001.	
XX			
PB		12-FEB-2001; 2001WO-DK00094.	
PR		11-FEB-2000; 2000DK-0000218.	
PR		18-OCT-2000; 2000DK-0001558.	
PA	(MAXY-) MAXYGEN APS.		
PI	Andersen KV, Pedersen AH, Bornaes C;		
XX			
XX	WPI; 2001-581807/65.		
PT	New conjugate, useful for treating Factor VIIa related diseases or disorders such as haemophilia, liver disease, myocardial infarction and deep-vein thrombosis, comprises non-polypeptide group covalently attached to polypeptide group -		
PS	Example 3; Page -: 89pp; English.		
CC	The invention relates to novel Factor VII (FVII) or Factor VIIA (FVIIA) polypeptide conjugates, comprising at least one non-polypeptide group covalently attached to a polypeptide, where the amino acid sequence of polypeptide differs from that of the wildtype FVIIA (AA52171) in that at least one amino acid residue containing an attachment group for the non-polypeptide group has been introduced or removed. The FVIIA conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and cerebroprotective activity and are useful for treating FVIIA/Fr-related diseases or disorders such as haemophilia, liver disease, myocardial infarction, thrombotic stroke and deep-vein thrombosis. The conjugates		

CC have increased functional in vivo half life and/or increased plasma half
 CC life, increased bioavailability and or reduced sensitivity to proteolytic
 CC degradation. Consequently medical treatment using the conjugates has a
 CC number of advantages over currently available such as longer duration
 CC between injections. The present sequence is that of a human FVII mutant,
 CC having an addition in vivo glycosylation site and tested for its
 CC amidolytic activity.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from the human wild-type FVII sequence shown in SEQ ID NO 1
 CC (AAM52171).
 XX
 SQ Sequence 406 AA;

Query Match 89.6%; Score 172; DB 22; Length 406;
 Best Local Similarity 100.0%; Pred. No. 4e-21;
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLXRXCKXXQCSFXHAXIFKDAKRTKLWISY 44
 ||||||||||||||||||||||||||||||||||||||||
 Db 1 anaflxxlrpsslrxckxxqcsfxhaxifkdxrtklwisy 44

RESULT 16
 AAM52187
 ID AAM52187 standard; Protein; 406 AA.
 XX
 AC AAM52187;
 XX
 DT 07-FEB-2002 (first entry)
 XX
 DE Human FVII mutant K143N/N145T/R315N/V317T.
 XX
 KW Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
 KM cardiant; hepatotrophic; cerebroprotective; haemophilia; liver disease;
 KM myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;
 XX muteln.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX
 FH Key Location/Qualifiers
 FT MISC-difference 6 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT MISC-difference 7 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT MISC-difference 14 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT MISC-difference 16 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT MISC-difference 19 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT MISC-difference 20 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT MISC-difference 25 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT MISC-difference 26 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT MISC-difference 29 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT MISC-difference 35 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT Modified-site 52 /note= "OTHER = gamma carboxyglutamic acid"

FT /note= "O-glycosylated"
 FT Modified-site 60 /note= "O-glycosylated"
 FT MISC-difference 143 /note= "Wild-type Lys substituted by Asn"
 FT MISC-difference 145 /note= "Wild-type Asn substituted by Thr"
 FT Cleavage-site 152..153 /note= "proteolytic cleavage site converting FVII zymogen
 FT /note= "to an activated form, comprising two chains
 FT linked by a single disulphide bridge"
 FT MISC-difference 315 /note= "Wild-type Arg substituted by Asn"
 FT MISC-difference 317 /note= "Wild-type Val substituted by Thr"
 FT Modified-site 322 /note= "N-glycosylated"
 XX
 PN W0200158935-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 12-FEB-2001; 2001MO-DK00094.
 XX
 PR 11-FEB-2000; 2000DK-0000218.
 PR 18-OCT-2000; 2000DK-0001558.
 XX
 PA (MAXY-) MAXYGEN APS.
 XX
 PI Andersen KV, Pedersen AH, Bornaes C;
 XX
 DR WPI; 2001-581807/65.
 XX
 XX New conjugate, useful for treating Factor VIIa related diseases or
 PT disorders such as haemophilia, liver disease, myocardial infarction and
 PT deep-vein thrombosis, comprises non-polypeptide group covalently
 PT attached to polypeptide group -
 XX
 XX
 PS Example 3; Page -: 89pp; English.
 XX
 CC The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
 CC polypeptide conjugates, comprising at least one non-polypeptide group
 CC covalently attached to a polypeptide, where the amino acid sequence of
 CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
 CC least one amino acid residue containing an attachment group for the
 CC non-polypeptide group has been introduced or removed. The FVIIa
 CC conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and
 CC cerebroprotective activity and are useful for treating FVIIa/TF-related
 CC diseases or disorders such as haemophilia, liver disease, myocardial
 CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
 CC have increased functional in vivo half life and/or increased plasma half
 CC life, increased bioavailability and or reduced sensitivity to proteolytic
 CC degradation. Consequently medical treatment using the conjugates has a
 CC number of advantages over currently available such as longer duration
 CC between injections. The present sequence is that of a human FVII mutant,
 CC having an addition in vivo glycosylation site and tested for its
 CC amidolytic activity.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from the human wild-type FVII sequence shown in SEQ ID NO 1
 CC (AAM52171).
 XX
 SQ Sequence 406 AA;

Query Match 89.6%; Score 172; DB 22; Length 406;
 Best Local Similarity 100.0%; Pred. No. 4e-21;
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLXRXCKXXQCSFXHAXIFKDAKRTKLWISY 44
 ||||||||||||||||||||||||||||||||||||||||
 Db 1 anaflxxlrpsslrxckxxqcsfxhaxifkdxrtklwisy 44

RESULT 17
 AAB84866
 ID AAB84866 standard; Protein: 406 AA.
 AC AAB84866;
 DT 31-JUL-2001 (first entry)
 DE Wild-type human blood coagulant factor VII (FVII).
 KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia.
 OS Homo sapiens.
 FT Disulfide-bond 159..164
 FT Location/Qualifiers
 JP2001061479-A.
 PD 13-MAR-2001.
 PF 24-AUG-1999; 99JP-0237610.
 PR 24-AUG-1999; 99JP-0237610.
 PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 DR WPI: 2001-310677/33.
 DR N-PSDB: AAH19459.
 PT Mutant of blood coagulant factor VII, used for substitution therapy in
 PT the treatment of hemophilia -
 PS Disclosure; Page 8-9; 29pp; Japanese.
 CC The present invention relates to mutants of blood coagulant factor VII
 CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
 CC sequence represents the protein sequence for wild-type human FVII. The
 CC mutants can be used as an agent for the substitution therapy of
 CC hemophilia inhibitor patients.
 CC
 SQ Sequence 406 AA;
 Query Match 89.6%; Score 172; DB 22; Length 406;
 Best Local Similarity 77.3%; Pred. No. 4e-21;
 Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 Oy 1 ANAFLLXXLRPGSLRXCKXXCQSFXXARXIFKDXRRTLEWISY 44
 Db 1 anaflleirpyslereckeegcsfeareltkdaertklfwisy 44
 RESULT 18
 AAB84867
 ID AAB84867 standard; Protein: 406 AA.
 AC AAB84867;
 DT 31-JUL-2001 (first entry)
 DE Mutant blood coagulant factor VII (FVII-5).
 KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
 KW mutant; mutein.
 OS Homo sapiens.
 OS Synthetic.
 FT Key Location/Qualifiers
 FT Misc-difference 159 /note= "Wild-type Cys substituted by Ala"
 FT

FT Misc-difference 164 /note= "Wild-type Cys substituted by Ala"
 FT
 FT
 XX
 PN JP2001061479-A.
 PD 13-MAR-2001.
 PF 24-AUG-1999; 99JP-0237610.
 PR 24-AUG-1999; 99JP-0237610.
 PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 DR WPI: 2001-310677/33.
 DR N-PSDB: AAH19460.
 PT Mutant of blood coagulant factor VII, used for substitution therapy in
 PT the treatment of hemophilia -
 PS Claim 3; Page 11-12; 29pp; Japanese.
 CC The present invention relates to mutants of blood coagulant factor VII
 CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
 CC sequence is one such mutant FVII: VII-5. In the wild-type protein
 CC (AAB84866), there is a disulphide bond (159Cys-164Cys). In the present
 CC protein, the disulphide bond is disrupted. The mutants can be used as an
 CC agent for the substitution therapy of haemophilia inhibitor patients.
 CC
 SQ Sequence 406 AA;
 Query Match 89.6%; Score 172; DB 22; Length 406;
 Best Local Similarity 77.3%; Pred. No. 4e-21;
 Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 Oy 1 ANAFLLXXLRPGSLRXCKXXCQSFXXARXIFKDXRRTLEWISY 44
 Db 1 anaflleirpyslereckeegcsfeareltkdaertklfwisy 44
 RESULT 19
 AAB84868
 ID AAB84868 standard; Protein: 406 AA.
 AC AAB84868;
 DT 31-JUL-2001 (first entry)
 DE Mutant blood coagulant factor VII (FVII-6).
 KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
 KW mutant; mutein.
 OS Homo sapiens.
 OS Synthetic.
 FT Key Location/Qualifiers
 FT Misc-difference 164 /note= "Wild-type Cys substituted by Ala"
 FT Misc-difference 299 /note= "Wild-type Val substituted by Cys"
 FT
 FT
 XX
 PN JP2001061479-A.
 PD 13-MAR-2001.
 PF 24-AUG-1999; 99JP-0237610.
 PR 24-AUG-1999; 99JP-0237610.
 PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 DR WPI: 2001-310677/33.
 DR

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DR  N-PSDB; AAH19461.
XX
XX  Mutant of blood coagulant factor VII, used for substitution therapy in
PT  the treatment of hemophilia -
XX
XX  Claim 5; Page 14-15; 29pp; Japanese.
PS
XX  The present invention relates to mutants of blood coagulant factor VII
CC  (FVII) or activated blood coagulant factor VII (FVIIa). The present
CC  sequence is one such mutant FVII: VII-6. In the wild-type protein
CC  (AAB84866), there is a disulphide bond (159Cys-164Cys). In the present
CC  protein, the disulphide bond is disrupted. The mutants can be used as an
CC  agent for the substitution therapy of haemophilia inhibitor patients.
XX
SQ  Sequence 406 AA;

Query Match      89.6%; Score 172; DB 22; Length 406;
Best Local Similarity 77.3%; Pred. No. 4e-21;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY  1 ANAFLLXLRPGSLRXKXQCSFXXARXIFKDXARTKLFWISY 44
    ||||| ||||| | || ||||| ||||| ||||| |||||
Db  1 anafllelrpgslereckeegcsfeearelfkdaertklfwisy 44

RESULT 20
AAB84869
ID  AAB84869 standard; Protein; 406 AA.
XX
AC  AAB84869;
XX
DT  31-JUL-2001 (first entry)
XX
DE  Mutant blood coagulant factor VII (FVII-30).
XX
XX  Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
KM  mutant; mutelin.
XX
XX  Homo sapiens.
OS  Synthetic.
XX
XX  Key Location/Qualifiers
FH  Misc-difference 235..239
FT  /note= "Wild-type Val-Pro-Gly-Thr-Thr substituted by
ET  Asp-Arg-Lys-Thr-Leu"
XX
XX  JP2001061479-A.
PN
XX
PD  13-MAR-2001.
XX
XX  24-AUG-1999; 99JP-0237610.
PF
XX
XX  24-AUG-1999; 99JP-0237610.
PR
XX
XX  (KACA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
PA
XX
XX  WPI: 2001-310677/33.
DR  N-PSDB; AAH19462.
XX
XX  Mutant of blood coagulant factor VII, used for substitution therapy in
PT  the treatment of hemophilia -
XX
XX  Claim 9; Page 17-18; 29pp; Japanese.
PS
XX  The present invention relates to mutants of blood coagulant factor VII
CC  (FVII) or activated blood coagulant factor VII (FVIIa). The present
CC  sequence is one such mutant FVII: VII-30. The mutants can be used as an
CC  agent for the substitution therapy of haemophilia inhibitor patients.
XX
SQ  Sequence 406 AA;

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Query Match      89.6%; Score 172; DB 22; Length 406;
Best Local Similarity 77.3%; Pred. No. 4e-21;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY  1 ANAFLLXLRPGSLRXKXQCSFXXARXIFKDXARTKLFWISY 44
    ||||| ||||| | || ||||| ||||| ||||| |||||
Db  1 anafllelrpgslereckeegcsfeearelfkdaertklfwisy 44

RESULT 21
AAR64205
ID  AAR64205 standard; Protein; 444 AA.
XX
AC  AAR64205;
XX
XX  18-JUL-1995 (first entry)
DT
XX
DE  Factor VII - modified forms of this act as an anticoagulant.
XX
XX  Factor VII; plasma glycoprotein; derivative; tissue factor; TF;
KM  inhibition; vascular restenosis; platelet deposition; catalytic centre;
KW  factor IX; factor X; inactivation; thrombosis; embolism; stroke; ss.
XX
XX  Homo sapiens.
OS
XX
XX  Key Location/Qualifiers
FH  Active-site 193
FT  /note= "forms a catalytic triad with Ser344 and Asp242"
ET  Active-site 242
FT  /note= "forms catalytic triad with Ser344 and His193"
ET  Active-site 344
FT  /note= "forms catalytic triad with Asp242 and His193"
ET  Cleavage-site 152..153
FT  /note= "internal cleavage site - cleavage activates
ET  the zymogen into active 2-chain Factor VIIa"
XX
XX  MO9427631-A.
PN
XX
XX  08-DEC-1994.
PD
XX
XX  23-MAY-1994; 94WO-US05779.
PF
XX
XX  21-MAY-1993; 93US-0065725.
PR
XX
XX  (NOVO ) NOVO-NORDISK AS.
PA  (ZYMO ) ZYMOGENETICS INC.
XX
XX  Berkner KL, Hart CE, Petersen LC;
PI
XX
XX  WPI: 1995-022464/03.
DR  N-PSDB; AAO80296.
XX
XX  Inhibition of tissue factor, vascular restenosis and platelet
PT  deposition - using modifier factor VII unable to activate
PT  factors IX and X, e.g. for treating thrombosis, embolism, stroke
PT  etc..
XX
XX  Disclosure; Page 39-40; 51pp; English.
PS
XX  AAR64205 shows the amino acid sequence of human Factor VII, encoded
CC  by AAO80296. Factor VII is a trace plasma glycoprotein that circulates
CC  in blood as a single-chain zymogen. The zymogen is catalytically
CC  inactive, and is converted into a two-chain active mol. by cleavage of an
CC  internal peptide bond located approx. in the middle of the mol. Factor
CC  VIIa rapidly activates Factor X or Factor IX by limited proteolysis.
CC  Modified Factor VII, partic. where the Ser344 in the catalytic triad is
CC  substituted with alanine, has anticoagulant properties, for preventing
CC  the coagulation cascade. The modified Factor VII has an active site
CC  modified by at least one amino acid substitution, and in its modified
CC  form is capable of binding tissue factor and inhibiting its action.
XX
SQ  Sequence 444 AA;

```


XX Sequence 444 AA;
SQ

Query Match
Best Local Similarity 77.3%; Score 172; DB 21; Length 444;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANAFLLXLRPGSLRXCKXXQCSFXRXARXIFKDXARTKLFWISY 44
Db 39 anafllelrpgslereckeegcsfeearelfkdaertklfwisy 82

RESULT 24
AAB61992
ID AAB61992 standard; Protein; 444 AA.
XX
AC AAB61992;
XX
DT 14-MAY-2001 (first entry)
XX
DE Human Factor VII polypeptide.
XX
KM Factor VIIa; thrombus; vascular patency; blood coagulation; Factor X;
KM plasma factor; Factor IX; myocardial injury; human; Factor VII.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..38 /note="signal peptide"
FT Protein 39..444 /note="mature peptide"
FT MISC-difference 10 /note="indicated incorrectly as Trp under sequence listing ID 2"
FT
FT
XX US6183743-B1.
XX
XX
XX 06-FEB-2001.
XX
PD
XX
PF 20-AUG-1999; 99US-0378907.
XX
XX
PR 06-JUN-1997; 97US-0871003.
PR 28-FEB-1991; 91US-0662920.
PR 28-FEB-1992; 92WO-US01636.
PR 21-MAY-1993; 93US-0065725.
PR 23-MAY-1994; 94WO-US05779.
PR 24-OCT-1994; 94US-0327690.
PR 07-JUN-1995; 95US-0475845.
PR 07-JUN-1996; 96US-0660289.
XX
XX
XX (ZYMO) ZYMOGENETICS INC.
XX (NOVO) NOVO NORDISK AS.
XX
XX
XX Hart CE, Petersen LC, Hedner U, Rasmussen ME;
XX
XX WPI: 2001-201993/20.
XX N-PSDB; AAF57099.
XX
XX
XX use of modified human factor VIIa with a covalent modification in its
XX catalytic center, to inhibit thrombus formation or to maintain vascular
XX patency -
XX
XX Example; Columns 43-48; 34pp; English.
XX
XX
XX The invention relates to the use of modified human Factor VIIa for
XX inhibiting thrombus formation, or maintaining or improving vascular
XX patency in a patient. The modified factor VIIa comprises a covalent
XX modification in its catalytic center which effectively interrupts the
XX blood coagulation cascade. The modifications render Factor VIIa
XX substantially unable to activate plasma factor IX or X. The modified
XX Factor VIIa can be used for preventing or treating myocardial injury

CC associated with post-ischemic reperfusion, for improving regional
CC myocardial blood flow during reperfusion and maintaining or improving
CC vascular patency in a patient. The present sequence represents the
CC human Factor VII polypeptide.
XX
XX
SQ Sequence 444 AA;
SQ

Query Match
Best Local Similarity 77.3%; Score 172; DB 22; Length 444;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANAFLLXLRPGSLRXCKXXQCSFXRXARXIFKDXARTKLFWISY 44
Db 39 anafllelrpgslereckeegcsfeearelfkdaertklfwisy 82

RESULT 25
AAP60056
ID AAP60056 standard; protein; 466 AA.
XX
AC AAP60056;
XX
DT 23-MAY-1991 (first entry)
XX
DE Factor VII peptide encoded by cDNA clone lambda VII2463.
XX
KM Factor VII; Factor VIIa; DNA construct;
XX
XX EP200421-A.
XX
XX 10-DEC-1986.
XX
PD
XX
PF 16-APR-1986; 86EP-0302855.
XX
XX
PR 16-DEC-1985; 85US-0810002.
PR 17-APR-1985; 85US-0724311.
XX
XX
XX (ZYMO-) ZYMOGENETICS INC.
XX
XX
XX Hagen FS, Murry MJ, Berkner KL, Insley MY, Woodbury RG;
XX Gray CL;
XX
XX
XX WPI: 1986-326899/50.
XX N-PSDB; AAN60064.
XX
XX
XX DNA construct used to transfect hosts - to produce protein which
XX activates to give factor VIIa
XX
XX
XX Disclosure; Fig. 1B; 55pp; English.
XX
XX
XX The partial factor VII cDNA sequence encoding the peptide is from
XX cDNA clone lambda VII2463. It is used in a DNA construct which contains
XX a nucleotide sequence encoding a protein which, on activation, has the
XX same biological activity for blood coagulation as Factor VIIa. The
XX cDNA sequence encodes at least partially for Factor VII and comprises a
XX sequence encoding a calcium binding domain joined to a second sequence
XX downstream of this encoding a catalytic domain for the serine protease
XX activity of Factor VIIa. The calcium binding domain comprises a gene
XX encoding Factor VII, IX, X, protein C, prothrombin or Protein S. The
XX construct is used to transfect host cells to produce the protein which,
XX on activation, yields Factor VIIa.
XX
XX
SQ Sequence 466 AA;
SQ

Query Match
Best Local Similarity 77.3%; Score 172; DB 7; Length 466;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANAFLLXLRPGSLRXCKXXQCSFXRXARXIFKDXARTKLFWISY 44
Db 61 anafllelrpgslereckeegcsfeearelfkdaertklfwisy 104

RESULT 26
 AAR52562 ID AAR52562 standard; Protein: 466 AA.
 XX
 AC AAR52562;
 XX
 DT 27-MAY-1994 (first entry)
 XX
 DE Factor VIII.
 XX
 KW Truncated tissue factor: tTF; factor VIIa: FVIIa; activator:
 KW bleeding disorder; haemophilia; liver cirrhosis; coagulation;
 KW transmembrane domain; extracellular domain; soluble.
 XX
 OS Homo sapiens.
 XX
 PN MO9323074-A.
 XX
 PD 25-NOV-1993.
 XX
 PF 12-MAY-1993; 93WO-US04493.
 XX
 PR 13-MAY-1992; 92US-0882202.
 PR 19-FEB-1993; 93US-0021615.
 XX
 PA (OKLA-) OKLAHOMA MED RES FOUND.
 XX
 PI Comp PC, Morrissey JH;
 XX
 DR WPI: 1993-386218/48.
 DR N-PSDB; AAO62299.
 XX
 PT Compn. of truncated tissue factor and factor-VIIa or activator
 PT of VII - useful for treating bleeding disorders, e.g. haemophilia
 PT or liver cirrhosis
 XX
 PS Disclosure: Page 26-28; 43pp; English.
 CC A compsn. for treatment of patients with prolonged or excessive
 CC bleeding disorders comprises truncated tissue factor (tTF) (AA052439)
 CC and a substance effective to produce a plasma level of factor VIIa
 CC which in combination with tTF will control or stop the excessive
 CC bleeding. The substance may be factor VIIa itself or an activator
 CC which promotes the conversion of endogenous factor VII to factor VIIa.
 CC
 CC Sequence 466 AA;
 XX
 SQ
 Query Match 89.6%; Score 172; DB 14; Length 466;
 Best Local Similarity 77.3%; Pred. No. 4.6e-21;
 Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 OY 1 ANAFLXLRPGSLXRXCKXQCSPFXARXIFPDARTKLFWISY 44
 DB 61 anafllelrpgslereckeegcsfearelfkdaertklfwisy 104

RESULT 27
 AAM69606 ID AAM69606 standard; Protein: 466 AA.
 XX
 AC AAM69606;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Human Factor VIIa.
 XX
 KW Human; truncated; tissue factor; tTF; TF; tumour; coagulation;
 KW blood vessel; Factor VIIa; FVIIa; benign growth; vascularised;
 KW benign prostatic hypertrophy; malignant; necrosis; angiogenesis;
 KW diabetic retinopathy; restenosis; neovascular glaucoma; psoriasis;

KW Rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 PN MO9831394-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 20-JAN-1998; 98WO-US01012.
 XX
 PR 27-MAR-1997; 97US-0042427.
 PR 22-JAN-1997; 97US-0035920.
 PR 27-JAN-1997; 97US-0036205.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Gao B, King SW, Thorpe PE;
 XX
 DR WPI: 1998-413821/35.
 DR N-PSDB; AAV40389.
 XX
 PT Composition containing coagulation-defective tissue factor for
 PT treating, e.g. tumours - useful for, e.g. promoting coagulation in
 PT pro:thrombotic and tumour-associated vasculature, used with, e.g.
 PT factor 7 or anti-cancer agent
 XX
 PS Claim 35; Page 196-197; 225pp; English.
 CC A composition has been developed which comprises at least 1 coagulation-
 CC deficient tissue factor (TF) compound that is modified to increase its
 CC biological half-life, but excluding modification that involves attachment
 CC to an antibody (or its antigen-binding region) that binds to a component
 CC (cells, vasculature or stroma) of tumours. Also described in the present
 CC invention are compositions containing any coagulation-deficient TF for
 CC promoting coagulation. The coagulation-deficient TFs are used to promote
 CC coagulation preferentially in prothrombotic vessels, particularly those
 CC associated with: (i) benign growths (e.g. benign prostatic hypertrophy);
 CC (ii) vascularised, malignant tumours of medium or large size (where they
 CC also induce tumour necrosis), or (iii) other disorders that involve
 CC angiogenesis, e.g. diabetic retinopathy, restenosis, neovascular
 CC glaucoma, psoriasis and rheumatoid arthritis. The composition can be
 CC administered systemically, particularly intravenously, typically at
 CC 0.2-200 mg, given 3 times over 7 days. Truncated TF, and its variants,
 CC localise specifically in tumour-associated blood vessels after systemic
 CC administration, even though they contain no targeting agent. They cause
 CC little if any injury to normal tissue; may produce a synergistic response
 CC when used with other antitumour agents and they eliminate the multi-step,
 CC and expensive, preparation of antibody-based targeting constructs. The
 CC present sequence is human Factor VIIa, from the present invention.
 CC
 CC Sequence 466 AA;
 XX
 SQ
 Query Match 89.6%; Score 172; DB 19; Length 466;
 Best Local Similarity 77.3%; Pred. No. 4.6e-21;
 Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 OY 1 ANAFLXLRPGSLXRXCKXQCSPFXARXIFPDARTKLFWISY 44
 DB 61 anafllelrpgslereckeegcsfearelfkdaertklfwisy 104

RESULT 28
 AAM14507 ID AAM14507 standard; Protein: 406 AA.
 XX
 AC AAM14507;
 XX
 DT 14-MAY-1997 (first entry)
 XX
 DE Modified blood coagulation Factor VII (K320).
 XX
 KW Blood coagulation; factor 7; mutein; mutation; modification;

KW	thrombocytopenia: von Willebrand's disease; plasma substitute.	
XX	Homo sapiens.	
OS	Synthetic.	
XX		
FT	Key	Location/Qualifiers
FT	Modified-site	6
FT		/label= OTHER
FT	Modified-site	/note= "gamma-carboxyglutamic acid"
FT		7
FT	Modified-site	/label= OTHER
FT		/note= "gamma-carboxyglutamic acid"
FT	Modified-site	14
FT		/label= OTHER
FT		/note= "gamma-carboxyglutamic acid"
FT	Modified-site	16
FT		/label= OTHER
FT		/note= "gamma-carboxyglutamic acid"
FT	Modified-site	19
FT		/label= OTHER
FT		/note= "gamma-carboxyglutamic acid"
FT	Modified-site	20
FT		/label= OTHER
FT		/note= "gamma-carboxyglutamic acid"
FT	Disulfide-bond	17..22
FT	Modified-site	25
FT		/label= OTHER
FT	Modified-site	/note= "gamma-carboxyglutamic acid"
FT		26
FT	Modified-site	/label= OTHER
FT		/note= "gamma-carboxyglutamic acid"
FT	Modified-site	29
FT		/label= OTHER
FT		/note= "gamma-carboxyglutamic acid"
FT	Cleavage-site	32..33
FT		/note= "proteolytic site in unmodified factor VII"
FT	Misc-difference	32
FT		/note= "native Lys32 has been substituted by Gln to provide a proteolytically more stable peptide bond"
FT	Modified-site	35
FT		/label= OTHER
FT		/note= "gamma-carboxyglutamic acid"
FT	Cleavage-site	38..39
FT		/note= "proteolytic site"
FT	Cleavage-site	42..43
FT		/note= "proteolytic site"
FT	Cleavage-site	44..45
FT		/note= "proteolytic site"
FT	Disulfide-bond	50..61
FT	Disulfide-bond	55..70
FT	Modified-site	63
FT		/label= OTHER
FT		/note= "beta-hydroxy-aspartic acid"
FT	Disulfide-bond	72..81
FT	Disulfide-bond	91..102
FT	Disulfide-bond	98..112
FT	Disulfide-bond	114..127
FT	Disulfide-bond	135..162
FT	Cleavage-site	143..144
FT		/note= "proteolytic site"
FT	Modified-site	145
FT		/note= "glycosylation site"
FT	Disulfide-bond	159..164
FT	Disulfide-bond	178..194
FT	Active-site	193
FT	Active-site	242
FT	Active-site	344
FT	Cleavage-site	290..291
FT		/note= "proteolytic site"
FT	Disulfide-bond	310..329
FT	Cleavage-site	315..316
FT		/note= "proteolytic site"

FT	Modified-site	322	
FT	/note="glycosylation site"		
FT	Disulfide-bond	340..368	
FT	Cleavage-site	341..342	
FT	/note="proteolytic site"		
FT	Cleavage-site	392..393	
FT	/note="proteolytic site"		
FT	Cleavage-site	396..397	
FT	/note="proteolytic site"		
FT	Cleavage-site	402..403	
FT	/note="proteolytic site"		
XX			
XX	US5580560-A.		
XX			
XX	03-DEC-1996.		
XX			
XX	13-NOV-1989;	89US-0434149.	
XX			
XX	09-AUG-1993;	93US-0104509.	
PR	13-NOV-1989;	89US-0434149.	
PR	12-JUN-1992;	92US-0898248.	
PR	22-AUG-1994;	94US-0293778.	
XX			
PA	(NOVO) NOVO-NORDISK AS.		
XX			
PI	Bjorn SE, Nicolaisen EM, Wiberg FC, Woodbury R;		
XX			
DR	WPI: 1997-033523/03.		
XX			
PT	Mutated human factor VII or VIIa proteins - with amino acid		
XX	substitutions to improve proteolytic stability		
PS	Claim 3; Page -: 28pp; English.		
XX			
CC	Modified human factor VII or VIIa proteins are stabilised against		
CC	proteolytic cleavage by substitution of one of the residues Lys32,		
CC	Lys38, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and		
CC	Lys341 by an amino acid that provides a proteolytically more stable		
CC	peptide bond, provided that Lys32 is replaced by Gln, Glu, His,		
CC	Gly, Thr, Ala or Ser. The modified proteins are useful for treating		
CC	bleeding disorders such as thrombocytopenia and von Willebrand's		
CC	disease. They are also suitable for addition to plasma substitutes.		
CC	The present sequence is a specific example of a modified factor VII		
CC	protein.		
XX			
XX	Sequence 406 AA:		
SQ			
	Query Match 87.5%; Score 168; DB 18; Length 406;		
	Best Local Similarity 75.0%; Pred. No. 2e-20;		
	Matches 33; Conservative 1; Mismatches 10; Indels 0; Gaps 0;		
OY	1 ANAFLXXLRPGSLKRXCKXXQCSFXRXRIFFDAXRTKLEWISY 44		
Db	1 anaflleelrpgslereckeegcsfeaeirelfgdaertklfwisy 44		
RESULT 29			
AAVY18313			
ID	AAV18313 standard; peptide: 44 AA.		
XX			
AC	AAV18313;		
XX			
DT	17-AUG-1999 (first entry)		
XX			
DE	Modified GLA domain of vitamin K-dependent protein.		
XX			
KW	GLA domain; muteln; vitamin K-dependent protein; clotting disorder;		
XX	therapy.		
XX			
OS	Homo sapiens.		
OS	Synthetic.		
XX			

FH	Key	Location/Qualifiers
FT	Misc-difference	1..44 /note- "Xaa- gamma-carboxyglutamic acid, or glutamic acid"
FT		
FT		
FN		WO9920767-A1.
PD		29-APR-1999.
XX		
XX	20-OCT-1998;	98WO-US22152.
XX		
PR	23-OCT-1997;	97US-0955636.
XX		
PA	(MINU) UNIV MINNESOTA.	
XX		
PI	Nelgestuen GL;	
DR	WPI; 1999-288309/24.	
XX		
PT	Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders	
XX		
PS	Disclosure; Page 81; 86pp; English.	
XX		
CC	This sequence represents a modified GIIA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GIIA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the GIIA domain results in a protein which has enhanced membrane binding affinity as compared to the native protein.	
CC		
XX		
SQ	Sequence	44 AA:

FT	/note=	"gamma-carboxyglutamic acid"
FT	19	
FT	/label=	OTHER
FT	/note=	"gamma-carboxyglutamic acid"
FT	20	
FT	/label=	OTHER
FT	/note=	"gamma-carboxyglutamic acid"
FT	17..22	
FT	25	
FT	/label=	OTHER
FT	/note=	"gamma-carboxyglutamic acid"
FT	26	
FT	/label=	OTHER
FT	/note=	"gamma-carboxyglutamic acid"
FT	29	
FT	/label=	OTHER
FT	/note=	"gamma-carboxyglutamic acid"
FT	32..33	
FT	/note=	"gamma-carboxyglutamic acid"
FT	35	
FT	/label=	OTHER
FT	/note=	"gamma-carboxyglutamic acid"
FT	38..39	
FT	/note=	"proteolytic site in unmodified factor VII"
FT	38	
FT	/note=	"native Lys38 has been substituted by Thr to provide a proteolytically more stable peptidic bond"
FT	42..43	
FT	/note=	"proteolytic site"
FT	44..45	
FT	/note=	"proteolytic site"
FT	50..61	
FT	55..70	

Query Match	86.5%	Score 166;	DB 20;	Length 44;
Best Local Similarity	97.7%;	Pred. No. 4.4e-21;		
Matches 43; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;
OY	1 ANAFPLXLRPGSLXRCKXXQCSFPXXARIRFDAXRTRKLFWISY	44 		
Db	1 anaflxrlrpgslxrckxxqcsfpxxarirfdaxrtklfwisy	44		
RESULT 30				
AAM14508				
ID AAM14508	standard; protein; 406 AA.			
XX				
AC AAM14508;				
XX				
DT 14-MAY-1997	(first entry)			
XX				
DE Modified blood coagulation Factor VII (K38T).				
XX				
KM Blood coagulation; factor 7; mutein; mutation; modification;				
KW thrombocytopenia; von Willebrand's disease; plasma substitute.				
XX				
OS Homo sapiens.				
OS Synthetic.				
XX				
FH Key	Location/Qualifiers			
FT FT	6			
FT Modified-site	/label= OTHER			
FT FT	/note= "gamma-carboxylutamic acid"			
FT Modified-site	7			
FT FT	/label= OTHER			
FT Modified-site	/note= "gamma-carboxylutamic acid"			
FT FT	14			
FT Modified-site	/label= OTHER			
FT FT	/note= "gamma-carboxylutamic acid"			
FT Modified-site	16			
FT FT	/label= OTHER			

FT	Disulfide-bond	/note= "beta-hydroxy-aspartic acid"
FT	Disulfide-bond	72..81
FT	Disulfide-bond	91..102
FT	Disulfide-bond	98..112
FT	Disulfide-bond	114..127
FT	Disulfide-bond	135..162
FT	Cleavage-site	143..144
FT	Cleavage-site	/note= "proteolytic site"
FT	Modified-site	145
FT	Disulfide-bond	/note= "glycosylation site"
FT	Disulfide-bond	159..164
FT	Disulfide-bond	178..194
FT	Active-site	193
FT	Active-site	242
FT	Active-site	344
FT	Cleavage-site	290..291
FT	Cleavage-site	/note= "proteolytic site"
FT	Disulfide-bond	310..329
FT	Cleavage-site	315..316
FT	Cleavage-site	/note= "proteolytic site"
FT	Modified-site	322
FT	Modified-site	/note= "glycosylation site"
FT	Disulfide-bond	340..368
FT	Cleavage-site	341..342
FT	Cleavage-site	/note= "proteolytic site"
FT	Cleavage-site	392..393
FT	Cleavage-site	/note= "proteolytic site"
FT	Cleavage-site	396..397
FT	Cleavage-site	/note= "proteolytic site"
FT	Cleavage-site	402..403
FT	Cleavage-site	/note= "proteolytic site"
XX		
PN	US5580560-A.	
XX		
PD	03-DEC-1996.	
XX		
3P	13-NOV-1989;	89US-0434149.

XX	09-AUG-1993;	93US-0104509.
PR	13-NOV-1989;	89US-0434149.
PR	12-JUN-1992;	92US-0898248.
PR	22-AUG-1994;	94US-0293778.
XX		
PA	(NOVO) NOVO-NORDISK AS.	
PI	Bjorn SE, Nicolaisen EM, Wlberg FC, Woodbury R;	
XX		
DR	WPI; 1997-033523/03.	
XX		
PT	Mutated human factor VII or VIIa proteins - with amino acid	
PT	substitutions to improve proteolytic stability	
XX		
PS	Example 2; Page -: 28pp: English.	
XX		
CC	Modified human factor VII or VIIa proteins are stabilised against	
CC	proteolytic cleavage by substitution of one of the residues Lys32,	
CC	Lys38, Ile44, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and	
CC	Lys341 by an amino acid that provides a proteolytically more stable	
CC	peptide bond, provided that Lys32 is replaced by Gln, Glu, His,	
CC	Gly, Thr, Ala or Ser. The modified proteins are useful for treating	
CC	bleeding disorders such as thrombocytopenia and von Willebrand's	
CC	disease. They are also suitable for addition to plasma substitutes.	
CC	The present sequence is a specific example of a modified factor VII	
CC	protein.	
XX		
SO	Sequence 406 AA;	
	Query Match 86.5%; Score 166; DB 18; Length 406;	
	Best Local Similarity 75.0%; Pred. No. 4.3e-20;	
	Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;	
OY	1 ANAFLXLRPGSLRXCKXXOCSEFXAXRIKFDAXRTKLFWISY 44	
Db	1 anaflaelrpgslereckeegcsfeaearelfkdaertlflwisy 44	
	RESULT 31	
AA18310		
ID	AA18310 standard; peptide; 44 AA.	
XX		
AC	AA18310;	
XX		
DT	17-AUG-1999 (first entry)	
DE	Modified GLA domain of vitamin K-dependent protein.	
XX		
KW	GLA domain; mutein; vitamin K-dependent protein; clotting disorder;	
XX	therapy.	
OS	Homo sapiens.	
XX	Synthetic.	
FT	Key Location/Qualifiers	
FT	Misc-difference 1..44	
FT	/note= "Xaa= gamma-carboxyglutamic acid, or glutamic	
FT	acid"	
XX		
PN	W09920767-A1.	
XX		
PD	29-APR-1999.	
XX		
PF	20-OCT-1998; 98WO-US22152.	
XX		
PR	23-OCT-1997; 97US-0955636.	
XX		
PA	(MINU) UNIV MINNESOTA.	
XX		
PI	Nejsestuen GL;	
XX		

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DR      WPI: 1999-288309/24.
XX
XX      Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
PT      acid domain, useful for treating clotting disorders
XX
PS      Disclosure: Page 80; 86pp; English.
XX
CC      This sequence represents a modified GLA (gamma-carboxyglutamic acid)
CC      domain. The invention relates to a vitamin K-dependent polypeptide
CC      comprising a modified GLA domain containing an amino acid substitution
CC      which enhances membrane binding of the modified polypeptide as compared
CC      to the native polypeptide. The polypeptide is used to treat a clotting
CC      disorder by decreasing or increasing clot formation. Modification of the
CC      GLA domain results in a protein which has enhanced membrane binding
CC      affinity as compared to the native protein.
XX
SQ      Sequence      44 AA:

Query Match          85.4%; Score 164; DB 20; Length 44;
Best Local Similarity 97.7%; Pred. No. 9.7e-21;
Matches    43; Conservative   0; Mismatches    1; Indels     0; Gaps     0;

OY      1 ANAFLLXLRPGSLRXKXCXXQCSEFXAXRIFKDAARFKLEWTSY 44
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB       1 anaflxlrlregslxrxcxxqcsfxaxrxlfrkdxrtklfwisy 44

RESULT  32
AAV18311
ID      AAV18311 standard; peptide: 44 AA.
XX
AC      AAY18311;
XX
DT      17-AUG-1999 (first entry)
XX
DE      Modified GLA domain of vitamin K-dependent protein.
XX
KM      GLA domain; muten; vitamin K-dependent protein; clotting disorder;
KW      therapy.
XX
OS      Homo sapiens.
OS      Synthetic.
XX
FH      Key Location/Qualifiers
FT      Misc-difference 1..44 /note= "Xaa" gamma-carboxyglutamic acid, or glutamic
FT      acid"
FT
PN      WO9920767-A1.
XX
PD      29-APR-1999.
XX
PE      20-OCT-1998; 98WO-US22152.
XX
PR      23-OCT-1997; 97US-0955636.
XX
PA      (MINN ) UNIV MINNESOTA.
XX
XX      Neisestuen GL;
PI
DR      WPI: 1999-288309/24.
XX
XX      Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
PT      acid domain, useful for treating clotting disorders
XX
PS      Disclosure: Page 80; 86pp; English.
XX
CC      This sequence represents a modified GLA (gamma-carboxyglutamic acid)
CC      domain. The invention relates to a vitamin K-dependent polypeptide
CC      comprising a modified GLA domain containing an amino acid substitution
CC      which enhances membrane binding of the modified polypeptide as compared
CC      to the native polypeptide. The polypeptide is used to treat a clotting
CC      disorder by decreasing or increasing clot formation. Modification of the
CC      GLA domain results in a protein which has enhanced membrane binding
CC      affinity as compared to the native protein.
XX

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FT Disulfide-bond 72..81
FT Disulfide-bond 91..102
FT Disulfide-bond 98..112
FT Disulfide-bond 114..127
FT Disulfide-bond 135..162
FT Cleavage-site 143..144
FT Modified-site 145
FT Modified-site 145
FT Disulfide-bond /note="glycosylation site"
FT Disulfide-bond 159..164
FT Disulfide-bond 178..194
FT Active-site 193
FT Active-site 242
FT Active-site 344
FT Cleavage-site 290..291
FT Disulfide-bond /note="proteolytic site"
FT Disulfide-bond 310..329
FT Cleavage-site 315..316
FT Modified-site 322
FT Modified-site 322
FT Disulfide-bond /note="glycosylation site"
FT Disulfide-bond 340..368
FT Cleavage-site 341..342
FT Cleavage-site 392..393
FT Cleavage-site /note="proteolytic site"
FT Cleavage-site /note="proteolytic site"
FT Cleavage-site 396..397
FT Cleavage-site /note="proteolytic site"
FT Cleavage-site 402..403
FT Cleavage-site /note="proteolytic site"
XX US5580560-A.
XX
XX
XX 03-DEC-1996.
XX
XX 13-NOV-1989; 89US-0434149.
XX
XX 09-AUG-1993; 93US-0104509.
XX 13-NOV-1989; 89US-0434149.
XX 12-JUN-1992; 92US-0898248.
XX 22-AUG-1994; 94US-0293778.
XX
XX (NOVO ) NOVO-NORDISK AS.
XX
XX Bjorn SE, Nicolaisen EM, Wlberg FC, Woodbury R;
XX WPI; 1997-033523/03.
XX
XX Mutated human factor VII or VIIa proteins - with amino acid
XX substitutions to improve proteolytic stability
XX
XX Claim 8; Page -: 28pp; English.
XX
XX Modified human factor VII or VIIa proteins are stabilised against
XX proteolytic cleavage by substitution of one of the residues Lys32,
XX Lys38, Ile44, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and
XX Lys341 by an amino acid that provides a proteolytically more stable
XX peptide bond, provided that Lys32 is replaced by Gln, Glu, His,
XX Gly, Thr, Ala or Ser. The modified proteins are useful for treating
XX bleeding disorders such as thrombocytopenia and von Willebrand's
XX disease. They are also suitable for addition to plasma substitutes.
XX The present sequence is a specific example of a modified factor VII
XX protein.
XX
XX Sequence 406 AA;

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Query Match 84.4%; Score 162; DB 18; Length 406;
Best Local Similarity 72.7%; Pred. No. 2.1e-19;
Matches 32; Conservative 1; Mismatches 11; Indels 0; Gaps 0;
QY 1 ANAFLLXLRGSLXRXCKXXQCSFXRXRXIFKDXRRLKRWISY 44
||||| ||||||| || ||||| || ||||| || |||||||

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Db 1 anafleelrpgslereckeegcsfeearlfgdaertllwisy 44
RESULT 35
AAV18302
ID AAV18302 standard; peptide; 44 AA.
XX
XX AAV18302;
XX
XX 17-AUG-1999 (first entry)
XX
XX Modified GLA domain of vitamin K-dependent protein.
XX
XX GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
XX therapy.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FT MISC-difference 1..44
XX FT /note="Xaa-gamma-carboxyglutamic acid, or glutamic
XX FT acid"
XX
XX WO9920767-A1.
XX
XX 29-APR-1999.
XX
XX 20-OCT-1998; 98WO-US22152.
XX
XX 23-OCT-1997; 97US-0955636.
XX
XX (MINU ) UNIV MINNESOTA.
XX
XX Nelsestuen GL;
XX
XX WPI; 1999-288309/24.
XX
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
XX acid domain, useful for treating clotting disorders
XX
XX Claim 11; Page 81; 86pp; English.
XX
XX This sequence represents a modified GLA (gamma-carboxyglutamic acid)
XX domain. The invention relates to a vitamin K-dependent polypeptide
XX comprising a modified GLA domain containing an amino acid substitution
XX which enhances membrane binding of the modified polypeptide as compared
XX to the native polypeptide. The polypeptide is used to treat a clotting
XX disorder by decreasing or increasing clot formation. Modification of the
XX GLA domain results in a protein which has enhanced membrane binding
XX affinity as compared to the native protein.
XX
XX Sequence 44 AA;

```

```

RESULT 36
AAW11904
ID AAW11904 standard; peptide; 41 AA.
XX
XX AAW11904;
XX
XX 01-APR-1997 (first entry)
XX
XX Factor VII GLa region.
DE

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CC		method of the invention for the determination of PIYKA in a specimen.
CC		The determination of PIYKA is clinically useful, as PIYKA is produced in
CC		blood as a result of incomplete gamma-carboxylation in a state of
CC		vitamin K deficiency or suppression. The determination of PIYKA can
CC		therefore be used as a marker of the state of vitamin K deficiency or
CC		suppression.
XX		
SQ	Sequence	41 AA;
Oy	Query Match	81.8%; Score 157; DB 16; Length 41;
	Best Local Similarity	100.0%; Pred. NO. 1.4e-19;
Matches	41: Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Db	1 ANAFLEXLRPGSLRXRCXKXOCSPFXAXIRKDARTKLFW 41 1 anafixxlrpgslrxrcxxqcsfxaxirxfidartklfw 41	
RESULT	37	
ID	AAW14506	
AC	AAW14506 standard; protein: 406 AA.	
XX	AAW14506;	
XX	14-MAY-1997 (first entry)	
DE	Modified blood coagulation Factor VII.	
XX	Blood coagulation; factor 7; muten; mutation; modification;	
KW	Thrombocytopenia; von Willebrand's disease; plasma substitute.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Modified-site	6 /label= OTHER
FT	Modified-site	/note= "gamma-carboxyglutamic acid"
FT	Modified-site	7 /label= OTHER
FT	Modified-site	/note= "gamma-carboxyglutamic acid"
FT	Modified-site	14 /label= OTHER
FT	Modified-site	/note= "gamma-carboxyglutamic acid"
FT	Modified-site	16 /label= OTHER
FT	Modified-site	/note= "gamma-carboxyglutamic acid"
FT	Modified-site	19 /label= OTHER
FT	Modified-site	/note= "gamma-carboxyglutamic acid"
FT	Modified-site	20 /label= OTHER
FT	Disulfide-bond	/note= "gamma-carboxyglutamic acid"
FT	Modified-site	17..22
FT	Modified-site	25 /label= OTHER
FT	Modified-site	/note= "gamma-carboxyglutamic acid"
FT	Modified-site	26 /label= OTHER
FT	Modified-site	/note= "gamma-carboxyglutamic acid"
FT	Modified-site	29 /label= OTHER
FT	Cleavage-site	/note= "gamma-carboxyglutamic acid"
FT	Cleavage-site	32..33 /note= "gamma-carboxyglutamic acid"
FT	Misc-difference	32 /note= "proteolytic site in unmodified factor VII"
FT	Misc-difference	/label= Lys, Glu, Gly, His, Gly, Thr, Ala, Ser
FT	Misc-difference	/note= "if native Lys32 is substituted by an amino
FT	Misc-difference	acid which provides a proteolytically more
FT	Misc-difference	stable peptide bond, then it must be substituted
FT	Misc-difference	by one of the amino acids Glu, Gly, His, Gly,
FT	Misc-difference	Thr, Ala or Ser"
FT	Modified-site	35

FT /label- OTHER
 FT /note- "gamma-carboxyglutamic acid"
 FT Cleavage-site 38..39 /note- "proteolytic site in unmodified factor VII"
 FT MISC-difference 38 /note- "if native Lys38 is substituted by an amino acid which provides a proteolytically more stable peptide bond, then it is pref. substituted by one of the amino acids Thr, Asp, Leu, Gly, Ala, Ser, Asn or His"
 FT Cleavage-site 42..43 /note- "proteolytic site in unmodified factor VII"
 FT MISC-difference 42 /note- "native Ile42 may be substituted by an amino acid which provides a proteolytically more stable peptide bond"
 FT Cleavage-site 44..45 /note- "proteolytic site in unmodified factor VII"
 FT MISC-difference 44 /note- "native Tyr44 may be substituted by an amino acid which provides a proteolytically more stable peptide bond"
 FT Disulfide-bond 50..61
 FT Disulfide-bond 55..70
 FT Modified-site 63 /label- OTHER
 FT Disulfide-bond 72..81 /note- "beta-hydroxy-aspartic acid"
 FT Disulfide-bond 91..102
 FT Disulfide-bond 98..112
 FT Disulfide-bond 114..127
 FT Disulfide-bond 135..162
 FT Cleavage-site 143..144 /note- "proteolytic site"
 FT Modified-site 145 /note- "glycosylation site"
 FT Disulfide-bond 159..164
 FT Disulfide-bond 178..194
 FT Active-site 193
 FT Active-site 242
 FT Active-site 344
 FT MISC-difference 278 /note- "native Phe278 may be substituted by an amino acid which provides a proteolytically more stable peptide bond"
 FT Cleavage-site 290..291 /note- "proteolytic site in unmodified factor VII"
 FT MISC-difference 290 /note- "if native Arg290 is substituted by an amino acid which provides a proteolytically more stable peptide bond, then it is pref. substituted by one of the amino acids Gly, Thr, Ala, Ser or Lys"
 FT MISC-difference 304 /note- "if native Arg304 is substituted by an amino acid which provides a proteolytically more stable peptide bond, then it is pref. substituted by one of the amino acids Gly, Thr, Ala, Ser or Gln"
 FT Disulfide-bond 310..329
 FT Cleavage-site 315..316 /note- "proteolytic site in unmodified factor VII"
 FT MISC-difference 315 /note- "if native Arg315 is substituted by an amino acid which provides a proteolytically more stable peptide bond, then it is pref. substituted by one of the amino acids Gly, Thr, Ala, Ser or Gln"
 FT Modified-site 322 /note- "glycosylation site"
 FT MISC-difference 332 /note- "native Tyr332 may be substituted by an amino acid which provides a proteolytically more stable peptide bond, then it is pref. substituted by one of the amino acids Gly, Thr, Ala, Ser or Gln"

PT Disulfide-bond 340..368 stable peptide bond"
 FT Cleavage-site 341..342 /note- "proteolytic site in unmodified factor VII"
 FT MISC-difference 341 /note- "if native Lys341 is substituted by an amino acid which provides a proteolytically more stable peptide bond, then it is pref. substituted by one of the amino acids Glu, Gln, Gly, Thr Ala or Ser"
 FT Cleavage-site 392..393 /note- "proteolytic site"
 FT Cleavage-site 396..397 /note- "proteolytic site"
 FT Cleavage-site 402..403 /note- "proteolytic site"
 FT US5580560-A.
 PN 03-DEC-1996.
 PD 13-NOV-1989; 89US-0434149.
 PF 09-AUG-1993; 93US-0104509.
 PR 13-NOV-1989; 89US-0434149.
 PR 12-JUN-1992; 92US-0898248.
 PR 22-AUG-1994; 94US-0293778.
 XX (NOVO) NOVO-NORDISK AS.
 PA Bjorn SE, Nicolaisen EM, Wiberg FC, Woodbury R; WPI; 1997-033523/03.
 XX Mutated human factor VII or VIIa proteins - with amino acid substitutions to improve proteolytic stability
 PT Claim 1; Page -: 28pp; English.
 PS Modified human factor VII or VIIa proteins are stabilised against proteolytic cleavage by substitution of one of the residues Lys32, Lys38, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and Lys341 by an amino acid that provides a proteolytically more stable peptide bond, provided that Lys32 is replaced by Gln, Glu, His, Gly, Thr, Ala or Ser. The modified proteins are useful for treating CC bleeding disorders such as thrombocytopenia and von Willebrand's CC disease. They are also suitable for addition to plasma substitutes.
 XX Sequence 406 AA:
 SQ
 Query Match 77.1%; Score 148; DB 18; Length 406;
 Best Local Similarity 69.8%; Pred. No. 5.3e-17;
 Matches 30; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 QY 1 ANAFLLXLRPSLXKRCXKXQCSFXRXKXIFKDAYRTKLPMIS 43
 DB 1 anafllelrpslxlrekeqcsfsearrelfxdaertxlrlwxs 43
 RESULT 38
 AAY18306
 ID AAY18306 standard; peptide; 44 AA.
 AC AAY18306;
 XX 17-AUG-1999 (first entry)
 DT Bovine factor VII GLA domain.
 XX
 DE GLA domain; vitamin K-dependent protein; clotting disorder;
 KW therapy.
 XX

[illegible]

XX	(MINU) UNIV MINNESOTA.
PA	Nelstescuen GL;
PI	WPl: 2001-007226/01.
Pt	Noval vitamin K-dependent polypeptide useful for treating clotting disorders such as thrombosis and hemophilia, comprises modified gamma-carboxy glutamic acid domain that enhances membrane binding affinity -
PS	Disclosure: Page 12; 8lpp: English.
SC	The present invention describes a vitamin K-dependent polypeptide (I) comprising a modified gamma-carboxy glutamic acid (GIA) domain having at least one amino acid substitution, that enhances membrane binding affinity and the activity of the polypeptide relative to a corresponding native vitamin K-dependent polypeptide and inhibits clot formation.
CC	(I) can have thrombolytic and haemostatic activities, and can be used as an inhibitor of clot formation. (I) is useful for decreasing clot formation in a mammal, a factor VII or factor IX containing a modified GIA domain is useful for increasing clot formation and for treating a bleeding disorder, including thrombosis and clotting disorders such as haemophilia A, haemophilia B and liver disease. The present sequence represents a wild type bovine factor VII GIA domain sequence, given in the exemplification of the present invention.
SQ	Sequence 44 AA:
Query Match	68.2%; Score 131; DB 22; Length 44;
Best Local Similarity	77.3%; Pred. No. 4.5e-15;
Matches	34; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
OY	1 ANAFLLXLRPGSLRXKCKXXXOCSEFXAXIRKDAAITLFWIST Y 44 II IIIIII II III I : : : : : Db 1 angflxlrlpgslrxrcxkxcisfxhxhlfrnxxtlrqfwvsy 44
RESULT 40	
AUO02959 ID	AUO02959 standard; Protein: 345 AA.
AC XX	AUO02959;
XZ XX	
Df XX	12-SEP-2001 (first entry)
DE	Angiotensin converting enzyme (ACEV) splice variant protein #59.
KM KM	Angiotensin converting enzyme splice variant; ACEV: interleukin 6; granulocyte colony stimulating factor receptor; glucagon: hypertrophy: platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen p53; cyclin-dependent kinase inhibitor IC; vasoactive intestinal polipeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality; vascular disorder; asbestososis. Mus sp.. WO200136632-A2. 25-MAY-2001. 17-NOV-2000; 200OWO-IL00766. xx xx PD xx PF xx PR 17-NOV-1999; 99IL-0132978. PR 10-DEC-1999; 99IL-0133455. PA (COMP-) COMPUGEN LTD.

KW Factor VII; Factor IX; fusion peptide.
 XX
 PN EP200421-A.
 XX
 PD 10-DEC-1986.
 XX
 PF 16-APR-1986; 86EP-0302855.
 XX
 PR 16-DEC-1985; 85US-0810002.
 PR 17-APR-1985; 85US-0724311.
 XX
 PA (ZYMO-) ZYMOGENETICS INC.
 XX
 PI Hagen FS, Murry MJ, Berkner KL, Insley MT, Woodbury RG;
 PI Gray CL;
 DR WPI: 1986-326899/50.
 DR N-PSDB; AAN60065.
 XX
 PT DNA construct used to transfect hosts - to produce protein which
 PT activates to give factor VIIa
 PS
 PS Disclosure: Fig. 7; 55pp; English.
 XX
 CC The peptide is encoded by a Factor IX/Factor VII fusion cDNA.
 CC cDNA encoding Factor VIIcan be used in a DNA construct which contains
 CC a nucleotide sequence encoding a protein which, on activation, has the
 CC same biological activity for blood coagulation as Factor Iia. The
 CC nucleotide codes at least partially for Factor VII and comprises sequence
 CC encoding a calcium binding domain joined to second sequence downstream of
 CC this encoding a catalytic domain for serine protease activity of Factor
 CC VIIa. Calcium binding domain comprises a gene encoding Factor VII, IX,
 CC X, Protein C, prothrombin or Protein S. The construct is used to
 CC transfect host cells to produce the protein which, on activation,
 CC yields Factor VIIa.
 XX
 SQ Sequence 453 AA;

 Query Match 55.7%; Score 107; DB 7; Length 453;
 Best Local Similarity 55.9%; Pred. No. 6.4e-10;
 Matches 19; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

 OY 11 GSLRXCKXKXQCSFXRXRIFFDARFKLFWISY 44
 Db 58 gnlerecmekscsfearventerklfwisy 91

 RESULT 43
 AAY18304
 ID AAY18304 standard; peptide: 44 AA.
 XX
 AC AAY18304;
 XX
 DT 17-AUG-1999 (first entry)
 XX
 DE Bovine protein C GLA domain.
 XX
 KW GLA domain; vitamin K-dependent protein; clotting disorder;
 KW therapy.
 XX
 OS Bos taurus.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 1..44
 FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
 FT acid"
 XX
 PN W09920767-A1.
 XX
 PD 29-APR-1999.
 XX
 PF 20-OCT-1998; 98WO-US22152.

XX
 PR 23-OCT-1997; 97US-0955636.
 XX
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Nelstuen GL;
 XX
 DR WPI: 1999-288309/24.
 XX
 PT vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
 PT acid domain, useful for treating clotting disorders
 XX
 PS Disclosure: Page 14; 86pp; English.
 XX
 CC This sequence is the protein C GLA (gamma-carboxyglutamic acid)
 CC domain. The invention relates to a vitamin K-dependent polypeptide
 CC comprising a modified GLA domain containing an amino acid substitution
 CC which enhances membrane binding of the modified polypeptide as compared
 CC to the native polypeptide. The polypeptide is used to treat a clotting
 CC disorder by decreasing or increasing clot formation. Modification of the
 CC GLA domain results in a protein which has enhanced membrane binding
 CC affinity as compared to the native protein.
 XX
 SQ Sequence 44 AA;

 Query Match 54.2%; Score 104; DB 20; Length 44;
 Best Local Similarity 68.2%; Pred. No. 1.9e-10;
 Matches 30; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

 OY 1 ANAFLLXLRPGSLRXCKXKXQCSFXRXRIFFDARFKLFWISY 44
 Db 1 anslfxlrlpgnvrxscxvctfxarxllqnlxdlafwisy 44

 RESULT 44
 AAB36403
 ID AAB36403 standard; peptide: 44 AA.
 XX
 AC AAB36403;
 XX
 DT 27-FEB-2001 (first entry)
 XX
 DE Bovine protein C gamma-carboxyglutamic acid domain SEQ ID NO:2.
 XX
 KW Vitamin K-dependent protein; factor VII; protein C; GLA domain;
 KW gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
 KW factor X; prothrombin; enhanced membrane binding affinity;
 KW clot formation; thrombolytic; haemostatic; bleeding disorder;
 KW Thrombosis; clotting disorder; haemophilia A; haemophilia B;
 KW liver disease.
 XX
 OS Bos taurus.
 XX
 PN W0200066753-A2.
 XX
 PD 09-NOV-2000.
 XX
 PF 28-APR-2000; 2000WO-US11416.
 XX
 PR 29-APR-1999; 99US-0302239.
 XX
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Nelstuen GL;
 XX
 DR WPI: 2001-007226/01.
 XX
 XX Novel vitamin K-dependent polypeptide useful for treating clotting
 PT disorders such as thrombosis and hemophilia, comprises modified
 PT gamma-carboxy glutamic acid domain that enhances membrane binding
 PT affinity

PS Example 5; Page 42; 81pp; English.

CC The present invention describes a vitamin K-dependent polypeptide (1)

CC comprising a modified gamma-carboxy glutamic acid (Gla) domain having

CC at least one amino acid substitution, that enhances membrane binding

CC affinity and the activity of the polypeptide relative to a corresponding

CC native vitamin K-dependent polypeptide and inhibits clot formation.

CC (1) can have thrombolytic and haemostatic activities, and can be used

CC as an inhibitor of clot formation. (1) is useful for decreasing clot

CC formation in a mammal, a factor VII or factor IX containing a modified

CC Gla domain is useful for increasing clot formation and for treating a

CC bleeding disorder, including thrombosis and clotting disorders such as

CC haemophilia A, haemophilia B and liver disease. The present sequence

CC represents a bovine protein C Gla domain sequence, given in the

CC exemplification of the present invention.

XX Sequence 44 AA;

SQ

Query Match 54.2%; Score 104; DB 22; Length 44;

Best Local Similarity 68.2%; Pred. No. 1.9e-10;

Matches 30; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 ANAFLXXLRPGSLXRKCKXXQCSFXXARXIFKDXRRTKLFWISY 44

Db 1 ansflxxlrpgnvxxcxvxxcfxxxarxlfqntcdlmatwfy 44

RESULT 45

AAR13675

ID AAR13675 standard; Protein; 250 AA.

XX AAR13675;

AC AAR13675;

DT 09-OCT-1991 (first entry)

XX

DE Factor X-LACI hybrid protein.

KW Kunitz domain; blood; coagulation; inhibitor; Factor X;

KM tissue factor; TF; Lipoprotein-Associated Coagulation Inhibitor.

XX

FH Key Location/Qualifiers

FT 1..171

FT Peptide /label= X1c

FT 1..40

FT Domain /label= prepro_leader

FT 55..64

FT Domain /label= GLA_domain

FT 89..150

FT Domain /label= growth_factor_domains

FT 172..250

FT Domain /label= kunitz_domain

FT 57..62

FT Disulfide-bond 90..101

FT Disulfide-bond 95..110

FT Disulfide-bond 112..121

FT Disulfide-bond 129..140

FT Disulfide-bond 136..149

FT Disulfide-bond 151..164

FT Disulfide-bond 186..236

FT Disulfide-bond 195..219

FT Disulfide-bond 211..232

XX

XX EP439442-A.

XX

XX 31-JUL-1991.

XX

XX 21-JAN-1991; 91EP-0870008.

XX

XX 25-JAN-1990; 90US-0470289.

XX

XX (UNIV) UNIV OF WASHINGTON.

XX

PI Girard TJ, Broze GJ;

XX

DR WPI: 1991-224839/31.

DR N-PDB; AAQ12776.

XX

PT New factor X-LACI hybrid protein - comprises light chain of

PT factor X and LACI's first kunitz domain for use as anticoagulant

PS Disclosure; Page 12-14; 17pp; English.

XX

CC The protein is used as a blood coagulation inhibitor in mammals. It

CC is believed to mimic the Xa/LACI complex in binding to and

CC inhibiting VIIa/tissue factor. LACI inhibits via a novel feedback

CC mechanism requiring generation of Xa (a prod. of VIIa/TF activity);

CC XIcLACIK1 inhibits VIIa/TF activity directly.

CC The DNA allows prodn. of XIcLACIK1 by introduction of the gene into

CC cells suitable for expression, e.g. E. coli or CHO cells.

XX

SQ Sequence 250 AA;

Query Match 53.1%; Score 102; DB 12; Length 250;

Best Local Similarity 40.9%; Pred. No. 2.5e-09;

Matches 18; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANAFLXXLRPGSLXRKCKXXQCSFXXARXIFKDXRRTKLFWISY 44

Db 41 ansfleemkkghleremeetcsyeaearevfedsdktnetfwnky 84

RESULT 46

AAR22513

ID AAR22513 standard; Protein; 436 AA.

XX AAR22513;

AC AAR22513;

DT 28-JUL-1992 (first entry)

XX

DE Truncated precursor of human Factor Xa1.

KW Mutant; prothrombinase complex; proteolytic; precursor; thrombosis;

KM inflammation; restenosis; transplantation; haemophilia; antibodies.

XX

OS Homo sapiens.

XX

PN W09204378-A.

XX

PD 19-MAR-1992.

XX

PF 04-SEP-1991; 91WO-US06337.

XX

PR 04-SEP-1990; 90US-0578646.

XX

PA (CORR-) COR THERAPEUTICS IN.

XX

XX Wolf D;

XX

XX WPI: 1992-114303/14.

XX

DR New analogues of Factor Xa peptide - useful for treating

PT haemophilia, thrombosis, inflammation and transplant

PT complications, for in-vivo diagnosis

XX

PS Claim 7; Fig 1; 59pp; English.

XX

CC The full length cDNA of human factor X (wp19x) was converted to

CC encode a truncated form of human factor X, designated rx', by deletion

CC of the activation peptide by oligonucleotide site directed mutagenesis.

CC An oligonucleotide was used to align Arg 142 following the

CC C-terminus of the Factor X light chain with Ile 53 of the Factor X

CC activation peptide (1st residue of the heavy chain). When expressed

CC in CHO cells the truncated peptide was cleaved endogenously.

CC Modified Factor Xa was further produced by acylation e.g. with the

PT Factor X-derived polypeptide(s) inhibit binding of factor X to
PT Mac-1 - useful for treating thrombosis, atherosclerosis,
PT disseminated intravascular coagulation, septic shock etc.
PS Disclosure: Page 101-103; 122pp; English.
XX
CC The sequence shown represents the complete amino acid sequence of
CC human factor X. Fragments of this sequence corresp. to the Mac-1
CC (macrophage-monocyte adhesive receptor) recognition sites (see
CC features) of 10-25 amino acid residues may be used to inhibit Factor
CC X monocyte procoagulant activity, specifically inflammation. The
CC same effect may be achieved with antibodies raised to such fragments.
CC Typical applications include treatment of patients at risk of thrombosis
CC or atherosclerosis before surgery, disseminated intravascular
CC coagulation, septic shock, inflammation caused by infection (esp. by
CC herpes simplex) or autoimmune diseases, delayed hypersensitivity, etc.
CC The fragments also inhibit leucocyte/endothelial cell interaction and
CC thus regulate responses such as leucocyte recruitment, adhesion and
CC extravasation, haematopoiesis, antigen presentation, angiogenesis,
CC syncytial formation and haemostasis.
CC See also AAR37403-20.
CC
XX
SQ Sequence 448 AA;

Query Match 53.1%; Score 102; DB 14; Length 448;
Best Local Similarity 40.9%; Pred. No. 4.6e-09;
Matches 18; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANAFLLXLRPGSLXRXKXXQCSFXXARXIFKDAKXRTKLFWISY 44
| | | | | : | | | | | : | | : | | : | | |
Db 1 ansfleemkxghlercmeetsyeaarevfedsdktnelwnky 44

RESULT 49
AAW66092
ID AAW66092 standard; peptide; 448 AA.
XX
AC AAW66092;
XX
DT 16-NOV-1998 (first entry)
XX
DE Human factor X variant.
XX
KW factor X variant; factor V; fVa; diagnostic assay; heparin; thrombin;
KW blood coagulation.
XX
OS Homo sapiens.
XX
PN WO9839456-A1.
XX
PD 11-SEP-1998.
XX
PF 05-MAR-1998; 98WO-US03939.
XX
PR 07-MAR-1997; 97US-0040047.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Mletlich JP;
XX
DR WPI; 1998-495855/42.
XX
PT New human blood coagulation Factor X variant - with asparagine
PT residue at position 347, has reduced affinity for activated Factor V
PT and is useful for diagnostic assays
XX
PS Claim 1; Page -: 42pp; English.
XX
CC The invention relates to a human Factor X variant (nfx) where asparagine
CC replaces arginine at position 347. Also claimed is a method for
CC substantially reducing the affinity of human Factor X for activated
CC Factor V (fVa) without substantially reducing the catalytic impact of

CC fVa binding, by replacing arginine with asparagine at position 347. The
CC new fx variant is especially useful for in vitro assays and diagnostic
CC applications. Specifically, these include (1) quantifying the importance
CC of the interaction between the serine protease domain of activated Factor
CC X (fXa) and fVa by comparison of wild type fXa and nfx; (2) quantifying
CC the impact of specific inhibitors of fVa-fXa interaction by comparison
CC of wild type fXa and nfx, which is useful for treatment with inhibitors
CC like heparin and tissue factor pathway inhibitor (TFPI); and (3)
CC reactions where total specificity of thrombin activation to membrane
CC surfaces is required, as nfx has no significant interaction with fVa in
CC the absence of a sufficiently charged phospholipid surface. Substitution
CC of wild-type arginine by asparagine at position 347 of factor X
CC selectively attenuates the interaction between fXa and fVa without
CC affecting its catalytic (thrombogenic) activity (except in the presence
CC of sub-saturating heparin where the rate of inhibition by antithrombin
CC IIR is 15% of normal). The present sequence represents the specifically
CC claimed human Factor X variant having the arginine residue at position
CC 347 replaced with asparagine.
CC NB: This sequence does not appear as such in the present patent
CC specification but was created using the native factor X sequence as
CC shown in PIR Accession Number 538554.
CC
XX
SQ Sequence 448 AA;

Query Match 53.1%; Score 102; DB 19; Length 448;
Best Local Similarity 40.9%; Pred. No. 4.6e-09;
Matches 18; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANAFLLXLRPGSLXRXKXXQCSFXXARXIFKDAKXRTKLFWISY 44
| | | | | : | | | | | : | | : | | : | | |
Db 1 ansfleemkxghlercmeetsyeaarevfedsdktnelwnky 44

RESULT 50
AAW40283
ID AAW40283 standard; Protein; 467 AA.
XX
AC AAW40283;
XX
DT 16-JUN-1998 (first entry)
XX
DE Human Factor X protease.
XX
KW Factor X; factor IX; serine protease activity; catalytic domain; ZAD;
KW zymogen-activating domain; epidermal growth factor-like domain; EGFL;
KW EGF2; regulator; coagulation; fibrinolysis; homeostasis; X-ray structure;
KW detection; drug modelling; restriction protease.
XX
XX
OS Homo sapiens.
XX
PN WO9747737-A1.
XX
FH Key Location/Qualifiers
FH 108..153
FT Domain /label= EGF2 domain
FT 154..165
FT Domain /label= EGF2 domain
FT 166..216
FT Domain /label= Activating domain
FT 217..454
FT Domain /label= catalytic domain
XX
PN WO9747737-A1.
XX
PD 18-DEC-1997.
XX
PF 11-JUN-1997; 97WO-EP03027.
XX
PR 06-JUL-1996; 96EP-0110959.
PR 11-JUN-1996; 96EP-0109288.
PR 22-JUN-1996; 96EP-0110109.
XX
PA (BOE) BOEHRINGER MANNHEIM GMBH.

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OM protein - protein search, using sw model

Run on: August 30, 2002, 13:47:15 ; Search time 39.72 Seconds
(without alignments)
27.058 Million cell updates/sec

Title: US-09-302-239-3

Perfect score: 192
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 50 summaries

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6: /cgn2_6/prodata/2/1aa/backfilesl.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	172	89.6	44	3	US-08-955-636-3
2	172	89.6	406	1	US-08-293-778-24
3	172	89.6	406	1	US-08-295-411-5
4	172	89.6	406	2	US-08-955-471-5
5	172	89.6	406	5	PCT-US92-1024-5
6	172	89.6	444	1	US-08-475-845-2
7	172	89.6	444	2	US-08-327-690-2
8	172	89.6	444	2	US-08-660-289-2
9	172	89.6	444	2	US-08-537-807-2
10	172	89.6	444	2	US-08-871-003-2
11	172	89.6	444	3	US-08-464-233-2
12	172	89.6	444	4	US-09-189-607-2
13	172	89.6	444	4	US-09-378-907-2
14	172	89.6	444	5	PCT-US94-05779-2
15	172	89.6	466	1	US-07-882-202A-4
16	172	89.6	466	1	US-08-021-615A-4
17	172	89.6	466	1	US-08-321-777-4
18	172	89.6	466	4	US-09-009-217-14
19	172	89.6	466	5	PCT-US93-04493-4
20	172	89.6	466	5	PCT-US93-04493-4
21	166	86.5	44	3	US-08-955-636-29
22	164	85.4	44	3	US-08-955-636-26
23	164	85.4	44	3	US-08-955-636-27
24	164	85.4	44	3	US-08-955-636-28
25	160	83.3	44	3	US-08-955-636-30
26	157	81.8	41	1	US-08-229-280-4
27	131	68.2	44	3	US-08-955-636-4

28	111	57.8	139	1	US-08-330-978-2	Sequence 2, Appl1
29	111	57.8	139	1	US-08-474-042-2	Sequence 2, Appl1
30	111	57.8	139	1	US-08-484-558-2	Sequence 2, Appl1
31	111	57.8	139	1	US-08-774-592-2	Sequence 2, Appl1
32	111	57.8	437	1	US-08-487-037-2	Sequence 2, Appl1
33	111	57.8	437	1	US-08-487-037-3	Sequence 2, Appl1
34	111	57.8	488	1	US-08-487-037-1	Sequence 1, Appl1
35	104	54.2	44	3	US-08-955-636-2	Sequence 1, Appl1
36	102	53.1	448	1	US-08-295-411-3	Sequence 3, Appl1
37	102	53.1	448	2	US-08-955-471-3	Sequence 3, Appl1
38	102	53.1	448	5	PCT-US92-10066-1	Sequence 1, Appl1
39	102	53.1	448	5	PCT-US92-10242-3	Sequence 3, Appl1
40	101	52.6	44	3	US-08-955-636-18	Sequence 18, Appl1
41	101	52.6	487	1	US-08-469-486-53	Sequence 53, Appl1
42	101	52.6	487	2	US-08-469-486-53	Sequence 53, Appl1
43	101	52.6	492	1	US-08-469-486-2	Sequence 2, Appl1
44	101	52.6	492	2	US-08-469-486-2	Sequence 2, Appl1
45	98	51.0	41	1	US-08-229-280-2	Sequence 2, Appl1
46	96	50.0	44	3	US-08-955-636-24	Sequence 24, Appl1
47	96	50.0	44	3	US-08-955-636-35	Sequence 35, Appl1
48	95	49.5	44	3	US-08-955-636-23	Sequence 23, Appl1
49	90	46.9	44	3	US-08-955-636-20	Sequence 20, Appl1
50	90	46.9	44	3	US-08-955-636-21	Sequence 21, Appl1

ALIGNMENTS

```
RESULT 1
US-08-955-636-3
; Sequence 3, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Neilsen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa-gamma carboxylutamic acid of glutamic acid
US-08-955-636-3

Query Match      89.6%: Score 172; DB 3; Length 44;
Best Local Similarity 100.0%: Pred. No. 6.8e-23;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ANAFLLXLRPGSLKRCXKXCSFXXARXIFKDXRKLFWISY 44
Db 1 ANAFLLXLRPGSLKRCXKXCSFXXARXIFKDXRKLFWISY 44

RESULT 2
US-08-293-778-24
; Sequence 24, Application US/08293778
; Patent No. 5580560
; GENERAL INFORMATION:
; APPLICANT: Nicolaisen, Else M.
; APPLICANT: Bjorn, Soren E.
; APPLICANT: Wilberg, Finn C.
; APPLICANT: Woodbury, Richard
; TITLE OF INVENTION: MODIFIED FACTOR VII/VIIA
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: No. 55805600 No. 5580560disk of No. 5580560th America, Inc.
STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,778
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/104,509
FILING DATE:
APPLICATION NUMBER: DK 3235/87
FILING DATE: 25-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/434,149
FILING DATE: 13-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK88/00103
FILING DATE: 24-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/898,248
FILING DATE: 12-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Agtis, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3129.224-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-293-778-24

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Query Match      89.6%  Score 172;  DB 1;  Length 406;
Best Local Similarity 77.3%  Pred. No. 7.2e-22;
Matches 34;  Conservative 0;  Mismatches 10;  Indels 0;  Gaps 0;

      QY      1 ANAFXLRLPGSLKRXKXKXQCSFXXARXIFRDXAKRTKLFWMISY 44
      ||||| ||||| ||| ||| ||| ||||| ||||| |||||
      Db      1 ANAFLYILRPGSLRYKCYKQCSFYIANYIFRDKATRTKLFWMISY 44

RESULT 3
US-08-295-411-5
; Sequence 5, Application US/08295411
; Patent No. 5679639
;
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Westers, Rolf M.
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Office of Patent Counsel, The Scripps
ADDRESSSEE: Research Institute
STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA

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1 ZIP: 92037
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3 COMPUTER READABLE FORM:
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5 MEDIUM TYPE: floppy disk
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7 COMPUTER: IBM PC compatible
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9 OPERATING SYSTEM: PC-DOS/MS-DOS
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11 SOFTWARE: PatentIn Release #1.0, Version #1.25
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13 CURRENT APPLICATION DATA:
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15 APPLICATION NUMBER: US/08/295,411
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17 FILING DATE: 22-AUG-1994
18
19 CLASSIFICATION: 530
20
21 PRIOR APPLICATION DATA:
22
23 APPLICATION NUMBER: US 07/793,989
24
25 FILING DATE: 18-NOV-1991
26
27 CLASSIFICATION: 530
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29 ATTORNEY/AGENT INFORMATION:
30
31 NAME: Fitting, Thomas
32
33 REGISTRATION NUMBER: 34,163
34
35 REFERENCE/DOCKET NUMBER: TSR1263.0C1
36
37 TELECOMMUNICATION INFORMATION:
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39 TELEPHONE: 619-554-2937
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41 TELEFAX: 619-554-6312
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43 INFORMATION FOR SEQ ID NO: 5:
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45 SEQUENCE CHARACTERISTICS:
46
47 LENGTH: 406 amino acids
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49 TYPE: amino acid
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51 TOPOLOGY: linear
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53 MOLECULE TYPE: protein
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55 HYPOTHEICAL: NO
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57 ANTI-SENSE: NO
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59 FEATURE:
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61 NAME/KEY: Region
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63 LOCATION: 1..152
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65 OTHER INFORMATION: /note="Factor VII light Chain"
66
67 FEATURE:
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69 NAME/KEY: Region
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71 LOCATION: 153..406
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73 OTHER INFORMATION: /note="Factor VII Heavy Chain"
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Query Match          89.6%: Score 172: DB 1: Length 406;
Best Local Similarity 77.3%: Pred. No. 7.2e-22;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY      1 ANAEFLXXLRPGSLRXCCKXXQCSFXAXRFXKDAKRTKLFMISY 44
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Db       1 ANAELELRPGSLRECKEQQCSFEAREIRPKDAERTKLFMISY 44

RESULT  4
US-08-955-471-5
; Sequence 5, Application US/08955471
; Patent No. 5968751
; GENERAL INFORMATION:
; APPLICANT: Griffio, John H.
; APPLICANT: Meesters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; NUMBER OF SEQUENCES: 10 for Inhibiting Coagulation
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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FILING DATE: 28-FEB-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-475-845-2

Query Match 89.6%; Score 172; DB 1; Length 444;
Best Local Similarity 77.3%; Pred. No. 7.9e-22;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 1 ANAFLELRPGSLRXKCKXXQCSFXXARXIFKDAERTKLFWISY 44
Db 39 ANAFLELRPGSLRECKECCSFEEARREIFKDAERTKLFWISY 82

RESULT 7
US-08-327-690-2
Sequence 2, Application US/08327690
Patent No. 5817788
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/327,690
FILING DATE: 24-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-327-690-2

Query Match 89.6%; Score 172; DB 2; Length 444;
Best Local Similarity 77.3%; Pred. No. 7.9e-22;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 1 ANAFLELRPGSLRXKCKXXQCSFXXARXIFKDAERTKLFWISY 44
Db 39 ANAFLELRPGSLRECKECCSFEEARREIFKDAERTKLFWISY 82

RESULT 8
US-08-660-289-2
Sequence 2, Application US/08660289
Patent No. 5835982
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,289
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/475,845
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 08/327,690
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-660-289-2

Query Match 89.6%; Score 172; DB 2; Length 444;

Best Local Similarity 77.3%; Pred. No. 7.9e-22;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 ANAFLXLRPGSLRXKXKXOCSEFXKXARXIFKDAKRTKLFWISY 44
Db 39 ANAFLLELRPGSLERECKEEOCSFEAREIFKDAERTKLFWISY 82

RESULT 9

US-08-537-807-2
Sequence 2, Application US/08537807
Patent No. 5861374
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/537,807
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05779
FILING DATE: 23-MAY-1994
APPLICATION NUMBER: US 08/065,725
FILING DATE: 21-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,920
FILING DATE: 28-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-1PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
FAX: 206-467-9600
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-537-807-2

Query Match 89.6%; Score 172; DB 2; Length 444;
Best Local Similarity 77.3%; Pred. No. 7.9e-22;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 ANAFLXLRPGSLRXKXKXOCSEFXKXARXIFKDAKRTKLFWISY 44
Db 39 ANAFLLELRPGSLERECKEEOCSFEAREIFKDAERTKLFWISY 82

RESULT 10

US-08-871-003-2
Sequence 2, Application US/08871003
Patent No. 5997864
GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
APPLICANT: Petersen, Lars C.
APPLICANT: Hedner, Ulla
APPLICANT: Rasmussen, Mirella E.
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle

STATE: WA
COUNTRY: USA
ZIP: 98102

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,003
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 90-07C7
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-871-003-2

Query Match 89.6%; Score 172; DB 2; Length 444;
Best Local Similarity 77.3%; Pred. No. 7.9e-22;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 ANAFLXLRPGSLRXKXKXOCSEFXKXARXIFKDAKRTKLFWISY 44
Db 39 ANAFLLELRPGSLERECKEEOCSFEAREIFKDAERTKLFWISY 82

RESULT 11

US-08-464-233-2
Sequence 2, Application US/08464233
Patent No. 6039944
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stuart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,233
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/327,690
FILING DATE: 24-OCT-1994
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-464-233-2

Query Match      89.6%; Score 172; DB 3; Length 444;
Best Local Similarity 77.3%; Pred. No. 7.9e-22;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANAFLLXLRPGSLXRCKXXQCSFXXARXIFKDAERTKLEWISY 44
Db 39 ANAFLELRPGSLRECKEBCQCSFEERARLTKDAERTKLEWISY 82

RESULT 12
US-09-189-607-2
; Sequence 2, Application US/09189607
; Patent No. 6168789
; GENERAL INFORMATION:
; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hedner, Olla
; APPLICANT: Bregengaard, Claus
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourile and Crew
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/189,607
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/660,289
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/065,725
; FILING DATE: 21-MAY-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
```

```
; REFERENCE/DOCKET NUMBER: 13952-8-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-189-607-2

Query Match      89.6%; Score 172; DB 4; Length 444;
Best Local Similarity 77.3%; Pred. No. 7.9e-22;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANAFLLXLRPGSLXRCKXXQCSFXXARXIFKDAERTKLEWISY 44
Db 39 ANAFLELRPGSLRECKEBCQCSFEERARLTKDAERTKLEWISY 82

RESULT 13
US-09-378-907-2
; Sequence 2, Application US/09378907
; Patent No. 6183743
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hedner, Olla
; APPLICANT: Rasmussen, Mirella E.
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,907
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/871,003
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-378-907-2

Query Match      89.6%; Score 172; DB 4; Length 444;
Best Local Similarity 77.3%; Pred. No. 7.9e-22;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANAFLLXLRPGSLXRCKXXQCSFXXARXIFKDAERTKLEWISY 44
Db 39 ANAFLELRPGSLRECKEBCQCSFEERARLTKDAERTKLEWISY 82
```

RESULT 14
PCT-US94-05779-2
Sequence 2, Application PC/TUS9405779
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05779
FILING DATE: 23-MAY-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/065,725
FILING DATE: 21-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,920
FILING DATE: 28-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-1PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-05779-2

Query Match 89.6%; Score 172; DB 5; Length 444;
Best Local Similarity 77.3%; Pred. No. 7.9e-22;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANAFLLXLRPGSLXKCKXKXCSFXKXRXIFKDXKRTKLFWISY 44
||||| ||||| | || |||| | ||||| ||||| |||||
Db 39 ANAFLEELRPGSLRECKEKEQCSFEANEIRKDAERTKLFWISY 82

RESULT 15
US-07-882-202A-4
Sequence 4, Application US/07882202A
GENERAL INFORMATION:
APPLICANT: Morrissey, James H.
TITLE OF INVENTION: Treatment of Bleeding with Modified
TITLE OF INVENTION: Tissue Factor in Combination with FVIIa
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Richards, Medlock & Andrews
STREET: 1201 Elm Street, Suite 4500
CITY: Dallas
STATE: Texas
COUNTRY: US
ZIP: 75270-2197
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/882,202A

FILING DATE: 13-MAY-1992
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Hansen, Eugenia S.
REGISTRATION NUMBER: 31,966
REFERENCE/DOCKET NUMBER: OMRP B34290
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4500
TELEFAX: 214-939-4600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 466 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-882-202A-4

Query Match 89.6%; Score 172; DB 1; Length 466;
Best Local Similarity 77.3%; Pred. No. 8.3e-22;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANAFLLXLRPGSLXKCKXKXCSFXKXRXIFKDXKRTKLFWISY 44
||||| ||||| | || |||| | ||||| ||||| |||||
Db 61 ANAFLEELRPGSLRECKEKEQCSFEANEIRKDAERTKLFWISY 104

RESULT 16
US-08-021-615A-4
Sequence 4, Application US/08021615A
Patent No. 5504064
GENERAL INFORMATION:
APPLICANT: Morrissey, James H.
TITLE OF INVENTION: Treatment of Bleeding with Modified
TITLE OF INVENTION: Tissue Factor in Combination with an Activator of
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Richards, Medlock & Andrews
STREET: 1201 Elm Street, Suite 4500
CITY: Dallas
STATE: Texas
COUNTRY: US
ZIP: 75270-2197
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/021,615A
FILING DATE: 19-FEB-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/882,202
FILING DATE: 13-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hansen, Eugenia S.
REGISTRATION NUMBER: 31,966
REFERENCE/DOCKET NUMBER: OMRP B34290CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4500
TELEFAX: 214-939-4600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 466 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-021-615A-4

Query Match 89.6%; Score 172; DB 1; Length 466;
Best Local Similarity 77.3%; Pred. No. 8.3e-22;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRPGSLRXCKXXCSEFXRXRIFKDXRTKLFWISY 44
||||| ||||| | | ||||| ||||| ||||| |||||
Db 61 ANAFLELRPGSLRCKEKGCSFEAREIFKDAERTKLFWISY 104

RESULT 17
US-08-321-777-4
; Sequence 4, Application US/08321777
; Patent No. 5504067
; GENERAL INFORMATION:
; APPLICANT: Morrissey, James H.
; APPLICANT: Comp, Philip C.
; TITLE OF INVENTION: Treatment of Bleeding with Modified
; TITLE OF INVENTION: Tissue Factor in Combination with FvIIa
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richards, Medlock & Andrews
; STREET: 1201 Elm Street, Suite 4500
; CITY: Dallas
; STATE: Texas
; COUNTRY: US
; ZIP: 75270-2197
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/321,777
; FILING DATE:
; CLASSIFICATION: 514
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/882202
; FILING DATE: 13-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hansen, Eugene S.
; REGISTRATION NUMBER: 31,966
; REFERENCE/DOCKET NUMBER: OMRP B34290C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 214-939-4500
; TELEFAX: 214-939-4600
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 466 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-321-777-4

Query Match 89.6%; Score 172; DB 1; Length 466;
Best Local Similarity 77.3%; Pred. No. 8.3e-22;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRPGSLRXCKXXCSEFXRXRIFKDXRTKLFWISY 44
||||| ||||| | | ||||| ||||| ||||| |||||
Db 61 ANAFLELRPGSLRCKEKGCSFEAREIFKDAERTKLFWISY 104

RESULT 18
US-09-009-217-14
; Sequence 14, Application US/09009217
; Patent No. 6132729
; GENERAL INFORMATION:
; APPLICANT: Thorpe, Philip E.
; APPLICANT: King, Steven W.
; APPLICANT: Gao, Boming
; TITLE OF INVENTION: COMBINED TISSUE FACTOR AND
; TITLE OF INVENTION: CHEMOTHERAPEUTIC METHODS AND COMPOSITIONS FOR COAGULATION

;; TITLE OF INVENTION: AND TUMOR TREATMENT
;; NUMBER OF SEQUENCES: 27
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Arnold, White & Durkee
;; STREET: P.O. Box 4433
;; CITY: Houston
;; STATE: Texas
;; COUNTRY: USA
;; ZIP: 77210
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/009,217
;; FILING DATE: Concurrently Herewith
;; CLASSIFICATION:
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US 60/042,427
;; FILING DATE: 27-MAR-1997
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US 60/036,205
;; FILING DATE: 27-JAN-1997
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US 60/035,920
;; FILING DATE: 22-JAN-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hieber, David W.
;; REGISTRATION NUMBER: 41,071
;; REFERENCE/DOCKET NUMBER: UTSD:536
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 512/418-3000
;; TELEFAX: 512/474-7577
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 466 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; US-09-009-217-14

Query Match 89.6%; Score 172; DB 4; Length 466;
Best Local Similarity 77.3%; Pred. No. 8.3e-22;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRPGSLRXCKXXCSEFXRXRIFKDXRTKLFWISY 44
||||| ||||| | | ||||| ||||| ||||| |||||
Db 61 ANAFLELRPGSLRCKEKGCSFEAREIFKDAERTKLFWISY 104

RESULT 19
US-09-009-656-14
; Sequence 14, Application US/09009656
; Patent No. 6132730
; GENERAL INFORMATION:
; APPLICANT: Thorpe, Philip E.
; APPLICANT: King, Steven W.
; APPLICANT: Gao, Boming
; TITLE OF INVENTION: COMBINED TISSUE FACTOR AND FACTOR VIIa
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR COAGULATION AND TUMOR
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,656
FILING DATE: Concurrently Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/042,427
FILING DATE: 27-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,205
FILING DATE: 27-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,920
FILING DATE: 22-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hildier, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: UTSD:537
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 466 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-009-656-14
```

```
Query Match      89.6%; Score 172; DB 4; Length 466;
Best Local Similarity 77.3%; Pred. No. 8.3e-22;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
```

```
Oy 1 ANAFLXLRPGSLRXKXKXCSFXAXRIFKDXARTKLFWISY 44
||||| ||||| || ||||| ||||| ||||| ||||| |||||
Db 61 ANAFLLELRPGSLRECKEEOCSFEAREIFKDAERTKLFWISY 104

RESULT 20
PCT-US93-04493-4
: Sequence 4; Application PC/TUS9304493
: GENERAL INFORMATION:
: APPLICANT: Morrissey, James H.
: TITLE OF INVENTION: Truncated Tissue Factor and FvIa or
: TITLE OF INVENTION: FvII Activator for Blood Coagulation
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Richards, Medlock & Andrews
: STREET: 1201 Elm Street, Suite 4500
: CITY: Dallas
: STATE: Texas
: COUNTRY: US
: ZIP: 75270-2197
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/04493
: FILING DATE: 19930512
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/882202
: FILING DATE: 13-MAY-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/021615
: FILING DATE: 19-FEB-1993
: ATTORNEY/AGENT INFORMATION:
```

```
NAME: Trujillo, Doreen Y.
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: OMRF B34290CIPC/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4600
TELEFAX: 214-939-4600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 466 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-04493-4
```

```
Query Match      89.6%; Score 172; DB 5; Length 466;
Best Local Similarity 77.3%; Pred. No. 8.3e-22;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
```

```
Oy 1 ANAFLXLRPGSLRXKXKXCSFXAXRIFKDXARTKLFWISY 44
||||| ||||| || ||||| ||||| ||||| ||||| |||||
Db 61 ANAFLLELRPGSLRECKEEOCSFEAREIFKDAERTKLFWISY 104
```

```
RESULT 21
US-08-955-636-29
: Sequence 29; Application US/08955636A
: Patent No. 6017882
: GENERAL INFORMATION:
: APPLICANT: Nelstuen, Gary
: TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
: FILE REFERENCE: 09531/002001
: CURRENT APPLICATION NUMBER: US/08/955,636A
: CURRENT FILING DATE: 1997-10-23
: NUMBER OF SEQ ID NOS: 35
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 29
: LENGTH: 44
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: MOD_RES
: LOCATION: (0)...(0)
: OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid
US-08-955-636-29
```

```
Query Match      86.5%; Score 166; DB 3; Length 44;
Best Local Similarity 97.7%; Pred. No. 7.4e-22;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy 1 ANAFLXLRPGSLRXKXKXCSFXAXRIFKDXARTKLFWISY 44
||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 ANAFLXLRPGSLRXKXKXCSFXAXRIFDDARTKLFWISY 44
```

```
RESULT 22
US-08-955-636-26
: Sequence 26; Application US/08955636A
: Patent No. 6017882
: GENERAL INFORMATION:
: APPLICANT: Nelstuen, Gary
: TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
: FILE REFERENCE: 09531/002001
: CURRENT APPLICATION NUMBER: US/08/955,636A
: CURRENT FILING DATE: 1997-10-23
: NUMBER OF SEQ ID NOS: 35
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 26
: LENGTH: 44
: TYPE: PRT
```

```

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-26
```

```

Query Match          85.4%; Score 164; DB 3; Length 44;
Best Local Similarity 97.7%; Pred. No. 1.6e-21;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY 1 ANAFLLXLRPGSLXRXCKXXQCSFXXARXIFKDXARTKLFWISY 44
DB 1 ANAFLLXLRPGSLXRXCKXXQCSFXXARXIFKDXARTKLFWISY 44
```

```

RESULT 23
US-08-955-636-27
; Sequence 27, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelissestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 44
; TYPE: PR1
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-27
```

```

Query Match          85.4%; Score 164; DB 3; Length 44;
Best Local Similarity 97.7%; Pred. No. 1.6e-21;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY 1 ANAFLLXLRPGSLXRXCKXXQCSFXXARXIFKDXARTKLFWISY 44
DB 1 ANAFLLXLRPGSLXRXCKXXQCSFXXARXIFKDXARTKLFWISY 44
```

```

RESULT 24
US-08-955-636-28
; Sequence 28, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelissestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 44
; TYPE: PR1
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-28
```

```

Query Match          85.4%; Score 164; DB 3; Length 44;
Best Local Similarity 97.7%; Pred. No. 1.6e-21;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY 1 ANAFLLXLRPGSLXRXCKXXQCSFXXARXIFKDXARTKLFWISY 44
DB 1 ANAFLLXLRPGSLXRXCKXXQCSFXXARXIFKDXARTKLFWISY 44
```

```

RESULT 25
US-08-955-636-30
; Sequence 30, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelissestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 44
; TYPE: PR1
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-30
```

```

Query Match          83.3%; Score 160; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 8e-21;
Matches 42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```

QY 1 ANAFLLXLRPGSLXRXCKXXQCSFXXARXIFKDXARTKLFWISY 44
DB 1 ANAFLLXLRPGSLXRXCKXXQCSFXXARXIFKDXARTKLFWISY 44
```

```

RESULT 26
US-08-229-280-4
; Sequence 4, Application US/08229280
; Patent No. 5516640
; GENERAL INFORMATION:
; APPLICANT: WATANABE, kelsuke
; APPLICANT: : MARAKI, Toru
; TITLE OF INVENTION: METHOD OF DETERMINATION OF
; TITLE OF INVENTION: PIVKA OF EVERY KIND AND
; TITLE OF INVENTION: REAGENT THEREFOR
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS, P. C.
; STREET: 2026 Rambling Road
; CITY: Kalamazoo
; STATE: Michigan
; COUNTRY: USA
; ZIP: 49008-1699
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
; COMPUTER: IBM PC/XT/AT Compatible
; OPERATING SYSTEM: MS-DOS 5.0
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/229,280
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-130015
```


FILING DATE: MAY 7, 1993
APPLICATION NUMBER: JP 6-16348
FILING DATE: FEBRUARY 10, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Teriyence F. Chapman
REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Furuya Case 1312
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homosapiens
FEATURE:
OTHER INFORMATION: Xaa in the sequence is
OTHER INFORMATION: -carboxyglutamic acid
US-08-229-280-4

Query Match 81.8%; Score 157; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2.5e-20;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ANAFLXLRPGSLXKXKXKXCSFXXARXIFKDXARTKLFW 41
Db 1 ANAFLXLRPGSLXKXKXKXCSFXXARXIFKDXARTKLFW 41

RESULT 27
US-08-955-636-4
Sequence 4, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 44
TYPE: PRT
ORGANISM: Bos taurus
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid
US-08-955-636-4

Query Match 68.2%; Score 131; DB 3; Length 44;
Best Local Similarity 77.3%; Pred. No. 8.2e-16;
Matches 34; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 1 ANAFLXLRPGSLXKXKXKXCSFXXARXIFKDXARTKLFWISY 44
Db 1 ANGLXLRPGSLXKXKXKXCSFXXAHXIFRNXXKRTKQFWVS 44

RESULT 28
US-08-330-978-2
Sequence 2, Application US/08330978
Patent No. 5589571
GENERAL INFORMATION:
APPLICANT: King, Robert
TITLE OF INVENTION: PROCESS FOR PRODUCTION OF INHIBITED

TITLE OF INVENTION: FORMS OF ACTIVATED BLOOD FACTORS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Morrison & Roester
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,978
FILING DATE: 28-OCT-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,558
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2803-0007.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)887-1500
TELEFAX: (202)822-0168
TELEX: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 17..22
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 50..61
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 55..70
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 72..81
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 89..100
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 96..109
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 111..124
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 132
OTHER INFORMATION: /note="Disulfide linkage with
residue 160 of SEQ ID NO:1, residue 108 of SEQ ID NO:3 or
OTHER INFORMATION: residue 108 of SEQ ID:4"
US-08-330-978-2

Query Match 57.8%; Score 111; DB 1; Length 139;
Best Local Similarity 40.9%; Pred. No. 8e-12;
Matches 18; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

OY 1 ANAFLXLRPGSLXKXKXKXCSFXXARXIFKDXARTKLFWISY 44
Db 1 ANSLTMMKKGHLFRFCMTTCSTYTTARTVFTDSOKTWNKRY 44

RESULT 29
US-08-474-042-2
; Sequence 2, Application US/08474042
; Patent No. 5589572
; GENERAL INFORMATION:
; APPLICANT: King, Robert
; TITLE OF INVENTION: PROCESS FOR PRODUCTION OF INHIBITED
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Moritson & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,042
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,558
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2803-0007.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)822-0168
; TELEFAX: (202)822-0168
; TELEX: 90-4030 MRSNFOERSMNH
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 17..22
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 50..61
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 55..70
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 72..81
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 89..100
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 96..109
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 111..124
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 132
; OTHER INFORMATION: /note- "Disulfide linkage with
; OTHER INFORMATION: residue 160 of SEQ ID NO:1, residue 108 of SEQ ID NO:3 or
; OTHER INFORMATION: residue 108 of SEQ ID:4"
US-08-474-042-2

Query Match 57.8%; Score 111; DB 1; Length 139;
Best Local Similarity 40.9%; Pred. No. 8e-12;
Matches 18; Conservative 7; Mismatches 19; Indels 0; Gaps 0;
Cy 1 ANAFXXLRPGSLXRCKXXQCSFXXRXIIFKDXRPLFMISY 44
Db 1 ANSLFTTMKKGHLLRTCMTTTCSTTTARIVFTSDKINTWNNKI 44
RESULT 30
US-08-484-558-2
; Sequence 2, Application US/08484558
; Patent No. 5602233
; GENERAL INFORMATION:
; APPLICANT: King, Robert
; TITLE OF INVENTION: PROCESS FOR PRODUCTION OF INHIBITED
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Moritson & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,558
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2803-0007.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)822-0168
; TELEFAX: (202)822-0168
; TELEX: 90-4030 MRSNFOERSMNH
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 17..22
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 50..61
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 55..70
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 72..81
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 89..100
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 96..109
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 111..124
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 132
; OTHER INFORMATION: /note- "Disulfide linkage with


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? LOCATION: -17
? OTHER INFORMATION: /note= "Location of Intron A"
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: (37-38)
? OTHER INFORMATION: /note= "Location of Intron B"
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: 46
? OTHER INFORMATION: /note= "Location of Intron C"
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: 63
? OTHER INFORMATION: /note= "An amino acid represented
? OTHER INFORMATION: by the greek letter Beta"
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: 84
? OTHER INFORMATION: /note= "Location of Intron D"
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: 128
? OTHER INFORMATION: /note= "Location of Intron E"
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: (158-159)
? OTHER INFORMATION: /note= "Location of Intron F"
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: 198
? OTHER INFORMATION: /note= "Location of Intron G"
? FEATURE:
? NAME/KEY: Disulfide-bond
? LOCATION: group(17..22, 50..61, 55..70, 72..81, 89..100, 96
? LOCATION: ..109, 111..124, 132..251, 150..155, 170..186,
? LOCATION: 299..313, 324..352)
US-08-487-037-2

Query Match 57.8%; Score 111; DB 1; Length 437;
Best Local Similarity 40.9%; Pred. No. 2,7e-11;
Matches 18; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLLXLRPGSLXKCKXXQCSFXKXRIFKDAXRTKLFWISY 44
Db 41 ANSFLTTMKKGHLTRTCMTTCSYTAIVTDSKNTFNWXY 84

RESULT 33
US-08-487-037-3
? Sequence 3, Application US/08487037
? Patent No. 5795863
? GENERAL INFORMATION:
? APPLICANT: Wolf, David L.
? TITLE OF INVENTION: RECOMBINANT AGENTS AFFECTING THROMBOSIS
? NUMBER OF SEQUENCES: 11
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: MORRISON & FOERSTER
? STREET: 2000 Pennsylvania Avenue, NW
? CITY: Washington
? STATE: DC
? COUNTRY: USA
? ZIP: 20006-1812
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/487,037
? FILING DATE: 07-JUN-1995
? CLASSIFICATION: 514
? ATTORNEY/AGENT INFORMATION:
```

```

? NAME: Adler, Reid G.
? REGISTRATION NUMBER: 30,988
? REFERENCE/DOCKET NUMBER: 2803-0002.02
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (202) 887-1500
? TELEFAX: (202) 887-0763
? TELEX: 90-4030
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 437 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: both
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: -40..397
? OTHER INFORMATION: /note= "Same features apply from
? OTHER INFORMATION: SEQ ID NO:2"
? FEATURE:
? NAME/KEY: Protein
? LOCATION: 1..139
? OTHER INFORMATION: /note= "Factor Xa - Light Chain"
? FEATURE:
? NAME/KEY: Peptide
? LOCATION: -40..0
? OTHER INFORMATION: /note= "Pre-Pro leader sequence"
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: -17
? OTHER INFORMATION: /note= "Location of Intron A"
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: (37-38)
? OTHER INFORMATION: /note= "Location of Intron B"
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: 46
? OTHER INFORMATION: /note= "Location of Intron C"
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: 63
? OTHER INFORMATION: /note= "An amino acid represented
? OTHER INFORMATION: by the greek letter Beta"
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: 84
? OTHER INFORMATION: /note= "Location of Intron D"
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: 198
? OTHER INFORMATION: /note= "Location of Intron G"
? FEATURE:
? NAME/KEY: Disulfide-bond
? LOCATION: group(17..22, 50..61, 55..70, 72..81, 89..100, 96
? LOCATION: ..109, 111..124, 132..251, 150..155, 170..186,
? LOCATION: 299..313, 324..352)
US-08-487-037-3

Query Match 57.8%; Score 111; DB 1; Length 437;
Best Local Similarity 40.9%; Pred. No. 2,7e-11;
Matches 18; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLLXLRPGSLXKCKXXQCSFXKXRIFKDAXRTKLFWISY 44
Db 41 ANSFLTTMKKGHLTRTCMTTCSYTAIVTDSKNTFNWXY 84

RESULT 34
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OTHER INFORMATION: /note= "Pre-Pro leader sequence"
FEATURE:
NAME/KEY: Protein
LOCATION: 1..139
OTHER INFORMATION: /note= "Factor Xa- Light chain"
FEATURE:
NAME/KEY: Peptide
LOCATION: 143..194
OTHER INFORMATION: /note= "Activation Peptide"
FEATURE:
NAME/KEY: Protein
LOCATION: 195..448
OTHER INFORMATION: /note= "Factor Xa-Heavy Chain"
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: group(17..22, 50..61, 55..70, 72..81, 89..100, 96
LOCATION: ..109, 111..124, 132..302, 201..206, 221..237,
LOCATION: 350..364, 375..403)
US-08-487-037-1

Query Match          57.8%; Score 111; DB 1; Length 488;
Best Local Similarity 40.9%; Pred. No. 3e-11;
Matches 18; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

OY      1 ANAFLLXLRPGSLARXCXXKOCSEFYXAXRIFRDARTKLEFMYIS 44
        ||::||::| | | | | | | | | | | | | | | | | | | |
Db       41 ANSFLTMKKGHLFRCTMTTCSYTTRATVFDSDKTFTFNKY 84

RESULT 35
US-08-955-636-2
Sequence 2, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Nelstuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
FILE REFERENCE: POLYPEPTIDES
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 44
TYPE: PRT
ORGANISM: Bos taurus
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa-gamma carboxylutamic acid or glutamic acid
US-08-955-636-2

Query Match          54.2%; Score 104; DB 3; Length 44;
Best Local Similarity 68.2%; Pred. No. 3.8e-11;
Matches 30; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

OY      1 ANAFLLXLRPGSLARXCXXKOCSEFYXAXRIFRDARTKLEFMYIS 44
        ||::||::||::||::||::||::||::||::||::||::||::||
Db       1 ANSFLXLRPGNVRXCXYCXFXARXIFONTXDMAFMSFY 44

RESULT 36
US-08-295-411-3
Sequence 3, Application US/08295411
Patent No. 5679639
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Westers, Rolf M.
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
```

```
;
;
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Office of Patent Counsel, The Scripps
;   ADDRESSEE: Research Institute
;   STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
;   CITY: La Jolla
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 92037
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/295,411
;   FILING DATE: 22-AUG-1994
;   CLASSIFICATION: 530
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/793,989
;   FILING DATE: 18-NOV-1991
;   CLASSIFICATION: 530
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Fitting, Thomas
;   REGISTRATION NUMBER: 34,163
;   REFERENCE/DOCKET NUMBER: TSRI263.0C1
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 619-554-2937
;   TELEFAX: 619-554-6312
;   INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 448 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   FEATURE:
;   NAME/KEY: Region
;   LOCATION: 1..139
;   OTHER INFORMATION: /note= "Factor X Light Chain"
;   FEATURE:
;   NAME/KEY: Region
;   LOCATION: 140..142
;   OTHER INFORMATION: /note= "Factor X Connecting
;   OTHER INFORMATION: Tripeptide"
;   FEATURE:
;   NAME/KEY: Region
;   LOCATION: 143..448
;   OTHER INFORMATION: /note= "Factor X Heavy Chain"
;
US-08-295-411-3

Query Match      53.1%; Score 102; DB 1; Length 448;
Best Local Similarity 40.9%; Pred. No. 9.9e-10;
Matches 18; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

Qy      1 ANAFLLXLRPGSLRXKCKXXQCSFYXARXIFKDXARTKLPWISY 44
      11:111::| | | | | | | | | | | | | | | | | | | |
Db      1 ANSFLFMKKGHLEKCMETCSYEAREVFEEDSDKTNEFMNKY 44

RESULT 37
US-08-955-471-3
; Sequence 3, Application US/08955471
; Patent No. 5968751
; GENERAL INFORMATION:
; APPLICANT: Griflin, John H.
; APPLICANT: Masters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
```

```
;
;
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Office of Patent Counsel, The Scripps
;   ADDRESSEE: Research Institute
;   STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
;   CITY: La Jolla
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 92037
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/955,471
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/295,411
;   FILING DATE:
;   CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Fitting, Thomas
;   REGISTRATION NUMBER: 34,163
;   REFERENCE/DOCKET NUMBER: TSRI263.0C1
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 619-554-2937
;   TELEFAX: 619-554-6312
;   INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 448 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   FEATURE:
;   NAME/KEY: Region
;   LOCATION: 1..139
;   OTHER INFORMATION: /note= "Factor X Light Chain"
;   FEATURE:
;   NAME/KEY: Region
;   LOCATION: 140..142
;   OTHER INFORMATION: /note= "Factor X Connecting
;   OTHER INFORMATION: Tripeptide"
;   FEATURE:
;   NAME/KEY: Region
;   LOCATION: 143..448
;   OTHER INFORMATION: /note= "Factor X Heavy Chain"
;
US-08-955-471-3

Query Match      53.1%; Score 102; DB 2; Length 448;
Best Local Similarity 40.9%; Pred. No. 9.9e-10;
Matches 18; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

Qy      1 ANAFLLXLRPGSLRXKCKXXQCSFYXARXIFKDXARTKLPWISY 44
      11:111::| | | | | | | | | | | | | | | | | | | |
Db      1 ANSFLFMKKGHLEKCMETCSYEAREVFEEDSDKTNEFMNKY 44

RESULT 38
PCT-US92-10068-1
; Sequence 1, Application PC/TUS9210068
; GENERAL INFORMATION:
; APPLICANT: Altieri, Dario C
; APPLICANT: Edgington, Thomas S
; APPLICANT: Fair, Daryl S
; TITLE OF INVENTION: Factor X-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Inflammation
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESS: Research Institute
STREET: 10666 North Torrey Pines Road
City: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10068
FILING DATE: 19921120
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/798,221
FILING DATE: 22-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: SCR1221P
REFERENCE/DOCKET NUMBER: 34,163
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..139
OTHER INFORMATION: /note= "Factor X Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 140..142
OTHER INFORMATION: /note= "Factor X Connecting
Tripeptide"
FEATURE:
NAME/KEY: Region
LOCATION: 143..448
OTHER INFORMATION: /note= "Factor X Heavy Chain"
PCT-US92-10068-1
Query Match 53.1%; Score 102; DB 5; Length 448;
Best Local Similarity 40.9%; Pred. No. 9,9e-10;
Matches 18; Conservative 8; Mismatches 18; Indels 0; Gaps 0;
Qy 1 ANAFLXLRPGSLRXKCKXXOCSPFXARXIPKDXRRLFWISY 44
Db 1 ANSFLKMKKGHLRECMETCSTYEAREVPEDSKTNFVNKY 44
RESULT 39
PCT-US92-10242-3
Sequence 3, Application PC/TUS9210242
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESS: Research Institute
STREET: 10666 North Torrey Pines Road, TPC 8

CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10242
FILING DATE: 19921118
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR0472P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..139
OTHER INFORMATION: /note= "Factor X Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 140..142
OTHER INFORMATION: /note= "Factor X Connecting
Tripeptide"
FEATURE:
NAME/KEY: Region
LOCATION: 143..448
OTHER INFORMATION: /note= "Factor X Heavy Chain"
PCT-US92-10242-3
Query Match 53.1%; Score 102; DB 5; Length 448;
Best Local Similarity 40.9%; Pred. No. 9,9e-10;
Matches 18; Conservative 8; Mismatches 18; Indels 0; Gaps 0;
Qy 1 ANAFLXLRPGSLRXKCKXXOCSPFXARXIPKDXRRLFWISY 44
Db 1 ANSFLKMKKGHLRECMETCSTYEAREVPEDSKTNFVNKY 44
RESULT 40
US-08-955-636-18
Sequence 18, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Neilsen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 18
LENGTH: 44
TYPE: PRT
ORGANISM: Bos taurus

```
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid
US-08-955-636-18
```

```
Query Match          52.6%; Score 101; DB 3; Length 44;
Best Local Similarity 65.9%; Pred. No. 1.3e-10;
Matches 29; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
```

```
QY 1 ANAFLLXLRPGSLRXCKXXQCSFXAXRIFKDXRKLFWISY 44
||:||||:|:||||| || |||||:| ||:| ||
Db 1 ANSEFLXVKGQNLXRCLEACSLXARXVFEADQTDERWSKY 44
```

```
RESULT 41
US-08-469-486-53
; Sequence 53, Application US/08469486
; Patent No. 5739281
; GENERAL INFORMATION:
; APPLICANT: Thoegeersen, Hans Christian
; APPLICANT: Holteit, Thor Las
; APPLICANT: Elzerodt, Michael
; TITLE OF INVENTION: Improved method for the refolding of
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,486
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/192,060
; FILING DATE: February 4, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06363/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 542 5070
; TELEFAX: 617 542 8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-469-486-53
```

```
Query Match          52.6%; Score 101; DB 1; Length 487;
Best Local Similarity 43.2%; Pred. No. 1.6e-09;
Matches 19; Conservative 7; Mismatches 18; Indels 0; Gaps 0;
```

```
QY 1 ANAFLLXLRPGSLRXCKXXQCSFXAXRIFKDXRKLFWISY 44
||:||||:|:||||| || |||||:| ||:| ||
Db 41 ANSEFLXVKGQNLXRCLEACSLXARXVFEADQTDERWSKY 84
```

```
RESULT 42
US-08-469-658-53
; Sequence 53, Application US/08469658
; Patent No. 5917018
```

```
GENERAL INFORMATION:
APPLICANT: Thoegeersen, Hans Christian
APPLICANT: Holteit, Thor Las
APPLICANT: Elzerodt, Michael
TITLE OF INVENTION: IMPROVED METHOD FOR THE REFOOLDING OF
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02110-2804
```

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,658
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
```

```
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06363/002002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070
TELEFAX: 617 542 8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-469-658-53
```

```
Query Match          52.6%; Score 101; DB 2; Length 487;
Best Local Similarity 43.2%; Pred. No. 1.6e-09;
Matches 19; Conservative 7; Mismatches 18; Indels 0; Gaps 0;
```

```
QY 1 ANAFLLXLRPGSLRXCKXXQCSFXAXRIFKDXRKLFWISY 44
||:||||:|:||||| || |||||:| ||:| ||
Db 41 ANSEFLXVKGQNLXRCLEACSLXARXVFEADQTDERWSKY 84
```

```
RESULT 43
US-08-469-486-2
; Sequence 2, Application US/08469486
; Patent No. 5739281
; GENERAL INFORMATION:
; APPLICANT: Thoegeersen, Hans Christian
; APPLICANT: Holteit, Thor Las
; APPLICANT: Elzerodt, Michael
; TITLE OF INVENTION: Improved method for the refolding of
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
```



```
; LENGTH: 41 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homosapiens
; FEATURE:
; OTHER INFORMATION: Xaa in the sequence is
; OTHER INFORMATION: -carboxyglutamic acid
US-08-229-280-2
```

```
Query Match 51.0%; Score 98; DB 1; Length 41;
Best Local Similarity 63.4%; Pred. No. 3.9e-10;
Matches 26; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
```

```
Oy 1 ANAFLLXLRPGSLXRCCKXXQCSFYXARXIFKDXARTKLEW 41
||:||||:| ||||| ||||:||||:| ||: ||
Db 1 ANSFLXXMKKGHLXRCMXXTCSYXXARXVFXDSDKTNXFW 41
```

```
RESULT 46
US-08-955-636-24
; Sequence 24, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Neissestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-24
```

```
Query Match 50.0%; Score 96; DB 3; Length 44;
Best Local Similarity 70.7%; Pred. No. 9.2e-10;
Matches 29; Conservative 3; Mismatches 9; Indels 0; Gaps 0;
```

```
Oy 1 ANAFLLXLRPGSLXRCCKXXQCSFYXARXIFKDXARTKLEW 41
||:||||| ||||| || ||||:||||:| ||
Db 1 ANSFLXXLRGSLXRCCKXIXICDFXAKXIFEDVDTLAEW 41
```

```
RESULT 47
US-08-955-636-35
; Sequence 35, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Neissestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
```

```
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-35
```

```
Query Match 50.0%; Score 96; DB 3; Length 44;
Best Local Similarity 70.7%; Pred. No. 9.2e-10;
Matches 29; Conservative 3; Mismatches 9; Indels 0; Gaps 0;
```

```
Oy 1 ANAFLLXLRPGSLXRCCKXXQCSFYXARXIFKDXARTKLEW 41
||:||||| ||||| || ||||:||||:| ||
Db 1 ANSFLXXLRGSLXRCCKXIXICDFXAKXIFEDVDTLAEW 41
```

```
RESULT 48
US-08-955-636-23
; Sequence 23, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Neissestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-23
```

```
Query Match 49.5%; Score 95; DB 3; Length 44;
Best Local Similarity 65.9%; Pred. No. 1.4e-09;
Matches 29; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
```

```
Oy 1 ANAFLLXLRPGSLXRCCKXXQCSFYXARXIFKDXARTKLEWISY 44
||:||||| ||||| || ||||:||||:| ||
Db 1 ANSFLXXLRHGNVXRCSSXVCFXARXIFQNTXDTMAEWSFY 44
```

```
RESULT 49
US-08-955-636-20
; Sequence 20, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Neissestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-20
```

```
Query Match 46.9%; Score 90; DB 3; Length 44;
Best Local Similarity 68.3%; Pred. No. 1e-08;
```

Matches 28; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANAFLXXLRPGSLXRCXXQCSPFXAXRIFKDXARTKLEW 41
||:||||| ||||| || ||||:||||:| ||
Db 1 ANSFLXXLRQSSLXRCXCIXICDPFXAKXIFEDVDLTFW 41

RESULT 50
US-08-955-636-21
; Sequence 21, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelstuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid
US-08-955-636-21

Query Match 46.9%; Score 90; DB 3; Length 44;
Best Local Similarity 68.3%; Pred. No. 1e-08;
Matches 28; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANAFLXXLRPGSLXRCXXQCSPFXAXRIFKDXARTKLEW 41
||:||||| ||||| || ||||:||||:| ||
Db 1 ANSFLXXLRQSSLXRCXCIXICDPFXAKXIFEDVDLTFW 41

Search completed: August 30, 2002, 15:31:14
Job time: 6239 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2002, 13:55:25 : Search time 77.69 Seconds
(Without alignments)
54.421 Million cell updates/sec

Title: US-09-302-239-3

Sequence: 1 ANAFLXLRPGLXRXCKXX.....XXARXIFKDAKXKLEWISY 44

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database : PIR-71.*

1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	172	89.6	466	1 KFH07	coagulation factor
2	138	71.9	443	2 I46932	coagulation factor
3	123	64.1	407	1 KFB07	coagulation factor
4	109	56.8	461	1 JX0210	protein C (activat
5	104	54.2	456	1 KXBO	protein C (activat
6	102	53.1	488	1 EXHU	coagulation factor
7	101	52.6	492	1 EXBO	coagulation factor
8	100	52.1	461	1 S18994	protein C (activat
9	96	50.0	482	1 EXRT	coagulation factor
10	91	47.4	475	1 EXCH	coagulation factor
11	86	44.8	416	1 KFB0	coagulation factor
12	84	43.8	461	1 KXHU	protein C (activat
13	83	43.2	461	1 KFHU	coagulation factor
14	83	43.2	622	1 TBHU	thrombin (EC 3.4.2
15	79	41.1	617	2 S10511	thrombin (EC 3.4.2
16	78	40.6	618	2 A35827	thrombin (EC 3.4.2
17	78	40.6	452	1 A30351	coagulation factor
18	78	40.6	459	2 J00419	coagulation factor
19	71.5	37.2	576	2 G96763	probable MAP kinase
20	69	35.9	642	2 S53433	plasma protein S p
21	66	34.4	675	1 KXBOS	plasma protein S p
22	65.5	34.1	594	2 D84859	probable MAP kinase
23	65.5	34.1	603	2 G96575	probable MAP kinase
24	64	33.3	642	2 S53434	plasma protein S p
25	64	33.3	646	2 S38819	plasma protein S p
26	64	33.3	676	1 KKHUS	plasma protein S p
27	63	32.8	396	1 KXBOZ	thrombin (EC 3.4.2
28	63	32.8	675	1 KXRTS	plasma protein S p

30	58	30.2	422	1 KKHU2	plasma protein 2 p
31	56	29.2	675	1 KXMS5	plasma protein S p
32	55	28.6	673	2 A48089	growth arrest-spec
33	53	27.6	674	2 I55476	growth potentialin
34	53	27.6	678	2 B48089	growth arrest-spec
35	51.5	26.8	516	2 H84424	probable MAP kinase
36	46	24.0	543	2 H84724	probable ARI-like
37	45	23.4	245	2 AH0926	hypothetical prote
38	45	23.4	879	2 S55864	hypothetical prote
39	44	22.9	422	2 T39306	mitogen-activated
40	43.5	22.7	319	2 T15137	hypothetical prote
41	43.5	22.7	367	2 B56598	endothelial kinase
42	43.5	22.7	385	2 T15221	hypothetical prote
43	43.5	22.7	1298	2 A48999	protein-tyrosine k
44	43.5	22.7	1363	2 I58375	protein-tyrosine k
45	43.5	22.7	1379	2 JC4954	vascular endotheli
46	43	22.4	211	2 D96996	uncharacterized lo
47	43	22.4	402	2 C72226	hypothetical prote
48	43	22.4	455	2 C83494	probable 2-isoprop
49	42.5	22.1	105	2 PH0976	ig heavy chain V r
50	42.5	22.1	322	2 T20272	hypothetical prote

ALIGNMENTS

RESULT 1
KFH07
coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1989 #sequence-revision 19-May-1994 #text-change 08-Dec-2000
C:Accession: A28322; A28819; A31186; B31186; S65524
R:O'Hara, P.J.; Grant, F.J.; Haldeman, B.A.; Gray, C.L.; Insley, M.Y.; Hagen, F.S.; M
Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987
A:Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-dep
A:Accession: A28322; MUID:87260948
A:Molecule type: DNA
A:Residues: 1-466 <OHAG>
A:Cross-references: GB:J02933; NID:g180333; PIDN:AAA51983.1; PID:g180334
R:Hagen, F.S.; Gray, C.L.; O'Hara, P.J.; Grant, F.J.; Saarl, G.C.; Woodbury, R.G.; Hart
Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986
A:Title: Characterization of a cDNA coding for human factor VII.
A:Reference number: A28819; MUID:86205965
A:Accession: A23819
A:Molecule type: mRNA
A:Residues: 1-466 <RHAG>
A:Cross-references: GB:M1232; NID:g182799; PIDN:AAA8040.1; PID:g182801
R:Thim, L.; Bjorn, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen,
Biochemistry 27, 7785-7793, 1988
A:Title: Amino acid sequence and posttranslational modifications of human factor VII-
A:Reference number: A90539; MUID:89088153
A:Accession: A31186
A:Molecule type: Protein
A:Residues: 61-212 <THI>
A:Accession: B31186
A:Molecule type: Protein
A:Residues: 213-466 <TH2>
R:Bjorn, S.; Foster, D.C.; Thim, L.; Wlberg, F.C.; Christensen, M.; Komiyama, Y.; Pe
J. Biol. Chem. 266, 11051-11057, 1991
A:Title: Human plasma and recombinant factor VII. Characterization of O-glycosylation
A:Reference number: A40529; MUID:91250411
A:Contents: annotation; carbohydrate binding sites
R:Persson, E.; Petersen, L.C.
Eur. J. Biochem. 234, 293-300, 1995
A:Title: Structurally and functionally distinct Ca(2+) binding sites in the gamma-car
A:Reference number: S63524; MUID:96096752
A:Accession: S63524
A:Molecule type: Protein
A:Residues: 61-65;99-103;105-109;213-217;308-312 <PER>
C:Genetics:
A:Gene: GDB:F7
A:Cross-references: GDB:119897; OMIM:227500

A:Map position: 13q34-13q34
 A:Functions: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1
 C:Function:
 A:Description: catalyzes the proteolytic activation of coagulation factor X in the presence of calcium and tissue factor
 A:Pathway: blood coagulation extrinsic pathway
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamic acid
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-60/Domain: propeptide #status predicted <PRO>
 F:45-104/Domain: Gla domain homology <GLA>
 F:61-212/Product: coagulation factor VIIa light chain #status experimental <MA1>
 F:110-141/Domain: EGF homology <EG1>
 F:151-187/Domain: EGF homology <EG2>
 F:213-466/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
 F:213-447/Domain: trypsin homology <TRY>
 F:66/67,74,76,79,80,85,86,95/Modified site: gamma-carboxylglutamic acid (Glu) #status experimental
 F:77-82,110-121,115-130,132-141,151-162,158-172,174-187,195-322,219-224,238-254,370-389, F:112,120/Binding site: carbohydrate (Ser) (covalent) #status experimental
 F:123/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status absent
 F:205,382/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:212-213/Cleavage site: Arg-11e (coagulation factor XIIIa) #status experimental
 F:253,302,404/Active site: His, Asp, Ser #status predicted
 F:350-351/Cleavage site: Arg-Clj (coagulation factor Xa) #status predicted

Query Match 89.6%; Score 172; DB 1; Length 466;
 Best Local Similarity 77.3%; Pred. No. 3e-21;
 Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANAFELXLRPGSLXRXCKXKQCSFXXARXFFKAXRKLFWISY 44
 Db 61 ANAFELRLPGSLERCKEKCQSFEEARLTKDAERTKLEWISY 104

RESULT 2
 146932
 coagulation factor VII - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 12-Feb-1999
 C:Accession: I46932
 R:Brothers, A.B.; Clarke, B.J.; Sheffield, W.P.; Blajchman, M.A.
 Thromb. Res. 69, 231-238, 1993
 A:Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII
 A:Reference number: I46932; MUID:93190306
 A:Accession: I46932
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-443 <BRO>
 A:Cross-references: GB:556300; NID:9266294; PID:9266295
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 F:24-83/Domain: Gla domain homology <GLA>
 F:89-120/Domain: EGF homology <EG1>
 F:130-166/Domain: EGF homology <EG2>
 F:192-425/Domain: trypsin homology <TRY>

Query Match 71.9%; Score 138; DB 2; Length 443;
 Best Local Similarity 59.1%; Pred. No. 1.7e-15;
 Matches 26; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY 1 ANAFELXLRPGSLXRXCKXKQCSFXXARXFFKAXRKLFWISY 44
 Db 40 ANSFELRLPGSLERCKEKCQSFEEARLTKDAERTKLEWISY 83

RESULT 3
 KRB07
 coagulation factor VIIa (EC 3.4.21.21) - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 21-May-1990 #sequence_revision 23-Mar-1995 #text_change 16-Jul-1999
 C:Accession: A31979; C02074
 R:Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, S.

J. Biol. Chem. 263, 14868-14877, 1988
 A:Title: Bovine factor VII: its purification and complete amino acid sequence.
 A:Reference number: A31979; MUID:89008362
 A:Accession: A31979
 A:Molecule type: protein
 A:Residues: 1407 <TKA>
 R:McMullen, B.A.; Fujikawa, K.; Kistel, W.
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983
 A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood
 A:Reference number: A20274; MUID:83308813
 A:Accession: C20274
 A:Molecule type: protein
 A:Residues: 58-62, 'X', 64-68 <KCM>
 A:Note: the residue designated 'X' was determined to be hydroxyaspartic acid
 R:Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga, S.
 J. Biochem. 104, 867-868, 1988
 A:Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood
 A:Reference number: A44556; MUID:89213999
 A:Contents: annotation
 A:Note: structure and location of covalently bound carbohydrate
 C:Function:
 A:Description: catalyzes the proteolytic activation of coagulation factor X in the presence of calcium and tissue factor
 A:Pathway: blood coagulation extrinsic pathway
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamic acid
 F:1-152/Product: coagulation factor VIIa light chain #status experimental <MA1>
 F:1-44/Domain: Gla domain homology (fragment) <GLA>
 F:50-81/Domain: EGF homology <EG1>
 F:91-127/Domain: EGF homology <EG2>
 F:153-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
 F:153-387/Domain: trypsin homology <TRY>
 F:6,7,14,16,19,20,25,26,29,34,35/Modified site: gamma-carboxylglutamic acid (Glu) #status experimental
 F:17-22,50-61,55-70,72-81,91-102,98-112,114-127,135-262,159-164,178-194,310-329,340-352/Binding site: carbohydrate (Ser) (covalent) #status experimental
 F:63/Modified site: erythro-beta-hydroxyaspartic acid (Asp) (partial) #status experimental
 F:143,203/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:152-153/Cleavage site: Arg-11e (coagulation factor XIIIa) #status experimental
 F:193,242,344/Active site: His, Asp, Ser #status predicted
 F:290-291/Cleavage site: Arg-Clj (coagulation factor Xa) #status experimental

Query Match 64.1%; Score 123; DB 1; Length 407;
 Best Local Similarity 52.3%; Pred. No. 5.7e-13;
 Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANAFELXLRPGSLXRXCKXKQCSFXXARXFFKAXRKLFWISY 44
 Db 1 ANSFELRLPGSLERCKEKCQSFEEARLTKDAERTKLEWISY 44

RESULT 4
 JX0210
 protein C (activated) (EC 3.4.21.69) precursor - mouse
 N:Alternate names: Vitamin K-dependent serine proteinase
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
 C:Accession: JX0210
 R:Trada, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.
 J. Biochem. 111, 491-495, 1992
 A:Title: Isolation and characterization of a mouse protein C cDNA.
 A:Reference number: JX0210; MUID:92316897
 A:Accession: JX0210
 A:Molecule type: mRNA
 A:Residues: 1-461 <TRAD>
 A:Cross-references: GB:D10445; NID:9220385; PID:NBA01235.1; PID:9220386
 A:Experimental source: liver
 C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that
 S:
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamic acid
 F:1-33/Domain: signal sequence #status predicted <SIG>
 F:27-85/Domain: Gla domain homology <GLA>

F:34-41/Domain: propeptide #status predicted <PRO>
F:42-196/Domain: light chain #status predicted <PRC>
F:47-196/Domain: heavy chain #status predicted <PCL>
F:91-110/Domain: EGF homology <EG1>
F:139-174/Domain: EGF homology <EG2>
F:199-661/Domain: heavy chain #status predicted <PCH>
F:199-211/Domain: activation peptide #status predicted <ACT>
F:212-461/Product: vitamin K-dependent serine proteinase #status predicted <VIT>
F:212-445/Domain: trypsin homology <TRY>
F:47-48,55-57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status
F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F:121-130,135-150,146-159,161-174,182-319,238-254,373-387,398-426/Disulfide Bonds: #stat
F:214,390,355/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:253,299,402/Active site: His, Asp, Ser #status predicted

Query Match 56.8%; Score 109; DB 1; Length 461;
Best Local Similarity 47.7%; Pred. No. 1.1e-10;
Matches 21; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

1 ANAFLLXLRPGSLKRXCKXKXCSFXXARKXIFKDAKRTLFPMISY 44
Db 42 ANSFLELRPGSLRECEMEICDEFAOEIFQWEDTLAFWIKY 85

RESULT 5

KXBO
protein C (activated) (EC 3.4.21.69) precursor - bovine (fragment)
N:Alternate names: autoproteolysin IIA; Plasma protein C
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Nov-1980 #sequence-revision 17-Mar-1987 #text-change 16-Jul-1999
C:Accession: A26250; A18385; A18386; A00928
R:Long, G.L.; Balagaje, R.M.; MacCullivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 81, 5653-5656, 1984
A:Title: Cloning and sequence of liver cDNA coding for bovine protein C.
A:Reference number: A26250; MUID:85014826
A:Accession: A26250
A:Molecule type: mRNA
A:Residues: 1-456 <ION>
R:Fernlund, P.; Stenflo, J.
J. Biol. Chem. 257, 12170-12179, 1982
A:Title: Amino acid sequence of the light chain of bovine protein C.
A:Reference number: A18385; MUID:83007325
A:Accession: A18385
A:Molecule type: protein
A:Residues: 40-194 <PER>
A:Note: 82-Lys was also found
R:Drakenberg, T.; Fernlund, P.; Roepstorff, P.; Stenflo, J.
Proc. Natl. Acad. Sci. U.S.A. 80, 1802-1806, 1983
A:Title: beta-Hydroxyaspartic acid in vitamin K-dependent protein C.
A:Reference number: A19316; MUID:83169769
A:Contents: annotation; revision to residue 110
R:Stenflo, J.; Fernlund, P.
J. Biol. Chem. 257, 12180-12190, 1982
A:Title: Amino acid sequence of the heavy chain of bovine protein C.
A:Reference number: A18386; MUID:83007326
A:Accession: A18386
A:Molecule type: Protein
A:Residues: 197-454, 'PV' <STE>
R:Esmon, N.L.; Debault, L.E.; Esmon, C.T.
J. Biol. Chem. 258, 5548-5553, 1983
A:Title: Proteolytic formation and properties of gamma-carboxyglutamic acid-domainless F
A:Reference number: A37541; MUID:83213513
A:Contents: annotation; activation; calcium binding
R:Johnson, A.E.; Esmon, N.L.; Lane, T.M.; Esmon, C.T.
J. Biol. Chem. 258, 5554-5560, 1983
A:Title: Structural changes required for activation of protein C are induced by Ca2+ but
A:Reference number: A37542; MUID:83213514
A:Contents: annotation; activation; calcium binding
C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re
s.
C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is c
bin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this react

C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with s
cognition of the thrombin-thrombomodulin complex.
C:Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vita
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol
C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium bind
F:1-29/Domain: signal sequence (fragment) #status predicted <SIG>
F:24-83/Domain: Gla domain homology <GLA>
F:30-39/Domain: propeptide #status predicted <PRO>
F:40-194/Product: protein C light chain #status experimental <LCH>
F:98-128/Domain: EGF homology <EG1>
F:137-112/Domain: EGF homology <EG2>
F:197-456/Product: protein C heavy chain #status experimental <HCH>
F:197-210/Domain: activation peptide #status experimental <APT>
F:211-440/Domain: trypsin homology <TRY>
F:45,46,53,55,58,59,62,64,65,68,74/Modified site: gamma-carboxyglutamic acid (Glu) #s
F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F:119-128,137-148,144-157,159-172,180-318,237-253,368-382,393-421/Disulfide Bonds: #s
F:136,289,350/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:252,298,397/Active site: His, Asp, Ser #status predicted
F:366/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 54.2%; Score 104; DB 1; Length 456;
Best Local Similarity 45.5%; Pred. No. 1.1e-09;
Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

1 ANAFLLXLRPGSLKRXCKXKXCSFXXARKXIFKDAKRTLFPMISY 44
Db 40 ANSFLELRPGSLNVERECSEVECFEAREIFQWEDTLAFWISFY 83

RESULT 6

EXHU
coagulation factor Xa (EC 3.4.21.6) precursor [validated] - human
N:Alternate names: Stuart factor
C:Species: Homo sapiens (man)
C:Date: 15-Nov-1984 #sequence-revision 02-May-1994 #text-change 08-Dec-2000
C:Accession: A24478; J00917; A42485; A25853; A22208; A21284; A20362; S59415; I54051;
R:Leytus, S.P.; Foster, D.C.; Kurachi, K.; Davie, E.W.
Biochemistry 25, 5098-5102, 1986
A:Title: Gene for human Factor X: a blood coagulation factor whose gene organization
A:Reference number: A24478; MUID:87026600
A:Accession: A24478
A:Molecule type: DNA
A:Residues: 1-488 <LEV>
A:Cross-references: GB:L29433; GB:M14327; NID:q459609; PIDN:AAA52764.1; PID:g182831
R:Messier, T.L.; Pittman, D.D.; Long, G.L.; Kaufman, R.J.; Church, W.R.
Gene 99, 291-294, 1991
A:Title: Cloning and expression in COS-1 cells of a full-length cDNA encoding human c
A:Accession: J00917; MUID:91216473
A:Molecule type: mRNA
A:Residues: 1-488 <MES>
A:Cross-references: GB:M57285; NID:g182389; PIDN:AAA52421.1; PID:g182390
R:Mao, C.H.; Leytus, S.P.; Chung, D.W.; Davie, E.W.
J. Biol. Chem. 267, 7395-7401, 1992
A:Title: Liver-specific expression of the gene coding for human factor X, a blood coa
A:Reference number: A42485; MUID:92218390
A:Accession: A42485
A:Molecule type: DNA
A:Residues: 1-15 <MIA>
A:Experimental source: liver
A:Note: Sequence extracted from NCBI backbone (NCBI:93780, NCBIP:93787)
R:Kaul, R.K.; Hildebrand, B.; Roberts, S.; Jagadeeswaran, P.
Gene 41, 311-314, 1986
A:Title: Isolation and characterization of human blood-coagulation factor X cDNA.
A:Reference number: A25853; MUID:86221713
A:Accession: A25853
A:Molecule type: mRNA
A:Residues: 19-284, 'E', 289-488 <KAU>
A:Cross-references: GB:M22613; NID:g180335; PIDN:AAA51984.1; PID:g180336
R:Fung, M.R.; Hay, C.W.; MacCullivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985

A:Title: Characterization of an almost full-length cDNA coding for human blood coagulation factor X.
A:Reference number: A22208; MUID:85216545
A:Accession: A22208
A:Molecule type: mRNA
A:Residues: 13-441; 'S', 443-488 <FNU>
A:Cross-references: GB:K03194; NID:g182840; PIDN:AAA52490.1; PID:g182841
R:Kleytus, S.P.; Chung, D.W.; Kistiel, W.; Kurechi, K.; Dave, E.W.
Proc. Natl. Acad. Sci. U.S.A. 81, 3699-3702, 1984
A:Title: Characterization of a cDNA coding for human factor X.
A:Reference number: A21284; MUID:84222026
A:Accession: A21284
A:Molecule type: mRNA
A:Residues: 13-284; 'E', 289-488 <LE2>
A:Cross-references: GB:K01886
R:McMullen, B.A.; Fujikawa, K.; Kistiel, W.; Sasagawa, T.; Howald, W.N.; Kwa, E.Y.; Weiss
Biochemistry 22, 2875-2884, 1983
A:Title: Complete amino acid sequence of the light chain of human blood coagulation factor X.
A:Reference number: A20362; MUID:83257207
A:Accession: A20362
A:Molecule type: protein
A:Residues: 41-179 <MCM>
R:Inoue, K.; Morita, T.
Eur. J. Biochem. 218, 153-163, 1993
A:Title: Identification of O-linked oligosaccharide chains in the activation peptides of human blood coagulation factor X.
A:Reference number: S39414; MUID:94062825
A:Accession: S39415
A:Molecule type: protein
A:Residues: 183-234 <INO>
A:Note: glycosylation sites
A:Note: Identification and characterization of beta-hydroxyaspartic acid
R:Jugadeeswarar, P.; Reddy, S.V.; Rao, K.J.; Hamsabhusanam, K.; Lyman, G.
Gene 84, 517-519, 1988
A:Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human blood coagulation factor X.
A:Reference number: I54051; MUID:90128299
A:Accession: I54051
A>Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-23 <RES>
A:Cross-references: GB:M33297; NID:g183860; PIDN:AAA52636.1; PID:g553330
R:Padmanabhan, K.; Padmanabhan, K.P.; Tullinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Blad
J. Mol. Biol. 232, 947-966, 1993
A:Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.
A:Reference number: A49458; MUID:93360277
A:Contents: annotation; X-ray crystallography, 2.2 angstroms
C:Comment: The two chains held together by one disulfide bond are formed from a single-c
C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or
C:Genetics:
A:Gene: GDB:F10
A:Cross-references: GDB:119890; OMIM:227600
A:Map position: 13q34-13q34
A:Introns: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1
A:Note: deficiency of this factor causes Stuart disease
C:Function:
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
A:Pathway: blood coagulation
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamat
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-40/Domain: propeptide #status predicted <PRO>
F:25-84/Domain: Gla domain homology <GLA>
F:41-179/Product: coagulation factor X light chain #status experimental <LCH>
F:90-121/Domain: EGF homology <EGF>
F:129-164/Domain: EGF homology <EG2>
F:183-488/Product: coagulation factor X heavy chain #status experimental <HCH>
F:183-234/Domain: activation peptide #status experimental <APF>
F:235-488/Product: coagulation factor Xa heavy chain #status experimental <ACT>
F:235-462/Domain: trypsin homology <TRY>
F:46;47;54;56;59;60;65;66;69;72;79/Modified site: gamma-carboxylglutamic acid (Glu) #statu
F:57-62/Disulfide bonds: #status predicted
F:90-101;95-110;112-121;129-140;136-149;151-164;173-342;241-246;261-277;390-404;415-443;#statu
F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F:109/Binding site: carboxylate (Thr) (covalent) #status experimental
F:129;231/Binding site: carboxylate (Asn) (covalent) #status experimental
F:221;231/Binding site: carboxylate (Asn) (covalent) #status experimental

F:234-235/Cleavage site: Arg-116 (coagulation factor IXa, coagulation factor VIII) #3
F:276,322,419/Active site: His, Asp, Ser #status experimental

```
Query Match          53.1%   Score 102; DB 1; Length 488;
Best Local Similarity 40.9%   Pred. No. 2,5e-09;
Matches 18; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRPGSLKRXCKXOCSPFXARXIRPKDARKTLFWISY 44
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 41 ANSFLEEMKKGHLRECMEECTSYEARAREVEDSDKTNEFNKY 84

RESULT 7
EXBO
coagulation factor Xa (EC 3.4.21.6) precursor - bovine
N.Alternate names: Stuart factor
C.Species: Bos primigenius taurus (cattle)
C.Date: 24-Apr-1984 #sequence, revision 17-Mar-1987 #text, change 16-Jul-1999
C.Accession: A22867; A14997; A12030; A34412; S39414; A00925
R.Fung, M.R.; Campbell, R.M.; Macgillivray, T.A.
Nucleic Acids Res. 12, 4481-4492, 1984
A.Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containin
A.Reference number: A22867; MUID:84247315
A.Accession: A22867
A.Molecule type: mRNA
A.Residues: 1-487 <FUN>
A.Cross-references: GB:X00673; NID:g192; PIDN:CA25286.1; PID:g193
R.Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K.
Biochemistry 19, 659-667, 1980
A.Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).
A.Reference number: A14997; MUID:80130563
A.Accession: A14997
A.Molecule type: Protein
A.Residues: 41-102, 'N', 104-180 <ENF>
R.McMullen, B.A.; Fujikawa, K.; Kistel, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A.Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood
A.Reference number: A20274; MUID:83308813
A.Contents: annotation; revision to residue 103
R.Titani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.
Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975
A.Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.
A.Reference number: A12030; MUID:76053069
A.Accession: A12030
A.Molecule type: Protein
A.Residues: 183-292,294-295, 'GDE',299-334,336-348, 'AE',351-354,356-441, 'GRFG',446-492
A.Note: carboxyhydrate binding sites and disulfide bonds were determined
R.Persson, E.; Selander, M.; Linse, S.; Drakenberg, T.; Oehlin, A.K.; Stenflo, J.
J. Biol. Chem. 264, 16897-16904, 1989
A.Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epiderm
A.Reference number: A34412; MUID:89380326
A.Accession: A34412
A.Molecule type: Protein
A.Residues: 85-126 <PER>
A.Note: beta-hydroxyaspartic acid site
R.Inoue, K.; Morita, T.
Eur. J. Biochem. 218, 153-163, 1993
A.Title: Identification of O-linked oligosaccharide chains in the activation peptides
A.Reference number: S39414; MUID:94062825
A.Accession: S39414
A.Molecule type: Protein
A.Residues: 183-196,199-209,216-233 <INO>
A.Note: carboxyhydrate binding sites
R.Titani, K.; Hermanson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.
Biochemistry 11, 4899-4903, 1972
A.Title: Bovine factor X-1a (activated Stuart factor). Evidence of homology with mamm
A.Reference number: A12453; MUID:73053314
A.Contents: annotation; active site
R.Fujikawa, K.; Titani, K.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 72, 3358-3363, 1975
A.Title: Activation of bovine factor X (Stuart factor): conversion of factor Xaalpha
A.Reference number: A13504; MUID:76053121
```


F:64/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:158,168,173,261/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:222,270,366/Active site: His, Asp, Ser #status predicted

Query Match 44.8%; Score 86; DB 1; Length 416;
 Best Local Similarity 44.1%; Pred. No. 1.2e-06;
 Matches 15; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

RESULT 12

KXHD
 protein C (activated) (EC 3.4.21.69) precursor - human
 N:Alternate names: antithrombin IIA; plasma protein C
 C:Species: Homo sapiens (man)
 C:Date: 17-Mar-1987 #sequence,revision 17-Mar-1987 #text,change 16-Jul-1999
 C:Accession: A22331; A25426; A21781; A23789; A00927
 R:Poster, D.C.; Yoshitake, S.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985
 A:Title: The nucleotide sequence of the gene for human protein C.
 A:Reference number: A22331; MUID:85270390
 A:Accession: A22331
 A:Molecule type: DNA
 A:Residues: 1-461 <FOS1>
 A:Cross-references: GB:M1228; NID:g190333; PIDN:AAA60166.1; PID:g190334
 R:Plutsky, J.; Hoskins, J.A.; Long, G.L.; Crabtree, G.R.
 Proc. Natl. Acad. Sci. U.S.A. 83, 546-550, 1986
 A:Title: Evolution and organization of the human protein C gene.
 A:Reference number: A25426; MUID:86120978
 A:Accession: A25426
 A:Molecule type: DNA
 A:Residues: 1-445, 'L', 446-461 <PLU>
 A:Cross-references: GB:M12712; NID:g190330; PIDN:AAA60165.1; PID:g190332
 R:Foster, D.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 81, 4766-4770, 1984
 A:Title: Characterization of a cDNA coding for human protein C.
 A:Reference number: A21781; MUID:84272714
 A:Accession: A21781
 A:Molecule type: mRNA
 A:Residues: 'O', 107-461 <FOS2>
 A:Cross-references: GB:K02059; NID:g190322; PIDN:AAA60164.1; PID:g190323
 R:Beckmann, R.J.; Schmidt, R.J.; Santerre, R.F.; Plutsky, J.; Crabtree, G.R.; Long, G.L.
 Nucleic Acids Res. 13, 5233-5247, 1985
 A:Title: The structure and evolution of a 461 amino acid human protein C precursor and
 A:Reference number: A23789; MUID:85269639
 A:Accession: A23789
 A:Molecule type: mRNA
 A:Residues: 1-461 <BEC>
 A:Cross-references: GB:X02750; NID:g35689; PIDN:CAA26528.1; PID:g763120
 R:Meleisch, J.P.; Broze Jr., G.J.
 J. Biol. Chem. 265, 11397-11404, 1990
 A:Title: Beta protein C is not glycosylated at asparagine 329. The rate of translation
 A:Reference number: A44605; MUID:90293094
 A:Contents: annotation; carbohydrate binding sites; activation peptide
 A:Note: the alpha form of protein C is glycosylated at Asn-329, and the beta form is not
 J. Biol. Chem. 267, 5102-5107, 1992
 R:Haris, R.J.; Ling, V.T.; Spellman, M.W.
 A:Title: O-linked fucose is present in the first epidermal growth factor domain of factor
 A:Reference number: A44606; MUID:92184750
 A:Contents: annotation; beta-hydroxyaspartic acid
 C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that in
 ulation of factor Va is strongly enhanced by complexing with protein S. Protein C also
 C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is
 bin, which cleaves a dodecapeptide from the amino end of the heavy chain; this reaction,
 C:Genetics:

A:Gene: GDB:PROC
 A:Cross-references: GDB:120317; OMIM:176660
 A:Map position: 2q13-2q21
 A:Introns: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1

C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol
 C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium bind
 F:1-32/Domain: signal sequence #status predicted <SIG>
 F:27-86/Domain: Gla domain homology <GLA>
 F:33-42/Domain: propeptide #status predicted <PRO>
 F:43-197/Product: protein C light chain #status predicted <LCH>
 F:99-133/Domain: EGF homology <EG1>
 F:140-175/Domain: EGF homology <EG2>
 F:200-461/Product: protein C heavy chain #status predicted <HCH>
 F:200-211/Domain: activation peptide #status experimental <APT>
 F:212-445/Domain: trypsin homology <TRY>
 F:48,49,56,58,61,62,67,68,71/Modified site: gamma-carboxyglutamic acid (Glu) #status
 F:59-64,92-105,101-120,122-131,140-151,147-160,162-175,183-319,238-254,373-387,398-42
 F:106-111/Disulfide bonds: #status predicted
 F:110/Binding site: carbohydrate (Thr) (covalent) #status absent
 F:113/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:139,290,355/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:211-212/Cleavage site: Arg-Leu (thrombin) #status experimental
 F:253,299,402/Active site: His, Asp, Ser #status predicted
 F:371/Binding site: carbohydrate (Asn) (covalent) (partial) #status atypical

Query Match 43.8%; Score 84; DB 1; Length 461;
 Best Local Similarity 43.9%; Pred. No. 2.8e-06;
 Matches 18; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

RESULT 13

KFRU
 coagulation factor IXa (EC 3.4.21.22) precursor [validated] - human
 N:Alternate names: antihemophilic factor B; Christmas factor
 C:Species: Homo sapiens (man)
 C:Date: 17-Dec-1982 #sequence,revision 30-Jun-1987 #text,change 15-Sep-2000
 C:Accession: A00922; A37570; A30511; A32989; A22673; A21337; A37546; A30623; A60486;
 R:Yoshitake, S.; Schach, B.G.; Foster, D.C.; Davie, E.W.; Kurachi, K.
 Biochemistry 24, 3736-3750, 1985
 A:Title: Nucleotide sequence of the gene for human factor IX (antihemophilic factor B
 A:Reference number: A00922; MUID:86000558
 A:Accession: A00922
 A:Molecule type: DNA
 A:Residues: 1-461 <YOS>
 A:Cross-references: GB:K02402; NID:g182612; PIDN:AAB56620.1; PID:g182613
 R:Anson, D.S.; Choo, K.H.; Rees, D.J.G.; Giannelis, F.; Gould, K.; Huddleston, J.A.;
 EMBO J. 3, 1053-1060, 1984
 A:Title: The gene structure of human anti-hemophilic factor IX.
 A:Reference number: A37570; MUID:84236100
 A:Accession: A37570
 A:Molecule type: DNA
 A:Residues: 1-461 <ANS>
 A:Cross-references: GB:K02048
 R:Beltsman, P.H.; Bertling, R.M.; Ploos van Amstel, J.K.; Riemens, A.; Briel, E.
 Blood 72, 1074-1076, 1988
 A:Title: The putative factor IX gene promoter in hemophilia B Leyden.
 A:Reference number: A30511; MUID:88327116
 A:Accession: A30511
 A:Molecule type: DNA
 A:Residues: 8-24 <REI>
 A:Cross-references: EMBL:X55008; NID:g311288; PIDN:CAB38245.2; PID:g4469253
 R:Koebel, D.D.; Boltema, C.D.K.; Buetstedde, J.M.; Sommer, S.S.
 Am. J. Hum. Genet. 45, 448-457, 1989
 A:Title: Functionally important regions of the factor IX gene have a low rate of poly
 A:Reference number: A32989; MUID:89371752
 A:Accession: A32989
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 30-92 <KOE>
 R:McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Lundblad, R.L.; Roberts, H.R.; Graham, J.B.
 Proc. Natl. Acad. Sci. U.S.A. 82, 2847-2851, 1985
 A:Title: Evidence for a prevalent dimorphism in the activation peptide of human coagu

A:Reference number: A22673; MUID:85190593
 A:Accession: A22673
 A:Molecule type: mRNA
 A:Residues: 1-193, 'T', 195-461 <MCG>
 A:Cross-references: GB:M1309; NID:9180552; PIDN:AA52023.1; PID:9180553
 A:Note: The authors translated the codon ACA for residue 29 as Tyr
 R:Jaye, M.; de la Salle, H.; Schimber, F.; Balland, A.; Kohl, V.; Flindell, A.; Tolstosht
 Nucleic Acids Res. 11, 2325-2335, 1983
 A:Title: Isolation of a human anti-haemophilic factor IX cDNA clone using a unique 52-bp
 A:Reference number: A21337; MUID:83320788
 A:Accession: A21337
 A:Molecule type: mRNA
 A:Residues: 1-193, 'T', 195-461 <NAV>
 A:Cross-references: GB:J00137; NID:9182610; PIDN:AA52763.1; PID:9182611
 R:Jagdeeswaran, P.; Lavelle, D.E.; Kaul, R.; Mohandas, T.; Warren, S.T.
 Somat. Cell Mol. Genet. 10, 465-473, 1984
 A:Title: Isolation and characterization of human factor IX cDNA: Identification of Tag I
 A:Reference number: A37546; MUID:84300526
 A:Accession: A37546
 A:Molecule type: mRNA
 A:Residues: 38-193, 'T', 195-326 <JAG>
 A:Cross-references: GB:M35672
 R:Kurachi, K.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 79, 6461-6464, 1982
 A:Title: Isolation and characterization of a cDNA coding for human factor IX.
 A:Reference number: A30623; MUID:83065193
 A:Accession: A30623
 A:Molecule type: mRNA
 A:Residues: 1-12, 'S', 14-73, 'P', 75-82, 'K', 84-203, 'P', 205-216, 'G', 218-298, 'A', 299-356, 'A',
 A:Cross-references: GB:J00136; NID:9182608; PIDN:AA58726.1; PID:9182609
 R:Tharakan, J.; Strickland, D.; Burgess, W.; Drohan, W.N.; Clark, D.B.
 Vox Sang. 58, 21-29, 1990
 A:Title: Development of an immunoaffinity process for factor IX purification.
 A:Reference number: A60486; MUID:90194857
 A:Accession: A60486
 A:Molecule type: protein
 A:Residues: 47-52, 'X', 55-60, 'X', 62, 'XX', 65 <THA>
 R:McMullen, B.A.; Fujikawa, K.; Kistiel, W.
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983
 A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co
 A:Reference number: A20274; MUID:83308813
 A:Accession: A20274
 A:Molecule type: protein
 A:Residues: 105-109, 'X', 111-115 <MCN>
 R:Balland, A.; Faure, T.; Carvallo, D.; Cordier, P.; Ulrich, P.; Fournet, B.; de la Sall
 Eur. J. Biochem. 172, 565-572, 1988
 A:Title: Characterisation of two differently processed forms of human recombinant factor
 A:Reference number: S02527; MUID:88166735
 A:Accession: S02527
 A:Molecule type: protein
 A:Residues: 29-63 <BAL>
 A:Note: processed forms expressed in recombinant system
 R:Jallat, S.; Perraud, F.; Dalemans, W.; Balland, A.; Dieterle, A.; Faure, T.; Meulien,
 EMBO J. 9, 3295-3301, 1990
 A:Title: Characterization of recombinant human Factor IX expressed in transgenic mice an
 A:Reference number: S12058; MUID:91006024
 A:Accession: S12058
 A:Molecule type: mRNA; protein
 A:Residues: 1-68 <JAL>
 A:Note: processed forms expressed in recombinant system
 R:Hanford, P.A.; Baron, M.; Mayhew, M.; Willis, A.; Beesley, T.; Brownlee, G.G.; Campbe
 EMBO J. 9, 475-480, 1990
 A:Title: The first EGF-like domain from human factor IX contains a high-affinity calcium
 A:Reference number: S12377; MUID:90151623
 A:Accession: S12377
 A:Molecule type: protein
 A:Residues: 92-130 <HAN>
 A:Note: NMR detection of calcium binding by domain expressed in recombinant system
 R:de la Salle, C.; Charmanier, J.L.; Baas, M.J.; Schwartz, A.; Wiesel, M.L.; Grunbaum,
 Thromb. Haemost. 70, 370-371, 1993
 A:Title: A deletion located in the 3' non translated part of the factor IX gene responsi
 A:Reference number: I59612; MUID:94054350

A:Accession: I59612
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 444-461 <RES>
 A:Cross-references: GB:S66552; NID:9439773; PIDN:AA828588.1; PID:9439774
 R:Stoflet, E.S.; Koerber, D.D.; Sarkar, G.; Sommer, S.S.
 Science 239, 491-494, 1988
 A:Title: Genomic amplification with transcript sequencing.
 A:Reference number: I59529; MUID:88127096
 A:Accession: I59529
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 290-359 <RE2>
 A:Cross-references: GB:M19063; NID:9182622; PIDN:AA52456.1; PID:9182623
 R:Agarwala, K.L.; Kawabata, S.; Takao, T.; Murata, H.; Shimonishi, Y.; Nishimura, H.;
 Biochemistry 33, 5167-5171, 1994
 A:Title: Activation peptide of human factor IX has oligosaccharides O-glycosidically
 A:Reference number: A54255; MUID:94227047
 A:Accession: A54255
 A:Molecule type: protein
 A:Residues: 'D', 204, 'X', 206-211, 212, 'D', 214, 'X', 216-221, 'D' <AGA>
 A:Note: the residues designated 'X' were determined to be threonine bound to carbohyd
 R:Di Scipio, R.G.; Kurachi, K.; Davie, E.W.
 J. Clin. Invest. 61, 1528-1538, 1978
 A:Title: Activation of human factor IX (Christmas factor).
 A:Reference number: A18483; MUID:78194509
 A:Contents: annotation; activation; active site; carbohydrate binding
 R:McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Graham, J.B.; Roberts, H.R.; Stafford, D.W.
 Am. Soc. Hemtol. Abstr. 64(Suppl.1), 262a, 1984
 A:Reference number: A37569
 A:Contents: annotation
 A:Note: 194-Thr was also found
 R:Morita, T.; Isaacs, B.S.; Esmon, C.T.; Johnson, A.E.
 J. Biol. Chem. 259, 5698-5704, 1984
 A:Title: Derivatives of blood coagulation factor IX contain a high affinity Ca2+-bind
 A:Reference number: A37543; MUID:84185715
 A:Contents: annotation; calcium binding
 R:Morita, T.; Isaacs, B.S.; Esmon, C.T.; Johnson, A.E.
 J. Biol. Chem. 260, 2583, 1985
 A:Reference number: A37544
 A:Contents: annotation; calcium binding; correction
 R:Bentley, A.K.; Rees, D.J.G.; Rizza, C.; Brownlee, G.G.
 Cell 45, 343-348, 1986
 A:Title: Defective propeptide processing of blood clotting factor IX caused by mutat
 A:Reference number: A37545; MUID:86189947
 A:Contents: annotation; signal sequence cleavage site
 R:Suenhiro, K.; Kawabata, S.I.; Miyata, T.; Takeya, H.; Takamatsu, J.; Ogata, K.; Kam
 J. Biol. Chem. 264, 21257-21265, 1989
 A:Title: Blood clotting factor IX B(M) Nagoya: substitution of arginine 180 by trypto
 A:Reference number: A30622; MUID:90078229
 A:Contents: annotation; sequence of mutant B(M) Nagoya
 A:Note: carboxylation, glycosylation, and cleavage sites
 R:Baron, M.; Norman, D.G.; Harvey, T.S.; Hanford, P.A.; Mayhew, M.; Tse, A.G.D.; Brow
 submitted to the Brookhaven Protein Data Bank, November 1991
 A:Reference number: A51252; PDB:1IXA
 A:Contents: annotation; conformation by (1)H-NMR, residues 92-130
 A:Note: recombinant form expressed in yeast
 C:Comment: Factor IX is activated by factor Xla, which excises the activation peptide
 C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitam
 C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with s
 C:Genetics:
 A:Gene: GDB:F9
 A:Cross-references: GDB:119900; OMIM:306900
 A:Map position: Xq27.1-Xq27.2
 A:Intons: 30/1; 84/2; 93/1; 131/1; 174/1; 241/3; 280/1
 C:Function:
 A:Description: catalyzes the proteolytic activation of coagulation factor X in the pr
 A:Pathway: blood coagulation intrinsic pathway
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglu
 F1-28/Domain: signal sequence #status predicted <SIS>
 F1-29-46/Domain: propeptide #status experimental <EPT>
 F1-31-91/Domain: Gla domain homology <GLA>

A:Reference number: A42696; MUID:92212913
 A:Accession: B42696
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 383-617, 'E' <BAN>
 A:Cross-references: GB:M81397
 C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
 C:Keywords: blood coagulation; calcium binding; carboxyglutamic acid; glycoprotein; hydro-
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-43/Domain: propeptide #status predicted <PRO>
 F:28-88/Domain: Gla domain homology <GLA>
 F:44-617/Product: prothrombin #status experimental <PMAT>
 F:109-187/Domain: kringle homology <KR1>
 F:215-292/Domain: kringle homology <KR2>
 F:360-609/Domain: trypsin homology <TRY>
 F:50,51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #status
 F:51-66,91-104,109-187,130-170,158-182,215-292,236-276,264-288,332-478,387-403,532-546,5
 F:402,458,564/Active site: His, Asp, Ser #status predicted

Query Match 41.1%; Score 79; DB 2; Length 617;
 Best Local Similarity 37.2%; Pred. No. 2,6e-05;
 Matches 16; Conservative 5; Mismatches 22; Indels 0; Gaps 0;

QY 2 NAFLLXLRPGSLKRXCKXXQCSFXXARXIKKDAKRTKLFWISY 44
 Db 46 SGFLLELRKGNLRECEQCSYEAEFALESPODITVFWAKY 88

RESULT 16
 A35827
 thrombin (EC 3.4.21.5) B chain precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 22-Jun-1999
 C:Accession: A35827; A42696; S12081
 R:Beegen, S.J.F.; Schaefer, L.A.; Jamlson, C.S.; Grant, S.G.; Fitzgibbon, J.J.; Pal, J.A.
 DNA Cell Biol. 9, 487-498, 1990
 A:Title: Characterization of the cDNA coding for mouse prothrombin and localization of t
 A:Reference number: A35827; MUID:91025351
 A:Accession: A35827
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-618 <DEG>
 A:Cross-references: GB:X52308; NID:953813; PIDN:CAA36548.1; PID:953814
 A:Experimental source: strain C57BL/6
 A:Note: the data were obtained from females resulting from the cross of M. domesticus an
 R:Banfield, D.K.; MacGillivray, R.T.A.
 Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
 A:Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq
 A:Reference number: A42696; MUID:92212913
 A:Accession: A42696
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 384-618, 'E' <BAN>
 A:Cross-references: GB:M81394
 C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
 C:Keywords: blood coagulation; calcium binding; carboxyglutamic acid; glycoprotein; hydro-
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-43/Domain: propeptide #status predicted <PRO>
 F:28-88/Domain: Gla domain homology <GLA>
 F:44-618/Product: prothrombin B #status predicted <MAT>
 F:109-187/Domain: kringle homology <KR1>
 F:215-293/Domain: kringle homology <KR2>
 F:361-610/Domain: trypsin homology <TRY>
 F:50,51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #status
 F:51-66,91-104,109-187,130-170,158-182,215-293,236-276,264-288,333-479,388-404,533-547,5
 F:403,459,565/Active site: His, Asp, Ser #status predicted

Query Match 41.1%; Score 79; DB 2; Length 618;
 Best Local Similarity 37.2%; Pred. No. 2,6e-05;
 Matches 16; Conservative 5; Mismatches 22; Indels 0; Gaps 0;

QY 2 NAFLLXLRPGSLKRXCKXXQCSFXXARXIKKDAKRTKLFWISY 44
 Db 46 SGFLLELRKGNLRECEQCSYEAEFALESPODITVFWAKY 88

RESULT 17
 A30351
 coagulation factor IXa (EC 3.4.21.22) precursor - dog
 C:Species: Canis lupus familiaris (dog)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A30351; I46201
 R:Evans, J.P.; Matzke, H.H.; Ware, J.L.; Stafford, D.W.; High, K.A.
 Blood 74, 207-212, 1989
 A:Title: Molecular cloning of a cDNA encoding canine factor IX.
 A:Reference number: A30351; MUID:89323338
 A:Accession: A30351
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-452 <EVA>
 A:Cross-references: GB:M21757; NID:9972719; PIDN:AAV5006.1; PID:9163948
 R:Axelrod, J.H.; Read, M.S.; Brinkhaus, K.M.; Verma, I.M.
 Proc. Natl. Acad. Sci. U.S.A. 87, 5173-5177, 1990
 A:Title: Phenotypic correction of factor IX deficiency in skin fibroblasts of hemophi
 A:Reference number: I46201; MUID:90311364
 A:Accession: I46201
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-452 <AXE>
 A:Cross-references: GB:M33826; NID:9163949; PIDN:AAA3084.1; PID:9163950
 C:Superfamily: coagulation factor IX; EGF homology; Gla domain homology; trypsin homol
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglu
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-40/Domain: propeptide #status predicted <PRO>
 F:24-84/Domain: Gla domain homology <GLA>
 F:41-482/Product: coagulation factor IX #status predicted <MAT>
 F:90-121/Domain: EGF homology <EG1>
 F:127-163/Domain: EGF homology <EG2>
 F:218-445/Domain: trypsin homology <TRY>
 F:46,47,54,56,59,60,65,66,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu)
 F:57-62,90-101,95-110,112-121,127-138,144-148,150-163,171-326,243-259,373-387,398-426
 F:258,306,402/Active site: His, Asp, Ser #status predicted

Query Match 40.6%; Score 78; DB 1; Length 452;
 Best Local Similarity 41.2%; Pred. No. 2,9e-05;
 Matches 14; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY 11 GSLLKRXCKXXQCSFXXARXIFKDAKRTKLFWISY 44
 Db 51 GNLERCEIERKCSFEAREVFNTEKTFPMKQY 84

RESULT 18
 JQ0419
 coagulation factor IXa (EC 3.4.21.22) precursor - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Jul-1999
 C:Accession: JQ0419; I49667
 R:Wu, S.M.; Stafford, D.W.; Ware, J.
 Gene 86, 275-278, 1990
 A:Title: Deduced amino acid sequence of mouse blood-coagulation factor IX.
 A:Reference number: JQ0419; MUID:90215309
 A:Accession: JQ0419
 A:Molecule type: mRNA
 A:Residues: 1-459 <WUS>
 A:Cross-references: GB:M23109; NID:9193317; PIDN:AAA37629.1; PID:9387158
 A:Experimental source: liver
 R:Sarkar, G.; Koeberl, D.D.; Sommer, S.S.
 Genomics 6, 133-143, 1990
 A:Title: Direct sequencing of the activation peptide and the catalytic domain of the
 A:Reference number: I46580; MUID:90152675
 A:Accession: I49667
 A:Status: preliminary; translated from GB/EMBL/DBJ

F:288-567,449-475,638-665/Disulfide bonds: #status experimental
F:499/Binding site: carbohydrate (asn) (covalent) #status experimental
F:509/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 34.4%; Score 66; DB 1; Length 675;
Best Local Similarity 34.1%; Pred. No. 0.0046;
Matches 15; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRPGSLRXKXKXQCSFXXARXIFKDXRRTKLEWISY 44
Db 42 ANLLEETKKGNIERCIEELCKKEAREFEENPETEYPRYK 85

RESULT 22

probable MAP kinase [Imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C:Accession: D84859

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

Neus, D.; Mierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: AB4420; MUID:20083487

A:Accession: D84859

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-594 <STO>

C:Genetics: A:Cross-references: GB:AE002093; NID:g4512667; PIDN:AAD21721.1; GSPDB:GN00139

A:Gene: At2g42880

A:Map position: 2

Query Match 34.1%; Score 65.5; DB 2; Length 594;
Best Local Similarity 34.8%; Pred. No. 0.0049;

Matches 16; Conservative 5; Mismatches 22; Indels 3; Gaps 2;

Oy 1 ANAFLLXLRPGSLRXKXKXQCSFXXARXIFKDXRRTKLEWISY 44
Db 133 ANYHHDLKPKNLNANCKLKICDFGLARVAFND-TPTTTFWTDY 177

RESULT 23

C96575

probable MAP kinase ATPK9, 98271-101224 [Imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: C96575

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Malt, R.; Maritali,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakono, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: AB6141; MUID:21016719

A:Accession: C96575

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-603 <STO>

C:Genetics: A:Cross-references: GB:AE005173; NID:g10645353; PIDN:AA621473.1; GSPDB:GN00141

A:Gene: F22610.12

A:Map position: 1

Query Match 34.1%; Score 65.5; DB 2; Length 603;

Best Local Similarity 34.8%; Pred. No. 0.005;
Matches 16; Conservative 5; Mismatches 22; Indels 3; Gaps 2;

Oy 1 ANAFLLXLRPGSLRXKXKXQCSFXXARXIFKDXRRTKLEWISY 44
Db 133 ANYHHDLKPKNLNANCKLKICDFGLARVAFND-TPTTTFWTDY 177

RESULT 24

S53434

plasma protein S precursor, vitamin K dependent - rhesus macaque (fragment)

C:Species: Macaca mulatta (rhesus macaque)

C>Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 16-Jul-1999

C:Accession: S53434

R:Greenard, J.S.; Fernandez, J.A.; Radtke, K.P.; Griffin, J.H.

Biochem. J. 305, 397-403, 1995

A:Title: Identification of candidate residues for interaction of protein S with C4b

A:Reference number: S53433; MUID:95134217

A:Accession: S53434

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-642 <CR>

A:Cross-references: EMBL:L31380

A:Experimental source: tissue type liver

A:Note: the source is designated as rhesus monkey

C:Genetics:

A:Gene: PROS

C:Superfamily: Plasma protein S; EGF homology; Gla domain homology; laminin G repeat

F:1-51/Domain: Gla domain homology (fragment) <GLA>

F:1-7/Domain: signal sequence (fragment) #status predicted <SIG>

F:8-642/Product: plasma protein S #status predicted <MAT>

F:87-120/Domain: EGF homology <EG1>

F:127-165/Domain: EGF homology <EG2>

F:171-207/Domain: EGF homology <EG3>

F:213-248/Domain: EGF homology <EG4>

F:281-633/Domain: sex hormone-binding globulin homology <SHB>

F:291-444/Domain: laminin G repeat homology <LGR>

Query Match 33.3%; Score 64; DB 2; Length 642;
Best Local Similarity 31.8%; Pred. No. 0.0096;

Matches 14; Conservative 8; Mismatches 22; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRPGSLRXKXKXQCSFXXARXIFKDXRRTKLEWISY 44
Db 8 ANSMEETKKGNIERCIEELCKKEAREFEVENDPETYPRYK 51

RESULT 25

S38819

plasma protein S - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 18-Feb-1994 #sequence_revision 21-Jul-1995 #text_change 16-Jul-1999

C:Accession: S38819; S37238

R:He, X.; Dahlback, B.

Eur. J. Biochem. 217, 857-865, 1993

A:Title: Molecular cloning, expression and functional characterization of rabbit anti

A:Reference number: S38819; MUID:94039141

A:Accession: S38819

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-646 <HEX>

A:Cross-references: EMBL:226485

R:He, X.; Dahlback, B.

submitted to the EMBL Data Library, September 1993

A:Description: Molecular Cloning and Expression of Rabbit Anticoagulant Vitamin K-dep

A:Reference number: S37238

A:Accession: S37238

A:Molecule type: mRNA

A:Residues: 1-502, 'U', 504-646 <HE2>

C:Superfamily: Plasma protein S; EGF homology; Gla domain homology; laminin G repeat

F:1-56/Domain: Gla domain homology (fragment) <GLA>


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Query Match      32.8%; Score 63; DB 1; Length 396;
Best Local Similarity 35.0%; Pred. No. 0.009;
Matches 14; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

OY      5 LXXLRPGSLKRXCKXXQCSFXXXARXIFKDXARKTKLFWISY 44
      6 LEELEFGHLEKCEWMEELCYEEARVEFDEDTTFEWRIT 45

RESULT 28
TBBO
thrombin (EC 3.4.21.5) precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 24-Apr-1984 #sequence_revision 14-Jul-1994 #text_change 18-Jun-1999
C:Accession: S02537; A00915; A37552; I46045; S67518
R:Irwin, D.M.; Robertson, K.A.; Macgillivray, R.T.A.
J. Mol. Biol. 200, 31-45, 1988
A:Title: Structure and evolution of the bovine prothrombin gene.
A:Reference number: S02537; MUID:88245190
A:Accession: S02537
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-625 <TRM>
R:Macgillivray, R.T.A.; Davie, E.W.
Biochemistry 23, 1626-1634, 1984
A:Title: Characterization of bovine prothrombin mRNA and its translation product.
A:Reference number: A00915; MUID:84203525
A:Accession: A00915
A:Molecule type: mRNA
A:Residues: 1-230, 'H', 232-625 <MAC>
A:Note: 600-Asn was also found
R:Magnusson, S.; Soltup-Jensen, L.; Petersen, T.E.; Claeyss, H.
In Boerhaave Symposium on Prothrombin and Related Coagulation Factors, Hemker, H.C., and
A:Reference number: A37552
A:Accession: A37552
A:Molecule type: protein
A:Residues: 44-287, 'N', 289-352, 'E', 354, 'Q', 356-548, 'ND', 551-599, 'N', 601-625 <MAC>
A:Note: The evidence for 231-Ser is strong
A:Note: disulfide bonds and carbohydrate binding sites were determined
R:Park, C.H.; Tulinsky, A.
Biochemistry 25, 3977-3982, 1986
A:Title: Three-dimensional structure of the kringle sequence: structure of prothrombin
A:Reference number: A37553; MUID:86296631
A:Contents: annotation; residues 44-317, X-ray crystallography, 2.8 angstroms
R:Irwin, D.M.; Ahern, K.G.; Pearson, G.D.; Macgillivray, R.T.A.
Biochemistry 24, 6854-6861, 1985
A:Title: Characterization of the bovine prothrombin gene.
A:Reference number: A37554; MUID:86077733
A:Contents: annotation; gene structure
R:Macgillivray, R.T.; Degen, S.J.; Chandra, T.; Woo, S.L.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 77, 5153-5157, 1980
A:Title: Cloning and analysis of a cDNA coding for bovine prothrombin.
A:Reference number: I46045; MUID:81054926
A:Accession: I46045
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 466-599, 'N', 601-625 <MAC>
A:Cross-references: EMBL:V00135; NID:9772; PIDN:CA23451.1; PID:9808945
R:Pejler, G.; Karlstrom, A.R.; Berg, L.
Eur. J. Biochem. 227, 102-107, 1995
A:Title: Identification of the proteolytic thrombin fragments formed after cleavage with
A:Reference number: S67518; MUID:95154277
A:Accession: S67518
A:Status: preliminary
A:Molecule type: protein
A:Residues: 318-325, 333-338, 'X', 340, 367-374, 481-484, 'X', 486-488, 515-522 <PE>
C:Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibrin
C:Comment: Prothrombin is activated on the surface of a phospholipid membrane that binds
activation peptide and cleaves the remaining part into light and heavy chains. The activat
C:Comment: Thrombin can cleave the amino-terminal activation peptide 1 from prothrombin,
C:Comment: The gamma-carboxyglutamyl residues bind calcium ions, result from the carboxy

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ent interaction with the negatively charged phospholipid membrane surface.
C:Comment: The prothrombin precursor is synthesized in the liver.
C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C:Keywords: blood coagulation; calcium binding; carboxyglutamic acid; duplication; gl
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-43/Domain: propeptide #status predicted <PRO>
F:28-88/Domain: Gla domain homology <GLA>
F:44-625/Product: prothrombin #status experimental <MP>
F:44-199/Domain: activation peptide 1 #status experimental <FR1>
F:109-187/Domain: kringle homology <KR1>
F:200-317/Domain: activation peptide 2 #status experimental <FR2>
F:214-292/Domain: kringle homology <KR2>
F:318-366/Product: thrombin light chain #status experimental <LCH>
F:367-625/Product: thrombin heavy chain #status experimental <HCH>
F:367-616/Domain: trypsin homology <TRY>
F:50-51, 58, 60, 63, 64, 69, 70, 73, 76/Modified site: gamma-carboxyglutamic acid (Glu) #stat
F:61-66, 91-104, 109-187, 130-170, 158-182, 214-292, 235-275, 263-287, 339-485, 394-410, 539-55
F:120, 144, 419/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:409, 465, 571/Active site: His, Asp, Ser #status experimental

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Query Match      32.8%; Score 63; DB 1; Length 625;
Best Local Similarity 34.1%; Pred. No. 0.014;
Matches 14; Conservative 3; Mismatches 24; Indels 0; Gaps 0;

OY      4 FLXXLRPGSLKRXCKXXQCSFXXXARXIFKDXARKTKLFWISY 44
      48 FLEVRKRGNLRCLEPCSRFEAFALSLSTDAFMWAY 88

RESULT 29
KXRTS
plasma protein S precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 04-Oct-1995 #sequence_revision 26-Jan-1996 #text_change 16-Jul-1999
C:Accession: J04180
R:Yasuda, F.; Hayashi, T.; Tanitame, K.; Nishioke, J.; Suzuki, K.
J. Biochem. 117, 374-383, 1995
A:Title: Molecular cloning and functional characterization of rat plasma protein S.
A:Reference number: J04180; MUID:95332263
A:Accession: J04180
A:Molecule type: mRNA
A:Residues: 1-675 <YAS>
A:Cross-references: GB:S78744; NID:91041903; PIDN:AC60704.1; PID:91041904
C:Comment: This protein is a vitamin K-dependent plasma glycoprotein that has an anti
activation of coagulation factors Va and VIIa. This protein also binds to factor Va
C:Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat
C:Keywords: beta-hydroxyasparagine; beta-hydroxyaspartic acid; blood coagulation; car
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-41/Domain: propeptide #status predicted <PRO>
F:26-85/Domain: Gla domain homology <GLA>
F:42-675/Product: plasma protein S #status predicted <MP>
F:88-116/Domain: thrombin-sensitive #status predicted <HS>
F:121-154/Domain: EGF homology <EG1>
F:161-199/Domain: EGF homology <EG2>
F:205-241/Domain: EGF homology <EG3>
F:247-282/Domain: EGF homology <EG4>
F:315-666/Domain: sex hormone-binding globulin homology <SHB>
F:325-478/Domain: laminin G repeat homology <LGR>
F:77, 48, 55, 57, 60, 61, 66, 67, 70, 73, 77/Modified site: gamma-carboxyglutamic acid (Glu) #s
F:58-63, 88-113, 121-134, 126-143, 145-154, 161-175, 171-184, 186-199, 205-217, 212-226, 228-24
F:111-112/Cleavage site: Arg-Ser (thrombin) #status predicted
F:136/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F:177, 219, 258/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F:499, 509/Binding site: carbohydrate (Asn) (covalent) #status predicted

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Query Match      32.8%; Score 63; DB 1; Length 675;
Best Local Similarity 31.8%; Pred. No. 0.015;
Matches 14; Conservative 7; Mismatches 23; Indels 0; Gaps 0;

OY      1 ANFLXXLRPGSLKRXCKXXQCSFXXXARXIFKDXARKTKLFWISY 44
      11 : : : : : : : : : : : : : : : : : : :

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Db      42 ANTLEETKKGNLERECIEELCNKEAREVEFENNPTDYFYPKY 85
RESULT 30
KXHUZ
Plasma protein 2 precursor [validated] - human
N:Alternate names: Vitamin K-dependent glycoprotein 2
C:Species: Homo sapiens (man)
C>Date: 18-Jan-1991 #sequence_revision 05-Jan-1996 #text_change 08-Dec-2000
C:Accession: A36244; A35893; B35893
R:Ichinose, A.; Takeya, H.; Espilng, E.; Iwanaga, S.; Kistiel, W.; Davie, E.W.
Biochem. Biophys. Res. Commun. 172, 1139-1144, 1990
A:Title: Amino acid sequence of human protein Z, a vitamin K-dependent plasma glycoprotein
A:Reference number: A36244; MUID:91058548
A:Accession: A36244
A:Molecule type: mRNA
A:Residues: 1-422 <ICH>
A:Cross-references: GB:M55671; NID:g190465; PIDN:AAA36501.1; PID:g190466
A>Note: parts of this sequence, including the amino end of the mature protein, were detected
Biochem. Biophys. Res. Commun. 171, 661-668, 1990
A:Title: Primary structure of vitamin K-dependent human protein Z.
A:Reference number: A35893; MUID:90386637
A:Accession: A35893
A:Molecule type: protein
A:Residues: 63-68, 'XX', '71-72', 'X', '74-76', 'X', '78', 'XX', '81', 'XX', '84', 'X', '86-87', 'XX', '90', 'XX', '93'
A:Molecule type: mRNA
A:Residues: 103-422 <SE2>
A:Cross-references: GB:M59303; NID:g190461; PIDN:AAA36499.1; PID:g190462
C:Genetics:
A:Gene: GDB:PROZ
A:Cross-references: GDB:9957440; OMIM:176895
A:Map position: 13q34-13q34
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; calcium binding; carboxylglutamic acid; glycoprotein
F:1-10/Domain: signal sequence #status predicted <SIG>
F:41-62/Domain: propeptide #status predicted <PRO>
F:67-107/Domain: Gla domain homology <GLA>
F:63-422/Product: protein Z #status experimental <MAT>
F:113-144/Domain: EGF homology <EG1>
F:151-187/Domain: EGF homology <EG2>
F:199-417/Domain: trypsin homology <TRY>
F:69,70,73,77,79,82,83,88,89,92,95,97,102/Modified site: gamma-carboxylglutamic acid (Glu)
F:115/Binding site: carbohydrate (Ser) (covalent) #status experimental
F:121,247,253,328,334/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:126/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F:134,337/Binding site: carbohydrate (Thr) (covalent) #status predicted
F:225-241,349-363/Disulfide bonds: #status predicted
F:258/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match      30.2%; Score 58; DB 1; Length 422;
Best Local Similarity 32.5%; Pred. No. 0.068;
Matches 13; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

QY      5 LXXLRPGLXKXCKXXOCSPFXKXKXIFKDXKRTKLFWISY 44
Db      68 LEELEFEGNLEKECEYEICVYEAREVEFENNVDFWRRY 107

RESULT 31
KXMS
Plasma protein S precursor - mouse
N:Alternate names: Vitamin K-dependent glycoprotein S
C:Species: Mus musculus (house mouse)
C>Date: 13-Jan-1995 #sequence_revision 26-Jan-1996 #text_change 16-Jul-1999
C:Accession: S43504; I59616; S35962
R:Chu, M.D.; Sun, J.; Bird, P.
Biochim. Biophys. Acta 1217, 325-328, 1994
A:Title: Cloning and sequencing of a cDNA encoding the murine vitamin K-dependent protein
A:Reference number: S43504; MUID:94198297

A:Molecule type: mRNA
A:Residues: 1-675 <CHU>
A:Cross-references: EMBL:Z25469; NID:g396426; PIDN:CAA80961.1; PID:g396427
R:Lu, D.; Schmidel, D.K.; Long, G.L.
Thromb. Res. 74, 135-142, 1994
A:Title: Structure of mouse protein S as determined by PCR amplification and DNA sequencing
A:Reference number: I59616; MUID:94302659
A:Accession: I59616
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 33-492, 'L', '494-675 <RES>
A:Cross-references: GB:L27439; NID:g487866; PIDN:AAA40006.1; PID:g487867
C:Complex: in plasma forms a complex with C4b binding protein
C:Function:
A:Description: a cofactor for activated protein C (EC 3.4.21.69); thrombin cleavage
C:Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat
C:Keywords: beta-hydroxyasparagine; beta-hydroxyaspartic acid; blood coagulation; car
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-41/Domain: propeptide #status predicted <PRO>
F:26-85/Domain: Gla domain homology <GLA>
F:42-675/Product: plasma protein S #status predicted <MAT>
F:121-154/Domain: EGF homology <EG1>
F:161-199/Domain: EGF homology <EG2>
F:205-241/Domain: EGF homology <EG3>
F:247-282/Domain: EGF homology <EG4>
F:315-666/Domain: sex hormone-binding globulin homology <SHB>
F:325-478/Domain: laminin G repeat homology <LGR>
F:47,48,55,57,60,61,66,67,70,73,77/Modified site: gamma-carboxylglutamic acid (Glu) #
F:56-63,88-113,121-134,126-143,145-154,161-175,177-184,186-199,205-217,212-226,228-24
F:111-112/Cleavage site: Arg-Ser (thrombin) #status predicted
F:136/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F:177,219,258/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F:499,509/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      29.2%; Score 56; DB 1; Length 675;
Best Local Similarity 29.5%; Pred. No. 0.23;
Matches 13; Conservative 6; Mismatches 25; Indels 0; Gaps 0;

QY      1 ANAFLLXLRPGLXKXCKXXOCSPFXKXKXIFKDXKRTKLFWISY 44
Db      42 ANTLEETKKGNLERECIEELCNKEAREVEFENNPTDYFYPKY 85

RESULT 32
A48089
growth arrest-specific protein gas6 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 05-Nov-1999
C:Accession: A48089; S37437
R:Manfioletti, G.; Brancolini, C.; Avanzl, G.; Schneider, C.
Mol. Cell. Biol. 13, 4976-4985, 1993
A:Title: The protein encoded by a growth arrest-specific gene (gas6) is a new member
A:Reference number: A48089; MUID:93330291
A:Accession: A48089
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-673 <MAN>
A:Cross-references: GB:X59846; NID:g407060; PIDN:CAA42507.1; PID:g407061
C:Note: authors translated the codon CCC for residue 424 as Ile
C:Genetics:
A:Gene: gas6
C:Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat
F:38-89/Domain: Gla domain homology #status atypical <GLA>
F:117-150/Domain: EGF homology <EG1>
F:157-192/Domain: EGF homology <EG2>
F:198-233/Domain: EGF homology <EG3>
F:239-274/Domain: EGF homology <EG4>
F:308-666/Domain: sex hormone-binding globulin homology <SHB>
F:318-470/Domain: laminin G repeat homology <LGR>
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Query Match          28.6%; Score 55; DB 2; Length 673;
Best Local Similarity 33.3%; Pred. No. 0.34;
Matches 12; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

Oy      9  RPSLXKCKXXKQCSFXKXARXIFKDAKRTKLEWISY 44
      : | | | | | | | | | | | | | | | | | | |
Db      54  KQGLERECVEEVCSEKREAREVFNDEPDTDFYPRY 89

RESULT  33
155476
growth potentiating factor - rat
C:Species: Rattus sp. (rat)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Apr-2001
C:Accession: I55476
J: Nakano, T.; Higashino, K.; Kikuchi, N.; Kishino, J.; Nomura, K.; Fujita, H.; Ohara, O.
A:Title: Vascular smooth muscle cell-derived, Glu-containing growth-potentiating factor
A:Reference number: I55476; MUID:95197586
A:Accession: I55476
A:Molecule type: mRNA
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-674 <RES>
A:Cross-references: GB:DA2148; NID:g1526567; PIDN:BA07719.1; PID:g893402
C:Superfamily: plasma protein S; EGF homology; Glu domain homology; laminin G repeat hom
F:29-89/Domain: Glu domain homology <GLA>
F:117-150/Domain: EGF homology <EG1>
F:157-192/Domain: EGF homology <EG2>
F:198-233/Domain: EGF homology <EG3>
F:239-274/Domain: EGF homology <EG4>
F:308-667/Domain: sex hormone-binding globulin homology <SHB>
F:318-470/Domain: laminin G repeat homology <LGR>

Query Match          27.6%; Score 53; DB 2; Length 674;
Best Local Similarity 33.3%; Pred. No. 0.74;
Matches 12; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

Oy      9  RPSLXKCKXXKQCSFXKXARXIFKDAKRTKLEWISY 44
      : | | | | | | | | | | | | | | | | | | |
Db      54  KQGLERECVEEVCSEKREAREVFNDEPDTDFYPRY 89

RESULT  34
B48089
growth arrest-specific protein gas6 - human
C:Species: Homo sapiens (man)
C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 05-Nov-1999
C:Accession: B48089
R: Mantouletti, G.; Brancolini, C.; Avanzl, G.; Schneider, C.
Mol. Cell. Biol. 13, 4976-4985, 1993
A:Title: The protein encoded by a growth arrest-specific gene (gas6) is a new member of
A:Reference number: A48089; MUID:93330291
A:Accession: B48089
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-678 <MAN>
A:Cross-references: GB:LI3720; NID:g401766; PIDN:AAA58494.1; PID:g401767
C:Superfamily: plasma protein S; EGF homology; Glu domain homology; laminin G repeat hom
F:41-92/Domain: Glu domain homology #status atypical <GLA>
F:120-153/Domain: EGF homology <EG1>
F:160-195/Domain: EGF homology <EG2>
F:201-236/Domain: EGF homology <EG3>
F:242-277/Domain: EGF homology <EG4>
F:311-671/Domain: sex hormone-binding globulin homology <SHB>
F:321-473/Domain: laminin G repeat homology <LGR>

Query Match          27.6%; Score 53; DB 2; Length 678;
Best Local Similarity 33.3%; Pred. No. 0.75;
Matches 12; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

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Oy      9  RPSLXKCKXXKQCSFXKXARXIFKDAKRTKLEWISY 44
      : | | | | | | | | | | | | | | | | | | |
Db      57  KQGLERECVEEELCSREAREVFNDEPDTDFYPRY 92

RESULT  35
H84424
probable MAP kinase [Imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: H84424
R: Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: H84424
A:Molecule type: DNA
A:Status: preliminary
A:Residues: 1-516 <STO>
A:Cross-references: GB:AE002093; NID:g3785991; PIDN:ACG7338.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g01450
A:Map position: 2

Query Match          26.8%; Score 51.5; DB 2; Length 516;
Best Local Similarity 30.4%; Pred. No. 1;
Matches 14; Conservative 7; Mismatches 22; Indels 3; Gaps 2;

Oy      1  ANAFLLXLRPGSL--XRCKXXKQCSFXKXARXIFKDAKRTKLEWISY 44
      : | | | | | | | | | | | | | | | | | | |
Db      136 AHVFHRLDKPKNITLANADCKIKICDGLARVSPDTS-PSAVFWTDY 180

RESULT  36
H84724
probable ARI-like RING zinc finger protein [Imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: H84724
R: Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: H84724
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-543 <STO>
A:Cross-references: GB:AE002093; NID:g4887759; PIDN:AAD32295.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g31770
A:Map position: 2

Query Match          24.0%; Score 46; DB 2; Length 543;
Best Local Similarity 30.0%; Pred. No. 9.4;
Matches 9; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Oy      10  PSLXKCKXXKQCSFXKXARXIFKDAKRTKLEWISY 39
      : | | | | | | | | | | | | | | | | | | |
Db      166 PGCLRVKCPPEPSCSAVAGKMDIEDVETRV 195

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RESULT  37
AH0926
hypothetical protein STY3673 [Imported] - Salmonella enterica subsp. enterica serovar
C:Species: Salmonella enterica subsp. enterica serovar Typhimurium
A:Note: this species has also been called Salmonella typhimurium
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001

```

C:Accession: AH0926
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher, T.; Conington, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Mule, S.; O'Gea, P.
 Nature 413, 848-852, 2001
 A:Authors: Park, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov
 A:Reference number: AB0502; PMID:11677608
 A:Accession: AH0926
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-246 <PAR>
 A:Cross-references: GB:AL513382; PIDN:CAD09434.1; PID:g16504551; GSPDB:GN00176
 C:Genetics:
 A:Gene: STY3673

Query Match 23.4%; Score 45; DB 2; Length 246;
 Best Local Similarity 42.9%; Pred. No. 6.7;
 Matches 9; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

OY 1 ANAFXXLRPGSLKRXKXXQ 21
 ||| : ||| : ||| :
 Db 142 ANARVSELKPGQILRLCLDLQ 162

RESULT 38
 S55864
 hypothetical protein YNL325c - yeast (*Saccharomyces cerevisiae*)
 N:Alternate names: hypothetical protein N0330
 C:Species: *Saccharomyces cerevisiae*
 C:Date: 27-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 23-Mar-2001
 C:Accession: S55864; S51290; S63306
 R:Matfahl, M.; Niclaud, J.M.; Levesque, H.; Galliardin, C.
 Yeast 11, 567-572, 1995
 A:Title: Sequencing analysis of a 15.4 kb fragment of yeast chromosome XIV identifies th
 A:Reference number: S55859; MUID:95373280
 A:Accession: S55864
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-879 <MAF>
 A:Cross-references: EMBL:Z46259; NID:g633655; PIDN:CAA66373.1; PID:g633661
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
 R:Nicaud, J.J.
 submitted to the EMBL Data Library, January 1995
 A:Description: Sequence analysis of a 13.9 Kb fragment of yeast chromosome XIV identifies
 A:Reference number: S51285
 A:Accession: S51290
 A:Molecule type: DNA
 A:Residues: 1-879 <NIC>
 A:Cross-references: EMBL:Z46259; NID:g633655; PID:g633661
 R:Matfahl, M.; Niclaud, J.M.; Levesque, H.; Galliardin, C.
 submitted to the Protein Sequence Database, April 1996
 A:Reference number: S63287
 A:Accession: S63306
 A:Molecule type: DNA
 A:Residues: 1-879 <MAF>
 A:Cross-references: EMBL:Z71601; NID:g1302439; PID:e239571; PID:g1302440; MIPS:YNL325C
 A:Experimental source: strain 5288C
 C:Genetics:
 A:Gene: SGD:FIG4
 A:Cross-references: SGD:S0005269; MIPS:YNL325C
 A:Map position: 14L

Query Match 23.4%; Score 45; DB 2; Length 879;
 Best Local Similarity 60.0%; Pred. No. 22;
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 OY 30 IFKDAKRTKLFWISY 44
 |||| : ||| : ||| :
 Db 165 IFKDDLTKEFYFSY 179

RESULT 39
 T39306
 mitogen-activated protein kinase - fission yeast (*Schizosaccharomyces pombe*)
 C:Species: *Schizosaccharomyces pombe*
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
 C:Accession: T39306; T45129; T48694
 R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
 submitted to the EMBL Data Library, March 1998
 A:Reference number: Z21843
 A:Accession: T39306
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-422 <WOO>

A:Cross-references: EMBL:AL022117; PIDN:CAI17923.1; GSPDB:GN00067; SPDB:SPBC119.08
 A:Experimental source: strain 972h-; cosmid cl19
 R:Toda, T.; Dhut, S.; Superili-Furga, G.; Gotcho, Y.; Nishida, E.; Sugitara, R.; Kuno, T
 Mol. Cell. Biol. 16, 6752-6764, 1996
 A:Title: The fission yeast pmk1+ gene encodes a novel mitogen-activated protein kinase
 A:Reference number: Z07420; MUID:9709653
 A:Accession: T45129
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-422 <ROD>

A:Cross-references: EMBL:X98243; NID:g1666670; PIDN:CAA66899.1; PID:g1666671
 R:Zaitsevskaia-Carter, T.; Cooper, J.A.
 EMBO J. 16, 1318-1331, 1997
 A:Title: Spml, a stress-activated MAP kinase that regulates morphogenesis in *S. pombe*
 A:Reference number: Z24537; MUID:97280820
 A:Accession: T48694

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-422 <ZAI>
 A:Cross-references: EMBL:U65405; NID:g1513145; PIDN:AAC49707.1; PID:g1513146
 C:Genetics:

A:Gene: spml; SPBC119.08; pmk1
 A:Map position: 2
 A:Introns: 22/3; 82/3; 106/3
 C:Function:

A:Description: pmk1 probably lies on a novel MAPK pathway, which does not overlap fun
 ent stress-sensing pathway
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: phosphoprotein; protein kinase; signal transduction

Query Match 22.9%; Score 44; DB 2; Length 422;
 Best Local Similarity 28.3%; Pred. No. 16;
 Matches 13; Conservative 5; Mismatches 26; Indels 2; Gaps 1;

OY 1 ANAFXXLRPGSL--XRXCKXXQCFXXARXIFKDAKRTKLFWISY 44
 ||| : ||| : ||| :
 Db 143 ANVHRDLKPGNLVNADECKIKDFGLRGCSNPENPEFMTEY 188

RESULT 40
 T15137
 hypothetical protein T28F2.3 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C:Accession: T15137
 R:Madsen, C.; Fyonick, B.
 submitted to the EMBL Data Library, April 1997
 A:Description: The sequence of C. elegans cosmid T28F2.
 A:Reference number: Z18300
 A:Accession: T15137
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-319 <MAD>
 A:Cross-references: EMBL:AF000198; NID:g2047345; PID:g2047348; PIDN:AAB53054.1; GSPDB
 C:Experimental source: strain Bristol N2; clone T28F2
 C:Genetics:
 A:Gene: CESP:T28F2.3
 A:Map position: 1

A;introns: 90/2; 189/3; 266/3; 295/3

Query Match 22.7%; Score 43.5; DB 2; Length 319;
Best Local Similarity 31.6%; Pred. No. 15;
Matches 12; Conservative 6; Mismatches 19; Indels 1; Gaps 1;

OY 5 LXXLRGSLXKCKXQCSFXRXRIFKDXRRTKLEWI 42
DB 201 LINTLPQVIYKGECKLCSEDF-QTFPPVAKETKEFWM 237

RESULT 41
B56598
endothelial kinase Quek2 - qual1 (fragment)
N:Alternate names: vascular endothelial growth factor receptor homolog Quek2
C:Species: Coturnix coturnix (quail)
C>Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 24-Sep-1999
C:Accession: B56598
R:Richmann, A.; Marcelle, C.; Breant, C.; Le Douarin, N.M.
Mech. Dev. 42, 33-48, 1993
A:Title: Two molecules related to the VEGF receptor are expressed in early endothelial
A:Reference number: A56598; MUID:93378866
A:Contents: ssp. japonica, E4 embryo
A:Accession: B56598
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-367 <EIC>
A:Cross-references: GB:S65207; NID:q410682; PIDN:AAB28128.1; PID:q410683
A:Note: sequence extracted from NCBI backbone (NCBIN:137164, NCBIPI:137165)
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C:Keywords: ATP; growth factor receptor
F:1-16/Domain: protein kinase homology (fragment) <KIN>

Query Match 22.7%; Score 43.5; DB 2; Length 367;
Best Local Similarity 34.5%; Pred. No. 17;
Matches 10; Conservative 4; Mismatches 8; Indels 7; Gaps 1;

OY 22 CSFXRXRXIFKD-----AXRTKLEWIS 43
DB 54 CDFGLARDIYKDPDYVRKKSARLPKXMA 82

RESULT 42
T15221
hypothetical protein C53H9.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T15221
R:Galtung, S.
submitted to the EMBL Data Library, May 1997
A:Description: The sequence of C. elegans cosmid C53H9.
A:Reference number: Z18310
A:Accession: T15221
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-385 <GAT>
A:Cross-references: EMBL:AF003143; NID:g2088752; PID:g2088753; PIDN:AAB54192.1; GSPDB:GN
A:Experimental source: strain Bristol N2; clone C53H9
C:Genetics:
A:Gene: C53H9.2
A:Map position: 1
A:introns: 77/2; 200/1

Query Match 22.7%; Score 43.5; DB 2; Length 385;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 10; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

OY 22 CSFXRXRXIFKDXRRTKLEWI 41
DB 264 CS-RAARLMKDYVSGKLIW 282

RESULT 43
A48999
protein-tyrosine kinase (EC 2.7.1.112) flt4 precursor - human

N:Alternate names: class III receptor tyrosine kinase FLT4; fms-like tyrosine kinase
C:Species: Homo sapiens (man)
C>Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2000
C:Accession: A48999; A44930; G02316; S36130; A42010
R:Pajusola, K.; Aprilikova, O.; Korhonen, J.; Kaipainen, A.; Pertovaara, L.; Allitalo, C.
Cancer Res. 52, 5738-5743, 1992
A:Title: FLT4 receptor tyrosine kinase contains seven immunoglobulin-like loops and 1
A:Reference number: A48999; MUID:93007958
A:Accession: A48999
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1298 <PAJ>
A:Cross-references: PIDN:AAB23636.1; PID:g257352
A:Experimental source: HEL erythroleukemia cells
A:Note: sequence extracted from NCBI backbone (NCBIP:115335)
R:Aprilikova, O.; Pajusola, K.; Partanen, J.; Armstrong, E.; Allitalo, R.; Bailey, S.K.
Cancer Res. 52, 746-748, 1992
A:Title: FLT4, a novel class III receptor tyrosine kinase in chromosome 5q33-qter.
A:Reference number: A44930; MUID:92119639
A:Accession: A44930
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 761-1190 <APR>
A:Cross-references: GB:X68203; NID:g311433
A:Note: sequence extracted from NCBI backbone (NCBIP:78155)
R:Wood, W.I.
submitted to the EMBL Data Library, December 1995
A:Reference number: H01039
A:Accession: G02316
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1298 <WOO>
A:Cross-references: EMBL:U43143; NID:g1150990; PIDN:AA085215.1; PID:g1150991
R:Galland, F.
submitted to the EMBL Data Library, December 1992
A:Reference number: S36130
A:Accession: S36130
A:Molecule type: mRNA
A:Residues: 1-23, 'D', '25-744', 'P', '746-751', 'RP', '754-889', 'Q', '891-1127', 'V', '1129-1145', 'H', '1
A:Cross-references: EMBL:X69878; NID:g297049; PIDN:CAA49505.1; PID:g297050
R:Galland, F.; Karaymsheva, A.; Mattei, M.G.; Rosnet, O.; Marchetto, S.; Birnbaum, D.
Genomics 13, 475-478, 1992
A:Title: Chromosomal localization of FLT4, a novel receptor-type tyrosine kinase gene
A:Reference number: A42010; MUID:92307693
A:Accession: A42010
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
A:Molecule type: mRNA
A:Residues: 776-889, 'Q', '891-1127', 'V', '1129-1145', 'H', '1147-1163', 'D', '1165-1200 <GAL2>
C:Genetics:
A:Gene: GDB:FLT4
A:Cross-references: GDB:128732; OMIM:136352
A:Map position: 5q34-5q35
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; transmembra
F:1-23/Domain: signal sequence #status predicted <SID>
F:24-1298/Product: protein-tyrosine kinase FLT4 #status predicted <MAT>
F:843-1176/Domain: protein kinase homology <KIN>
F:851-859/Region: protein kinase ATP-binding motif

Query Match 22.7%; Score 43.5; DB 2; Length 1298;
Best Local Similarity 34.5%; Pred. No. 56;
Matches 10; Conservative 4; Mismatches 8; Indels 7; Gaps 1;

OY 22 CSFXRXRXIFKD-----AXRTKLEWIS 43
DB 1054 CDFGLARDIYKDPDYVRKKSARLPKXMA 1082

RESULT 44
158375
protein-tyrosine kinase (EC 2.7.1.112) flt4 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 04-Feb-2000
C:Accession: 158375; B42010
R:Finerty, H.; Kelleher, K.; Morris, G.E.; Bean, K.; Merberg, D.M.; Kitz, R.; Morris, J.
Oncogene 8, 2293-2298, 1993
A:Title: Molecular cloning of murine FLT4 and FLT4.
A:Reference number: 158375; MUID:9330572
A:Accession: 158375
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1363 <RES>
A:Cross-references: GB:L07296; NID:g293780; PIDN:AAA40077.1; PID:g293781
R:Galland, F.; Karamyshaya, A.; Mattei, M.G.; Rosnet, O.; Marchetto, S.; Birnbaum, D.
Genomics 13, 475-478, 1992
A:Title: Chromosomal localization of FLT4, a novel receptor-type tyrosine kinase gene.
A:Reference number: A42010; MUID:92307693
A:Accession: B42010
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: DNA
A:Residues: 1033-1072 <GAL>
C:Genetics:
A:Gene: FLT4
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C:Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F:843-1176/Domain: protein kinase homology <KIN>
F:851-859/Region: protein kinase ATP-binding motif

Query Match 22.7%; Score 43.5; DB 2; Length 1363;
Best Local Similarity 34.5%; Pred. No. 59;
Matches 10; Conservative 4; Mismatches 8; Indels 7; Gaps 1;
Oy 22 CSFXARXIFKD-----AXRTKLEWIS 43
Db 1054 CDFGLARDIYKDPVYRKGSARLPKMW 1082
RESULT 45
JC4954
vascular endothelial growth factor receptor 2 precursor - Japanese quail
N:Alternate names: Quail endothelial kinase 2; Quak 2
C:Species: Coturnix coturnix japonica (Japanese quail)
C>Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 24-Sep-1999
C:Accession: JC4954
R:Elchmann, A.; Marcelle, C.; Breant, C.; Le Douarin, N.M.
Gene 174, 3-8, 1996
A:Title: Molecular cloning of Quak 1 and 2, two quail vascular endothelial growth factor
A:Reference number: JC4953; MUID:97017121
A:Accession: JC4954
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1379 <ETC>
A:Cross-references: EMBL:X83287; NID:9619865; PIDN:CAA58267.1; PID:e283815; PID:q1707416
C:Comment: This protein is an endothelial-specific receptor and binds vascular endothel
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C:Keywords: ATP; embryo; growth factor receptor; transmembrane protein
F:1-20/Domain: signal sequence #status predicted <SIG>
F:789-810/Domain: transmembrane #status predicted <TM>
F:856-1186/Domain: protein kinase homology <KIN>
F:864-872/Region: protein kinase ATP-binding motif

Query Match 22.7%; Score 43.5; DB 2; Length 1379;
Best Local Similarity 34.5%; Pred. No. 60;
Matches 10; Conservative 4; Mismatches 8; Indels 7; Gaps 1;
Oy 22 CSFXARXIFKD-----AXRTKLEWIS 43
Db 1066 CDFGLARDIYKDPVYRKGSARLPKMW 1094

RESULT 46
D96996
uncharacterized low-complexity protein [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C:Accession: D96996
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Matkova, K.S.; Zeng, Q.; Gibson, R.; L
; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: D96996
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-211 <KOR>
A:Cross-references: GB:AE001437; PIDN:AAK78759.1; PID:g15023669; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC0783

Query Match 22.4%; Score 43; DB 2; Length 211;
Best Local Similarity 34.4%; Pred. No. 13;
Matches 11; Conservative 3; Mismatches 10; Indels 8; Gaps 1;
Oy 11 GSLRXCKXQCSFYXRXI-----FKDA 34
Db 46 GAHFKCMLYKCSFKHAEFISNLKGSDFKDA 77

RESULT 47
C72226
hypothetical protein TM1677 - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: C72226
R:Neelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwyn, M.L.; Dodson, R.J.; Haft, D.H.; Hic
garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A:Reference number: A72200; MUID:99287316
A:Accession: C72226
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-402 <ARN>
A:Cross-references: GB:AE001808; GB:AE000512; NID:g4982233; PIDN:AND36744.1; PID:g498
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM1677
C:Superfamily: hypothetical protein b1432

Query Match 22.4%; Score 43; DB 2; Length 402;
Best Local Similarity 25.6%; Pred. No. 23;
Matches 10; Conservative 7; Mismatches 18; Indels 4; Gaps 1;
Oy 10 PGSIXRCKXQCS-----FXXARXIFKDXRTKLEWIS 44
Db 14 PCHLSQTCBELNRTAARIYNKTMSTIVRKIKHKKGWLSW 52

RESULT 48
C83494
probable 2-isopropylmalate synthase PA1217 [imported] - Pseudomonas aeruginosa (strai
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: C83494
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
A:Reference number: A82950; MUID:20437337
A:Accession: C83494
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-455 <STO>
A:Cross-references: GB:AE004551; GB:AE004091; MID:g9947135; PIDN:ANG04606.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA1217

Query Match 22.4%; Score 43; DB 2; Length 455;
Best Local Similarity 36.8%; Pred. No. 26;
Matches 7; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 12 SLRXCKXXQCSEFXRXI 30
DB 8 TLREGCOARQCSEFXRXI 26

RESULT 49

PH0976
Ig heavy chain V region (clone 25.12m) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH0976
R:Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell
A:Reference number: PH0971; MUID:92381444
A:Accession: PH0976
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-105 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotrimer; Immunoglobulin
F:14-97/Domain: Immunoglobulin homology <IMM>

Query Match 22.1%; Score 42.5; DB 2; Length 105;
Best Local Similarity 28.9%; Pred. No. 8.1;
Matches 11; Conservative 6; Mismatches 20; Indels 1; Gaps 1;

OY 8 LRPSLXRXCKXXQCSEFXRXIF-KDAXRTKLFWISY 44
DB 12 VKRGSVKISCKASGYFTDYNDMDVWQSHGKSLWICGY 49

RESULT 50

T20272
hypothetical protein C5667.3 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C:Accession: T20272
R:percy, C.
submitted to the EMBL Data Library, November 1994
A:Reference number: Z19245
A:Accession: T20272
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-322 <WIL>
A:Cross-references: EMBL:Z46793; PIDN:CAA86771.1; GSPDB:GN00021; CESP:C5667.3
A:Experimental source: clone C5667
C:Genetics:
A:Gene: CESP:C5667.3
A:Map position: 3
A:Introns: 26/3; 225/3; 251/2; 294/1
C:Superfamily: *Caenorhabditis elegans* hypothetical protein C5667.3

Query Match 22.1%; Score 42.5; DB 2; Length 322;
Best Local Similarity 25.0%; Pred. No. 23;
Matches 9; Conservative 6; Mismatches 18; Indels 3; Gaps 1;

OY 4 FLXXLRPSLXRXCK--KXXQCSEFXRXIFKDXR 36
DB 262 FFSALHASAMCRCSIRKSKQCTLANQTIFSETTR 297

Search completed: August 30, 2002, 15:32:46
Job time: 5841 sec

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OM protein - protein search, using sw model

Run on: August 30, 2002, 15:31:20 ; Search time 77.99 Seconds

(Without alignments)
21.845 Million cell updates/sec

Title: US-09-302-239-3

Perfect score: 192
Sequence: 1 ANAFLLXLRPGSLXKRCXX.....XXARKLIFKDAKRLKLFWISY 44

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 50 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	172	89.6	466	FA7_HUMAN	P08709 homo sapien
2	138	71.9	444	FA7_RABIT	P98139 oryctolagus
3	127	66.1	446	FA7_MOUSE	P70375 mus musculu
4	123	64.1	407	FA7_BOVIN	P22457 bos taurus
5	114	59.4	459	PRTC_PIG	Q991P2 sus scrofa
6	109	56.8	461	PRTC_MOUSE	P33587 mus musculu
7	104	54.2	456	PRTC_BOVIN	P00745 bos taurus
8	102	53.1	488	FA10_HUMAN	P00742 homo sapien
9	101	52.6	492	FA10_BOVIN	P00743 bos taurus
10	100	52.1	461	PRTC_RAT	P31394 rattus norv
11	99	51.6	218	FA10_HUMAN	O14668 homo sapien
12	98	51.0	490	FA10_RABIT	O19045 oryctolagus
13	94	49.0	458	PRTC_RABIT	Q28661 oryctolagus
14	92	47.9	376	FA10_TROCA	P81428 tropidochis
15	91	47.4	475	FA10_CHICK	P25155 gallus gall
16	89	46.4	202	TMG2_HUMAN	O14669 homo sapien
17	88	45.8	231	TMG3_HUMAN	Q992d7 homo sapien
18	86	44.8	416	FA9_BOVIN	P00741 bos taurus
19	84	43.8	461	PRTC_HUMAN	P04070 homo sapien
20	83	43.2	461	FA9_HUMAN	P00740 homo sapien
21	83	43.2	622	THRB_HUMAN	P00734 homo sapien
22	82.5	43.0	226	TMG4_HUMAN	Q992d6 homo sapien
23	79	41.1	617	THRB_RAT	P18292 rattus norv
24	79	41.1	618	THRB_MOUSE	P19221 mus musculu
25	78	40.6	452	FA9_MOUSE	P19540 canis famli
26	78	40.6	459	FA9_MOUSE	P16294 mus musculu
27	66	34.4	675	PRTS_BOVIN	P07224 bos taurus
28	64	33.3	646	PRTS_RABIT	P98118 oryctolagus
29	64	33.3	649	PRTS_MACMO	Q28520 macaca mula
30	64	33.3	676	PRTS_HUMAN	P07225 homo sapien
31	63	32.8	396	PRT2_BOVIN	P00744 bos taurus
32	63	32.8	625	THRB_BOVIN	P00735 bos taurus
33	63	32.8	675	PRTS_RAT	P53813 rattus norv

34	58	30.2	400	1	PRT2_HUMAN	P22891 homo sapien
35	56	29.2	675	1	PRTS_MOUSE	O08761 mus musculu
36	45	23.4	879	1	YNG5_YEAST	P42837 saccharomyc
37	44	22.9	422	1	SPM1_SCHPO	Q92398 schizosacch
38	43.5	22.7	1298	1	VGR3_HUMAN	P35916 homo sapien
39	43.5	22.7	1363	1	VGR3_MOUSE	P35917 mus musculu
40	42.5	22.1	322	1	YOL3_CAEEL	O09292 caenorhabdi
41	42	21.9	263	1	PRLA_STRUD	O06575 streptococc
42	42	21.9	753	1	NAPA_DESDE	P81186 desulfovibr
43	41.5	21.6	1348	1	VGR2_COTUA	P52583 coturnix co
44	41.5	21.6	1356	1	VGR2_HUMAN	P35968 homo sapien
45	41.5	21.6	1367	1	VGR2_MOUSE	P35918 mus musculu
46	41	21.4	462	1	TBMP_SOCMV	P15628 soybean chl
47	41	21.4	484	1	STF2_YEAST	Q00772 saccharomyc
48	41	21.4	557	1	FM04_HUMAN	P31512 homo sapien
49	40.5	21.1	370	1	MPK1_ARAVH	Q39021 arabidopsis
50	40.5	21.1	1343	1	VGR2_RAT	O08775 rattus norv

ALIGNMENTS

RESULT 1
FA7_HUMAN
ID FA7_HUMAN STANDARD: PRT: 466 AA.
AC P08709; Q14339; (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator) (Eptacog alfa).
CN F7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=86205965; PubMed=3486420;
RA Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C.,
RA Woodbury R.G., Hart C.E., Insley M.Y., Kistel W., Kurachi K.,
RA Davyle E.W.;
RT "Characterization of a cDNA coding for human factor VII.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87260948; PubMed=3037537;
RA O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y.,
RA Hagen F.S., Murray M.J.;
RT "Nucleotide sequence of the gene coding for human factor VII, a
RT vitamin K-dependent protein participating in blood coagulation.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).
RN [3]
RP SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=89088153; PubMed=3264725;
RA Thim L., Bjørn S., Christensen M., Nicolaisen E.M., Lund-Hansen T.,
RA Pedersen A.H., Hedner U.;
RT "Amino acid sequence and posttranslational modifications of human
RT factor VIIa from plasma and transfected baby hamster kidney cells.";
RL Biochemistry 27:7785-7793(1988).
RN [4]
RP CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.
RX MEDLINE=91250411; PubMed=1904059;
RA Bjørn S., Foster D.C., Thim L., Wibeberg F.C., Christensen M.,
RA Komiyama Y., Pedersen A.H., Kistel W.;
RT "Human plasma and recombinant factor VII. Characterization of O-
RT glycosylations at serine residues 52 and 60 and effects of site-
RT directed mutagenesis of serine 52 to alanine.";
RL J. Biol. Chem. 266:11051-11057(1991).
RN [5]
RP STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=90062160; PubMed=2511201;

RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T., Takao T.,
 RA Shimomishi Y., Iwanaga S.;
 RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
 RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first
 RT epidermal growth factor-like domain of human factors VII and IX and
 RT protein Z and bovine protein Z.";
 RL J. Biol. Chem. 264:20320-20325(1989).
 RN [6]
 RP STRUCTURE OF CARBOHYDRATE ON SER-112.
 RX MEDLINE-91344709; PubMed-2129367;
 RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;
 RT "A new trisaccharide sugar chain linked to a serine residue in the
 RT first EGF-like domain of clotting factors VII and IX and protein Z.";
 RL Adv. Exp. Med. Biol. 281:121-131(1990).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE-96175641; PubMed-8598903;
 RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,
 RA Konigsberg W.H., Nemerson Y., Kirchhofer D.;
 RT "The crystal structure of the complex of blood coagulation factor
 RT VIIa with soluble tissue factor.";
 RL Nature 380:41-46(1996).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE-99126538; PubMed-9925787;
 RA Zhang E., St Charles R., Tulinsky A.;
 RT "Structure of extracellular tissue factor complexed with factor VIIa
 RT inhibited with a BPTI mutant.";
 RL J. Mol. Biol. 285:2089-2104(1999).
 RN [9]
 RP STRUCTURE BY NMR OF 105-145
 RX MEDLINE-98367502; PubMed-9692950;
 RA Muranyi A., Flinn B.E., Gippert G.P., Forsen S., Stenflo J.;
 RT "Solution structure of the N-terminal EGF-like domain from human
 RT factor VII.";
 RL Biochemistry 37:10605-10615(1998).
 RN [10]
 RP VARIANT GLN-364.
 RX MEDLINE-91300046; PubMed-2070047;
 RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,
 RA Meade T.W., Tuddenham E.G.D.;
 RT "Purification and characterization of factor VII 304-Gln: a variant
 RT molecule with reduced activity isolated from a clinically unaffected
 RT male.";
 RL Blood 78:132-140(1991).
 RN [11]
 RP VARIANTS GLN-364 AND PHE-370.
 RX MEDLINE-92340074; PubMed-1634227;
 RA Marchetti G., Patrachini P., Gemmati D., Derosa V., Pinotti M.,
 RA Rodotrig G., Casonato A., Girolami A., Bernardi F.;
 RT "Detection of two missense mutations and characterization of a repeat
 RT polymorphism in the factor VII gene (F7).";
 RL Hum. Genet. 89:497-502(1992).
 RN [12]
 RP VARIANT TYR-238.
 RX MEDLINE-93372811; PubMed-8364544;
 RA Marchetti G., Ferrati M., Patrachini P., Redaelli R., Bernardi F.;
 RT "A missense mutation (178Cys->Tyr) and two neutral dimorphisms
 RT (115His and 333Ser) in the human coagulation factor VII gene.";
 RL Hum. Mol. Genet. 2:1055-1056(1993).
 RN [13]
 RP VARIANTS.
 RX MEDLINE-94061028; PubMed-8242057;
 RA Takamiya O., Kemball-Cook G., Martin D.M.A., Cooper D.N.,
 RA von Felten A., Melli E., Hahn I., Prangnell D.R., Lumley H.,
 RA Tuddenham E.G.D., McVey J.H.;
 RT "Detection of missense mutations by single-strand conformational
 RT polymorphism (SSCP) analysis in five dysfunctional variants of
 RT coagulation factor VII.";
 RL Hum. Mol. Genet. 2:1355-1359(1993).
 RN [14]
 RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.

RX MEDLINE-94264305; PubMed-8204879;
 RA Chaling S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W.,
 RA Roberts H.R., Blakejman M., Monroe D.M., High K.A.;
 RT "Severe factor VII deficiency caused by mutations abolishing the
 RT cleavage site for activation and altering binding to tissue factor.";
 RL Blood 83:3524-3535(1994).
 RN [15]
 RP VARIANT VAL-354.
 RX MEDLINE-95072589; PubMed-7981691;
 RA Bernardi F., Castaman G., Redaelli R., Pinotti M., Lunghi B.,
 RA Rodeghiero F., Marchetti G.;
 RT "Topologically equivalent mutations causing dysfunctional coagulation
 RT factors VII (294Ala->Val) and X (334Ser->Pro).";
 RL Hum. Mol. Genet. 3:1175-1177(1994).
 RN [16]
 RP VARIANT MIE HIS-307.
 RX MEDLINE-95064662; PubMed-7974346;
 RA Ohwa M., Hayashi T., Wada H., Minamikawa K., Shirakawa S.,
 RA Suzuki K.;
 RT "Factor VII Mie: homozygous asymptomatic type I deficiency caused by
 RT an amino acid substitution of His (CAC) for Arg(247) (CGC) in the
 RT catalytic domain.";
 RL Thromb. Haemost. 71:773-777(1994).
 RN [17]
 RP VARIANT MET-419.
 RX MEDLINE-96247510; PubMed-8652821;
 RA Arbini A.A., Mannucci P.M., Bauer K.A.;
 RT "A Thr359Met mutation in factor VII of a patient with a hereditary
 RT deficiency causes defective secretion of the molecule.";
 RL Blood 87:5085-5094(1996).
 RN [18]
 RP VARIANTS W-283; K-325; V-358; Q-364; E-402 AND Q-413.
 RX MEDLINE-97001216; PubMed-8844208;
 RA Bernardi F., Castaman G., Pinotti M., Ferraresi P., di Iasio M.G.,
 RA Lunghi B., Rodeghiero F., Marchetti G.;
 RT "Mutation pattern in clinically asymptomatic coagulation factor VII
 RT deficiency.";
 RL Hum. Mutat. 8:108-115(1996).
 RN [19]
 RP VARIANT VAL-304.
 RX MEDLINE-97037613; PubMed-8883260;
 RA Tamay H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N.,
 RA Brenner B., Paz M., Luder A.S., Blau O., Korostilshesky M.,
 RA Zaitov R., Seligsohn U.;
 RT "Ala244Val is a common, probably ancient mutation causing factor VII
 RT deficiency in Moroccan and Iranian Jews.";
 RL Thromb. Haemost. 76:283-291(1996).
 RN [20]
 RP VARIANTS MALTA THR-194 AND VAL-304.
 RX MEDLINE-98112461; PubMed-9452082;
 RA Alshinawi C., Scerif C., Galdies R., Aquilina A., Felice A.E.;
 RT "Two new missense mutations (P134T and A244V) in the coagulation
 RT factor VII gene.";
 RL Hum. Mutat. Suppl. 1:5189-5191(1998).
 CC -I- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
 CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR
 CC THROMBIN BY MINOR PROTEOLYSES. IN THE PRESENCE OF TISSUE FACTOR
 CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
 CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
 CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.
 CC -I- CATALYTIC ACTIVITY: Hydrolyses one Arg-1-Ile bond in factor X to
 CC form factor Xa.
 CC -I- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
 CC BY A DISULFIDE BOND.
 CC -I- ALTERNATIVE PRODUCTS: 2 isoforms; A (shown here) and B; are
 CC produced by alternative splicing.
 CC -I- TISSUE SPECIFICITY: PLASMA.
 CC -I- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC -I- DISEASE: DEFECTS IN F7 CAN CAUSE COAGULOPATHY.
 CC -I- PHARMACEUTICAL: Available under the names Niasase or Novoseven
 CC (Novo Nordisk). Used for the treatment of bleeding episodes in

CC hemophilia A or B patients with antibodies to coagulation factors
CC VIII or IX.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.

Query Match 89.6%; Score 172; DB 1; Length 466;
Best Local Similarity 77.3%; Pred. No. 3.2e-23;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Oy 1 ANAEFLXLRPGSLKRXKXXCCSFYKXRXIKDAKRTLFWISY 44
Db 61 ANAEFLRLPGSLRECKEQQSFEEAREIFKDAERTKLFWISY 104

RESULT 2
FA7_RABIT STANDARD; PRT; 444 AA.
AC P98139; P79224;
DT 01-FEB-1996 (Rel. 33, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator).
GN F7.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
ON NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93190306; PubMed=8383365;
RA Brothers A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;
RT Complete nucleotide sequence of the cDNA encoding rabbit coagulation
RT factor VII.
RL Thomb. Res. Suppl. 69:231-238(1993).
RN [2]
RP REVISION TO 395.
RC TISSUE=Liver;
RA Ruiz S.R., Blajchman M.A., Clarke B.J.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR
CC THROMBIN BY MINOR PROTEOLYSES. IN THE PRESENCE OF TISSUE FACTOR
CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
CC SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Hydrolyses one Arg-|-Ile bond in factor X to
CC form factor Xa.
CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
CC BY A DISULFIDE BOND (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS 2 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.

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CC or send an email to license@isb-sib.ch).

CC EMBL: U77477; AAB37326.1; -
DR HSSP; P08709; 1BF9.
DR MEROPS; S01.215; -
DR InterPro; IPR002086; Aldehyde_dehydr.

DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR00742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Trypsin.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; tryp-spec; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Blood coagulation; zymogen; Glycoprotein;
KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
KW EGF-like domain; Repeat; Signal; Hydroxylation.
FT SIGNAL 1 21
FT PROPEP 22 39
FT CHAIN 40 191
FT CHAIN 192 444
FT DOMAIN 45 74
FT DOMAIN 85 121
FT DOMAIN 126 167
FT DOMAIN 192 444
FT SITE 191 192
FT ACT_SITE 232 232
FT ACT_SITE 281 281
FT ACT_SITE 383 383
FT BINDING 377 377
FT DISULFID 56 61
FT DISULFID 89 100
FT DISULFID 94 109
FT DISULFID 111 120
FT DISULFID 130 141
FT DISULFID 137 151
FT DISULFID 153 166
FT DISULFID 174 301
FT DISULFID 198 203
FT DISULFID 217 233
FT DISULFID 349 368
FT DISULFID 379 407
FT MOD_RES 45 45
FT MOD_RES 46 46
FT MOD_RES 53 53
FT MOD_RES 55 55
FT MOD_RES 58 58
FT MOD_RES 59 59
FT MOD_RES 64 64
FT MOD_RES 65 65
FT MOD_RES 68 68
FT MOD_RES 74 74
FT MOD_RES 102 102
FT CARBOHYD 211 211
FT CARBOHYD 242 242
FT CARBOHYD 306 306
SO SEQUENCE 444 AA; 49011 MM; 0481ABC4FE342F78 CRC64;

Query Match 71.9%; Score 138; DB 1; Length 444;
Best Local Similarity 59.1%; Pred. No. 4.1e-17;

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Matches 26; Conservative 4; Mismatches 14; Indels 0; Gaps 0;
Qy 1 ANAFLLXLRPGSLRXKXQCSEFXXARXIFKQAXRTKLEWISY 44
Db 40 ANSLEELRPGSLRECKELCSFEAREVFOSTERTKQWIVY 83

RESULT 3
FA7_MOUSE STANDARD; PRT; 446 AA.
AC P70375;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Coagulation factor VII precursor (BC 3.4.21.21) (Serum prothrombin
DE conversion accelerator).
FN F7 OR CF7.
GN
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97127167; PubMed=8972017;
RA Idusogie E., Rosen E.D., Carmeliet P., Collen D., Castellino F.J.;
RT "Nucleotide structure and characterization of the murine blood
RT coagulation factor VII gene."
RL Thromb. Haemost. 76:957-964(1996).
CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
CC CONVERTED TO FACTOR VIIa BY FACTOR XIa, FACTOR XIIa, FACTOR IXd, OR
CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
CC SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Hydrolyses one Arg-1-Ile bond in factor X to
CC form factor Xa.
CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
CC BY A DISULFIDE BOND (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM (BY SIMILARITY)
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
CC -----
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CC -----
DR EMBL: U66079; AAC33796.1; -.
DR HSSP: P08709; 1BF9.
DR MEROPS: S01.215; -.
DR MGD: MGI:109325; F7.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000361; EGF-like.
DR InterPro: IPR000742; EGF-2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Trypsin.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; gla_1.
DR Pfam: PF00089; trypsin_1.
DR PRINTS: PRO0722; CHYMOTRYPSIN.
DR PRINTS: PRO0001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 1.
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DR SMART: SM00001; EGF_like; 1.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; TRYP_SPC; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF-2; FALSE_NEG.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Serine protease; Blood coagulation; zymogen; glycoprotein;
KW Liver; Plasma; Vitamin K; Calcium-binding; gamma-carboxyglutamic acid;
KW EGF-like domain; Repeat; Signal; Hydroxylation.
FT SIGNAL 1 24
FT PROPEP 25 41
FT CHAIN 42 193
FT CHAIN 194 446
FT DOMAIN 47 76
FT DOMAIN 87 123
FT DOMAIN 128 169
FT DOMAIN 194 446
FT SITE 193 194
FT ACT_SITE 234 234
FT ACT_SITE 283 283
FT ACT_SITE 385 385
FT BINDING 379 379
FT DISULFID 58 63
FT DISULFID 91 102
FT DISULFID 96 111
FT DISULFID 113 122
FT DISULFID 132 143
FT DISULFID 139 153
FT DISULFID 155 168
FT DISULFID 176 303
FT DISULFID 200 205
FT DISULFID 219 235
FT DISULFID 351 370
FT DISULFID 381 409
FT MOD_RES 47 47
FT MOD_RES 48 48
FT MOD_RES 55 55
FT MOD_RES 57 57
FT MOD_RES 60 60
FT MOD_RES 61 61
FT MOD_RES 66 66
FT MOD_RES 67 67
FT MOD_RES 70 70
FT MOD_RES 76 76
FT MOD_RES 104 104
FT CARBOHYD 186 186
FT CARBOHYD 244 244
SQ SEQUENCE 446 AA; 50276 MW; 2512E44A4A5CB936 CRC64;

Query Match Score 127; DB 1; Length 446;
Best Local Similarity 59.1%; Pred. No. 4e-15;
Matches 26; Conservative 1; Mismatches 17; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRPGSLRXKXQCSEFXXARXIFKQAXRTKLEWISY 44
Db 42 ANSLEELRPGSLRECKELCSFEAREVFOSTERTKQWIVY 85

RESULT 4
FA7_BOVIN STANDARD; PRT; 407 AA.
ID FA7_BOVIN
AC P22457;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Coagulation factor VII (BC 3.4.21.21) (Serum prothrombin conversion
```

DE accelerator).

GN F7.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE.

RX MEDLINE=69008362; PubMed=3049594;

RA Takeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T.,

RA Iwanaga S.;

RT "Bovine factor VII. Its purification and complete amino acid

RT sequence.";

RL J. Biol. Chem. 263:14868-14877(1988).

RN [2]

RP STRUCTURE OF CARBOHYDRATE ON SER-52.

RX MEDLINE=8921399; PubMed=3149637;

RA Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T.,

RA Miyata T., Iwanaga S., Takao T., Shimomishi Y., Ikenaka T.;

RT "A new trisaccharide sugar chain linked to a serine residue in bovine

RT blood coagulation factors VII and IX.";

RL J. Biochem. 104:867-868(1988).

RN [3]

RP STRUCTURE OF CARBOHYDRATE ON SER-52.

RX MEDLINE=91344709; PubMed=2129367;

RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;

RT "A new trisaccharide sugar chain linked to a serine residue in the

RT first EGF-like domain of clotting factors VII and IX and protein Z.";

RL Adv. Exp. Med. Biol. 281:121-131(1990).

CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS

CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR

CC THROMBIN BY MINOR PROTEOLYSES. IN THE PRESENCE OF TISSUE FACTOR

CC AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA

CC BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO

CC FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.

CC -1- CATALYTIC ACTIVITY: Hydrolyses one Arg-Ile bond in factor X to

CC form factor Xa.

CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED

CC BY A DISULFIDE BOND.

CC -1- TISSUE SPECIFICITY: PLASMA.

CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAATIC CARBOXYLATION OF SOME

CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND

CC CALCIUM.

CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE

CC TRYPSIN FAMILY.

DR PIR: A31979; A31979.

DR HSSP: P08709; 1BF9.

DR MEROPS: S01.215; -.

DR InterPro: IPR000152; Asx_hydroxyl.

DR InterPro: IPR001314; Chymotrypsin.

DR InterPro: IPR000561; EGF_1like.

DR InterPro: IPR000742; EGF_2.

DR InterPro: IPR001881; EGF_Ca.

DR InterPro: IPR001438; EGF_II.

DR InterPro: IPR002383; GLA_blood.

DR InterPro: IPR001254; Trypsin.

DR InterPro: IPR000294; VitK_dep_GLA.

DR Pfam: PF00008; EGF_2.

DR Pfam: PF00594; gla_1.

DR Pfam: PF00089; trypsin_1.

DR PRINTS: PR00722; CHYMOTRYPSIN.

DR PRINTS: PR00010; EGFBL00D.

DR PRINTS: PR00001; GLABLOOD.

DR SMART: SM00179; EGF_CA_1.

DR SMART: SM00001; EGF_1like_1.

DR SMART: SM00069; GLA_1.

DR SMART: SM00020; TRYP_SF_1.

DR PROSITE: PS00010; ASX_HYDROXYL_1.

DR PROSITE: PS00022; EGF_1; 1.

DR PROSITE: PS01186; EGF_2; 2.

DR PROSITE: PS01187; EGF_CA_1.

DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.

DR PROSITE: PS50240; TRYPSIN_DOM; 1.

DR PROSITE: PS00134; TRYPSIN_HIS; 1.

DR PROSITE: PS00135; TRYPSIN_SER; 1.

KW Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;

KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;

KW EGF-like domain; Repeat.

FT CHAIN 1 152

FT CHAIN 153 407

FT DOMAIN 6 35

FT DOMAIN 46 82

FT DOMAIN 87 128

FT DOMAIN 153 407

FT SITE 152 153

FT ACT_SITE 193 193

FT ACT_SITE 242 242

FT ACT_SITE 344 344

FT BRINDING 338 338

FT DISULFID 17 22

FT DISULFID 50 61

FT DISULFID 55 70

FT DISULFID 72 81

FT DISULFID 91 102

FT DISULFID 98 112

FT DISULFID 114 127

FT DISULFID 135 262

FT DISULFID 159 164

FT DISULFID 178 194

FT DISULFID 310 329

FT DISULFID 340 368

FT MOD_RES 6 6

FT MOD_RES 7 7

FT MOD_RES 14 14

FT MOD_RES 16 16

FT MOD_RES 19 19

FT MOD_RES 20 20

FT MOD_RES 25 25

FT MOD_RES 26 26

FT MOD_RES 29 29

FT MOD_RES 35 35

FT MOD_RES 52 52

FT CARBOHYD 145 145

FT CARBOHYD 203 203

SO SEQUENCE 407 AA; 44431 MM; 703ELFE063677F10 CRC64;

Query Match 64.1%; Score 123; DB 1; Length 407;

Best Local Similarity 52.3%; Pred. No. 1, 9e-14;

Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Oy 1 ANAEPLXLRPGSLXRXCKXCCSFXXARXIFKXARKLEWISY 44

Db 1 ANGFLLEELPGLSLRECHREELCSFEAEHIEIRNEERTQFWVSY 44

RESULT 5

ID PRTC_PIG STANDARD; PRT; 459 AA.

AC Q9GLP2;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)

DE (Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation

DE factor XIV).

GN PROC.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

KM	EGF-like domain; Repeat;	Endothelial cell; Hydrolyase; Signal.
FT	SIGNAL	1 33 BY SIMILARITY.
FT	PROPEP	34 41 BY SIMILARITY.
FT	CHAIN	42 196 PROTEIN C LIGHT CHAIN (BY SIMILARITY).
FT	CHAIN	199 461 PROTEIN C HEAVY CHAIN (BY SIMILARITY).
FT	PEPTIDE	199 212 ACTIVATION PEPTIDE (BY SIMILARITY).
FT	SITE	212 213 CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
FT	DOMAIN	96 131 EGF-LIKE 1.
FT	DOMAIN	135 175 EGF-LIKE 2.
FT	DOMAIN	213 461 SERINE PROTEASE.
FT	MOD_RES	47 47 GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	48 48 (BY SIMILARITY).
FT	MOD_RES	55 55 GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	55 55 (BY SIMILARITY).
FT	MOD_RES	57 57 GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	57 57 (BY SIMILARITY).
FT	MOD_RES	60 60 GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	60 60 (BY SIMILARITY).
FT	MOD_RES	61 61 GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	61 61 (BY SIMILARITY).
FT	MOD_RES	66 66 GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	66 66 (BY SIMILARITY).
FT	MOD_RES	67 67 GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	67 67 (BY SIMILARITY).
FT	MOD_RES	70 70 GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	70 70 (BY SIMILARITY).
FT	MOD_RES	112 112 HYDROXYLATION (BY SIMILARITY).
FT	ACT_SITE	253 253 CHARGE RELAY SYSTEM.
FT	ACT_SITE	299 299 CHARGE RELAY SYSTEM.
FT	ACT_SITE	402 402 CHARGE RELAY SYSTEM.
FT	DISULFD	58 63 BY SIMILARITY.
FT	DISULFD	91 110 BY SIMILARITY.
FT	DISULFD	100 105 BY SIMILARITY.
FT	DISULFD	104 119 BY SIMILARITY.
FT	DISULFD	121 130 BY SIMILARITY.
FT	DISULFD	139 150 BY SIMILARITY.
FT	DISULFD	146 159 BY SIMILARITY.
FT	DISULFD	161 174 BY SIMILARITY.
FT	DISULFD	182 319 INTERCHAIN (BY SIMILARITY).
FT	DISULFD	238 254 BY SIMILARITY.
FT	DISULFD	373 387 BY SIMILARITY.
FT	CARBOHYD	398 426 BY SIMILARITY.
FT	CARBOHYD	214 214 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	328 MISSING (IN REF. 2).
FT	CONFLICT	393 N-> D (IN REF. 2).
FT	SEQUENCE	461 AA; 51945 MW; 53FAAD85B194D6E CRC64;
<hr/>		
Query Match 56.8%; Score 109; DB 1; Length 461;		
Best Local Similarity 47.7%; Pred.No. 7.2e-12;		
Matches 21; Conservative 5; Mismatches 18; Indels 0; Gaps 0;		
Oy	1 ANAFLLXLRPGSLRXCKXXQCSFYKAXXIIFRDAXRTLFMTSY 44	:
Db	42 ANSFLEMRPSGLERECMEIICDFEEAOEIFQVNEDTLAFWIKY 85	:
<hr/>		
RESULT 7		
PRTC_BOVIN	STANDARD:	PRT: 456 AA.
ID_PRTC_BOVIN	P00745:	
DR	21-JUL-1986 (Rel. 01, Created)	
DR	13-AUG-1987 (Rel. 05, Last sequence update)	
DR	16-OCT-2001 (Rel. 40, Last annotation update)	
DE	Vitamin-k dependent protein C precursor (EC 3.4.21.65)	
DE	(Autoproteolytic cleavage)	
DE	factor XIV (Fragment).	
OS	Bos taurus (Bovine).	

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bos.
 ON NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85014826; PubMed=6091100;
 RA Long G.L., Balagaje R.M., McGillivray R.T.A.;
 RT "Cloning and sequencing of liver cDNA coding for bovine protein C.;"
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).
 RP [2]
 RP SEQUENCE OF 40-194.
 RX MEDLINE=83007325; PubMed=6896876;
 RA Fernlund P., Stenflo J.;
 RT "Amino acid sequence of the light chain of bovine protein C.;"
 RL J. Biol. Chem. 257:12170-12179(1982).
 RN [3]
 RP REVISION TO 110.
 RX MEDLINE=83169769; PubMed=6572939;
 RA Drakenberg T., Fernlund P., Roepstorff P., Stenflo J.;
 RT "Beta-hydroxyaspartic acid in vitamin K-dependent protein C.;"
 RL Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).
 RN [4]
 RP SEQUENCE OF 197-456.
 RX MEDLINE=83007326; PubMed=6896877;
 RA Stenflo J., Fernlund P.;
 RT "Amino acid sequence of the heavy chain of bovine protein C.;"
 RL J. Biol. Chem. 257:12180-12190(1982).
 RN [5]
 RP PROCESSING, AND CALCIUM-BINDING DATA.
 RX MEDLINE=83213513; PubMed=6304092;
 RA Esmon N.L., Debault L.E., Esmon C.T.;
 RT "Proteolytic formation and properties of gamma-carboxyglutamic acid-
 domainless protein C.;"
 RL J. Biol. Chem. 258:5548-5553(1983).
 RN [6]
 RP PROCESSING, AND CALCIUM-BINDING DATA.
 RX MEDLINE=83213514; PubMed=6406503;
 RA Johnson A.E., Esmon N.L., Laue T.M., Esmon C.T.;
 RT "Structural changes required for activation of protein C are induced
 by Ca2+ binding to a high affinity site that does not contain gamma-
 carboxyglutamic acid.;"
 RL J. Biol. Chem. 258:5554-5560(1983).
 CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
 REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
 IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
 and VIIIA.
 CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
 INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
 BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
 TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
 REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
 CC STRONGLY PROMOTED BY THROMBOMODULIN.
 CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMIC CARBOXYLATION OF SOME
 CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
 CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
 CC THROMBIN-THROMBOMODULIN COMPLEX.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 CC -----
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DR EMBL: K02435; AAA30685.1; -.
 DR PIR: A00928; KXBO.
 DR HSSP: P04070; 1PCU.
 DR MEROPS: S01.218; -.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF-Ca.
 DR InterPro: IPR001254; Trypsin.
 DR InterPro: IPR000294; VitK_dep_Glu.
 DR Pfam: PF00008; EGF_2.
 DR Pfam: PF00594; gla_1.
 DR Pfam: PF00089; trypsin_1.
 DR SMART: SM00181; EGF_2.
 DR SMART: SM00069; GLA_1.
 DR SMART: SM00020; TRYP_SPE; 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; 1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF-Ca; 1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; FALSE_NEG.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Blood coagulation; Glycoprotein; Serine protease;
 KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 KW EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
 FT SIGNAL 1 29
 FT PROPEP 30 39
 FT CHAIN 40 194
 FT CHAIN 197 456
 FT PEPTIDE 197 210
 FT DOMAIN 94 129
 FT DOMAIN 133 173
 FT DOMAIN 211 456
 FT MOD_RES 45 45
 FT MOD_RES 46 46
 FT MOD_RES 53 53
 FT MOD_RES 55 55
 FT MOD_RES 58 58
 FT MOD_RES 59 59
 FT MOD_RES 62 62
 FT MOD_RES 64 64
 FT MOD_RES 65 65
 FT MOD_RES 68 68
 FT MOD_RES 74 74
 FT MOD_RES 110 110
 FT ACT_SITE 252 252
 FT ACT_SITE 298 298
 FT ACT_SITE 397 397
 FT ACT_SITE 56 61
 FT DISULFID 89 108
 FT DISULFID 98 103
 FT DISULFID 102 117
 FT DISULFID 119 128
 FT DISULFID 137 148
 FT DISULFID 144 157
 FT DISULFID 159 172
 FT DISULFID 180 318
 FT DISULFID 237 253
 FT DISULFID 368 382
 FT DISULFID 393 421
 FT DISULFID 136 136
 FT CARBOHYD 289 289
 FT CARBOHYD 350 350
 FT CARBOHYD 366 366
 FT VARIANT 82 82
 FT CONFLICT 455 456
 SQ SEQUENCE 456 AA; 51407 MW; 51407 MW; CAAR6833F894C209 CRC64;
 N-LINKED (GLCNAC. . .).
 N-LINKED (GLCNAC. . .).
 N-LINKED (GLCNAC. . .).
 N-LINKED (GLCNAC. . .).
 N-LINKED (GLCNAC. . .).
 F -> K.
 VP -> PV (IN REF. 4).
 CAAR6833F894C209 CRC64;

Query Match 54.28; Score 104; DB 1; Length 456;
 Best Local Similarity 45.58; Pred. No. 5.7e-11;

Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLLXLRPGSLRXKXKXOCSEFXKXARFKRDAKRTKLFMTSY 44
DB 40 ANSFLLELRPGNVERECSEWCEFEAREIFQNMEDTMAFSFY 83

RESULT 8
FA10_HUMAN STANDARD; PRT; 488 AA.
AC P00742; Q14340;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Coagulation factor X precursor (BC 3.4.21.6) (Stuart factor).
GN F10.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91216473; PubMed=1902434;
RA Messier T.L., Pittman D.D., Long G.L., Kaufman R.J., Church W.R.;
RT "Cloning and expression in COS-1 cells of a full-length cDNA encoding
human coagulation factor X.";
RL Gene 99:291-294(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87026600; PubMed=3768336;
RA Leytus S.P., Foster D.C., Kurachi K., Davie E.W.;
RT "Gene for human factor X: a blood coagulation factor whose gene
organization is essentially identical with that of factor IX and
protein C.";
RL Biochemistry 25:5098-5102(1986).
RN [3]
RP SEQUENCE OF 13-488 FROM N.A.
RX MEDLINE=85216545; PubMed=2582420;
RA Fung M.R., Hay C.W., McGillivray R.T.A.;
RT "Characterization of an almost full-length cDNA coding for human
blood coagulation factor X.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).
RN [4]
RP SEQUENCE OF 19-488 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=86221713; PubMed=3011603;
RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;
RT "Isolation and characterization of human blood-coagulation factor X
cDNA.";
RL Gene 41:311-314(1986).
RN [5]
RP SEQUENCE OF 41-179.
RX MEDLINE=83257207; PubMed=6871167;
RA McMillen B.A., Fujikawa K., Kistiel W., Sasagawa T., Howald W.N.,
RT Kwa E.Y., Weinstein B.;
RT "Complete amino acid sequence of the light chain of human blood
coagulation factor X: evidence for identification of residue 63 as
beta-hydroxyaspartic acid.";
RL Biochemistry 22:2875-2884(1983).
RN [6]
RP SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=Liver;
RX MEDLINE=84222026; PubMed=6587384;
RA Leytus S.P., Chung D.W., Kistiel W., Kurachi K., Davie E.W.;
RT "Characterization of a cDNA coding for human factor X.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702(1984).
RN [7]
RP SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=94062825; PubMed=8243461;
RA Inoue K., Morita T.;
RT "Identification of O-linked oligosaccharide chains in the activation
peptides of blood coagulation factor X. The role of the carbohydrate
moieties in the activation of factor X.";

RL Eur. J. Biochem. 218:153-163(1993).
RN [8]
RP SEQUENCE OF 1-23 FROM N.A.
RX MEDLINE=90128299; PubMed=2612918;
RA Jagadeeswaran P., Reddy S.V., Rao K.J., Hamsabhusanam K., Lyman G.;
RT "Cloning and characterization of the 5' end (exon 1) of the gene
encoding human factor X.";
RL Gene 84:517-519(1989).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.
RX MEDLINE=93360277; PubMed=8355279;
RA Padmanabhan K., Padmanabhan K.P., Tulinsky A., Park C.H., Bode W.,
RA Huber R., Blankenship D.T., Cardin A.D., Kistiel W.;
RT "Structure of human des(1-45) factor Xa at 2.2-A resolution.";
RL J. Mol. Biol. 232:947-966(1993).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.
RX MEDLINE=98283982; PubMed=9618463;
RA Kamata K., Kawamoto H., Honma T., Iwama T., Kim S.H.;
RT "Structural basis for chemical inhibition of human blood coagulation
factor Xa.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).
CC -I- FUNCTION: FACTOR XA IS A VITAMIN K-DEPENDENT GLYCOPROTEIN THAT
CC CONVERTS PROTHROMBIN TO THROMBIN IN THE PRESENCE OF FACTOR VA,
CC CA++ AND PHOSPHOLIPID DURING BLOOD CLOTTING.
CC -I- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
CC Arg-|-Ile bonds in prothrombin to form thrombin.
CC -I- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
CC MORE DISULFIDE BONDS.
CC -I- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
CC -I- PTR: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM.
CC -I- PTR: N- AND O-GLYCOSYLATED.
CC -I- PTR: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
CC -I- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
CC -----
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CC -----
DR EMBL: K03194; AAA52490.1; -;
DR EMBL: M57285; AAA52421.1; -;
DR EMBL: L29433; AAA52764.1; -;
DR EMBL: L00390; AAA52764.1; JOINED.
DR EMBL: L00391; AAA52764.1; JOINED.
DR EMBL: L00392; AAA52764.1; JOINED.
DR EMBL: L00393; AAA52764.1; JOINED.
DR EMBL: L00394; AAA52764.1; JOINED.
DR EMBL: L00395; AAA52764.1; JOINED.
DR EMBL: M22613; AAA51984.1; -;
DR EMBL: K01886; AAA52486.1; -;
DR EMBL: M33297; AAA52636.1; -;
DR PIR: A00924; EXHU.
DR PIR: A25853; A25853.
DR PIR: A24478; A24478.
DR PDB: 1HCG; 08-MAY-95.
DR PDB: 1FAX; 29-OCT-97.
DR PDB: 1FXV; 17-JUN-98.
DR PDB: 1XKA; 23-MAR-99.
DR MEROPS: S01.216; -;
DR CarBank: CCSD:29393; -;
DR GlycoSuiteDB: P00742; -;

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DR MTM: 134530: -
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF-2.
DR InterPro: IPR001881; EGF-Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Trypsin.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; gla_1.
DR Pfam: PF00089; trypsin_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA_1.
DR SMART: SM00001; EGF_Like_1.
DR SMART: SM00069; GLA_1.
DR SMART: SM00020; Tryp_Spc_1.
DR PROSITE: PS00010; ASX_HYDROXYL_1.
DR PROSITE: PS00022; EGF_1_1.
DR PROSITE: PS01186; EGF_2_2.
DR PROSITE: PS00011; GLU_CARBOXYLATION_1.
DR PROSITE: PS50240; TRYPSIN_DOM_1.
DR PROSITE: PS00135; TRYPSIN_HIS_1.
DR PROSITE: PS00134; TRYPSIN_SER_1.
DR GlycoProtein: Hydrolase; Serine protease; Plasma; blood coagulation;
KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
KW Signal; Zymogen; EGF-like domain; Repeat; 3D-structure.
FT SIGNAL 1 31
FT PROPEP 32 40
FT CHAIN 41 179
FT PROPEP 183 488
FT CHAIN 183 234
FT CHAIN 235 488
FT DOMAIN 86 122
FT DOMAIN 125 165
FT DOMAIN 235 488
FT MOD_RES 46 46
FT MOD_RES 47 47
FT MOD_RES 54 54
FT MOD_RES 55 55
FT MOD_RES 59 59
FT MOD_RES 60 60
FT MOD_RES 65 65
FT MOD_RES 66 66
FT MOD_RES 69 69
FT MOD_RES 72 72
FT MOD_RES 79 79
FT MOD_RES 103 103
FT CARBOHYD 199 199
FT CARBOHYD 211 211
FT CARBOHYD 221 221
FT CARBOHYD 231 231
FT ACT_SITE 276 276
FT ACT_SITE 322 322
FT ACT_SITE 419 419
FT DISULFID 90 101
FT DISULFID 95 110
FT DISULFID 112 121

Query Match 53.1%; Score 102; DB 1; Length 488;
Best Local Similarity 40.9%; Pred. No. 1,4e-10;
Matches 18; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

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QY 1 ANAFLLXLRGSLARXCKXQCSEFXARXIFKQAXRTKLFWISY 44
DB 41 ANSFLSEMKKGHLRECEMEETCSYEAREVFEEDSDKTNEFWNKY 84

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RESULT 9
FA10_BOVIN STANDARD; PRT; 492 AA.
AC P00743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
GN F10.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
ON NCBI_TaxID=9913;
RX MEDLINE=84247315; PubMed=6330671;
RA Fung M.R., Campbell R.M., McGillivray R.T.A.;
RT "Blood coagulation factor X mRNA encodes a single polypeptide chain
RT containing a prepro leader sequence.";
RL Nucleic Acids Res. 12:4481-4492(1984).
[2]
RX MEDLINE=80130563; PubMed=6766735;
RA Enfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
RA Neurath K.;
RT "Amino acid sequence of the light chain of bovine factor XI (Stuart
RT factor).";
RL Biochemistry 19:659-667(1980).
[3]
RX MEDLINE=83308813; PubMed=6688526;
RA McMullen B.A., Fujikawa K., Kisiel W.;
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
RT K-dependent blood coagulation zymogens.";
RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
[4]
RX MEDLINE=76053069; PubMed=1059093;
RA Tiltani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,
RA Neurath H.;
RT "Bovine factor XI (Stuart factor): amino-acid sequence of heavy
RT chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).
[5]
RX MEDLINE=94062825; PubMed=8243461;
RA Inoue K., Morita T.;
RT "Identification of O-linked oligosaccharide chains in the activation
RT peptides of blood coagulation factor X. The role of the carbohydrate
RT moieties in the activation of factor X.";
RL Eur. J. Biochem. 218:153-163(1993).
[6]
RX MEDLINE=73053314; PubMed=4264286;
RA Tiltani K., Hermanson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
RA Neurath H., Davie E.W.;
RT "Bovine factor X Ia (activated Stuart factor). Evidence of homology
RT with mammalian serine proteases.";
RL Biochemistry 11:4899-4903(1972).
[7]
RX MEDLINE=76053121; PubMed=1059122;
RA Fujikawa K., Tiltani K., Davie E.W.;
RT "Activation of bovine factor X (Stuart factor): conversion of factor
RT Xa-alpha to factor Xa-beta.";
RL Proc. Natl. Acad. Sci. U.S.A. 72:3359-3365(1975).
[8]
RX MEDLINE=84185716; PubMed=6546930;
RA Sugo T., Björk I., Holmgren A., Stenflo J.;
RT "Calcium-binding properties of bovine factor X lacking the gamma-
RT carboxyglutamic acid-containing region.";

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RL J. Biol. Chem. 259:5705-5710(1984).
RN [9]
RP SUFATION
RX MEDLINE-86140210; PubMed-3949800;
RA Morita T., Jackson C.M.;
RT "Localization of the structural difference between bovine blood
RT coagulation factors XI and X2 to tyrosine 18 in the activation
RT peptide".
RL J. Biol. Chem. 261:4008-4014(1986).
RN [10]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE-91084483; PubMed-2261466;
RA Selander M., Persson E., Stenflo J., Drakenberg T.;
RT "1H NMR assignment and secondary structure of the Ca(2+)-free form of
RT the amino-terminal epidermal growth factor like domain in coagulation
RT factor X".
RL Biochemistry 29:8111-8118(1990).
RN [11]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE-92329412; PubMed-1627540;
RA Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,
RA Teleman O.;
RT "Three-dimensional structure of the apo form of the N-terminal
RT EGF-like module of blood coagulation factor X as determined by NMR
RT spectroscopy and simulated folding".
RL Biochemistry 31:5974-5983(1992).
RN [12]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE-92406922; PubMed-1527084;
RA Selander M., Ullner M., Persson E., Teleman O.,
RA Stenflo J., Drakenberg T.;
RT "How an epidermal growth factor (EGF)-like domain binds calcium. High
RT resolution NMR structure of the calcium form of the NH2-terminal EGF-
RT like domain in coagulation factor X".
RL J. Biol. Chem. 267:19642-19649(1992).
RN [13]
RP STRUCTURE BY NMR OF 41-126.
RX MEDLINE-96387194; PubMed-8794734;
RA Sunnerhagen M., Olah G.A., Stenflo J., Forsen S., Drakenberg T.,
RA Trewhella J.;
RT "The relative orientation of Gla and EGF domains in coagulation
RT factor X is altered by Ca2+ binding to the first EGF domain. A
RT combined NMR-small angle X-ray scattering study".
RL Biochemistry 35:11547-11559(1996).
RN [14]
RP FUNCTION: FACTOR XA IS A VITAMIN K-DEPENDENT GLYCOPROTEIN THAT
RP CONVERTS PROTHROMBIN TO THROMBIN IN THE PRESENCE OF FACTOR VA,
RP CA2+, AND PHOSPHOLIPID DURING BLOOD CLOTTING.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
CC Arg-|-Ile bonds in prothrombin to form thrombin.
CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
CC MORE DISULFIDE BONDS.
CC -1- PTM: THE VITAMIN K-DEPENDENT ENZYMAIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM.
CC -1- PTM: N- AND O-GLYCOSYLATED.
CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
CC INTRINSIC PATHWAY) OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
CC -----
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CC -----
CC EMBL; X00673; CAA25286.1; -

DR PIR; A00925; EXBO.
DR PDB; 1A0; 31-JAN-94.
DR PDB; 1CCF; 31-MAY-94.
DR PDB; 1WHE; 15-MAY-97.
DR PDB; 1WHF; 15-MAY-97.
DR MEROPS; S01.216; -.
DR CarBank; CCSD:7747; -.
DR CarBank; CCSD:7899; -.
DR CarBank; CCSD:11506; -.
DR CarBank; CCSD:11508; -.
DR GlycoSuiteDB; P00743; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Trypsin.
DR InterPro; IPR000294; Vitk_dep_GLA.
DR Pfam; PF00008; BGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYF_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
KW Signal; Zymogen; EGF-like domain; Repeat; Sulfation; 3D-structure.
FT SIGNAL; 1; 23
FT PROPEP; 41; 40
FT CHAIN; 24; 180
FT CHAIN; 183; 492
FT PROPEP; 183; 233
FT CHAIN; 234; 492
FT PROPEP; 476; 492
FT DOMAIN; 86; 122
FT DOMAIN; 125; 165
FT DOMAIN; 234; 492
FT ACT_SITE; 275; 275
FT ACT_SITE; 321; 321
FT ACT_SITE; 418; 418
FT MOD_RES; 46; 46
FT MOD_RES; 47; 47
FT MOD_RES; 54; 54
Query Match 52.6%; Score 101; DB 1; Length 492;
Best Local Similarity 43.2%; Pred. No. 2; 1e-10;
Matches 19; Conservative 7; Mismatches 18; Indels 0; Gaps 0;
OY 1 ANAFLLXLRPGSLXKCKXKSCFFXXKXIFDARTLFWISY 44
DB 41 ANSFLFVKKQGNLRECEACSLAEAREVFDADQDTEFWSKY 84
RESULT 10
PRTC_RAT STANDARD; PRT; 461 AA.
AC P31394;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Vitamin K dependent protein C precursor (EC 3.4.21.69)
 DE (Aucrothrombin IIA) (Anticoagulant protein C) (Blood coagulation
 DE factor XIV).
 GN PROC.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MSTAR; TISSUE=Liver;
 RX MEDLINE=92329550; PubMed=1627650;
 RA Okafuji T., Maekawa K., Nawa K., Marumoto Y.;
 RT "The CDNA cloning and mRNA expression of rat protein C.";
 RL Biochim. Biophys. Acta 1131:329-332(1992).
 CC -1 FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
 CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
 CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
 CC -1 CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
 CC and VIIIA.
 CC -1 SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
 CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
 CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
 CC TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN. THIS
 CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
 CC STRONGLY PROMOTED BY THROMBOMODULIN.
 CC -1 TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
 CC -1 PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
 CC -1 MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
 CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
 CC THROMBIN-THROMBOMODULIN COMPLEX.
 CC -1 SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 CC -----
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 CC -----
 DR EMBL: X64336; CAA45617.1; -
 DR PIR: S18994; S18994.
 DR PIR: S24312; S24312.
 DR HSSP: P04070; PCU.
 DR MEROPS: S01.218; -
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Trypsin.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam: PF00008; EGF_2.
 DR Pfam: PF00594; gla_1.
 DR Pfam: PF00089; trypsin_1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00179; EGF_CA_1.
 DR SMART: SM00001; EGF_like_1.
 DR SMART: SM00069; GLA_1.
 DR SMART: SM00020; TRYP_SPC_1.
 DR PROSITE: PS00010; ASX_HYDROXYL_1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF_CA_1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION_1.
 DR PROSITE: PS0240; TRYPSIN_DOM_1.
 DR PROSITE: PS00134; TRYPSIN_HIS_1.

DR PROSITE: PS00135; TRYPSIN_SER_1.
 KW Blood coagulation; Glycoprotein; Serine protease;
 KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 KW EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
 FT SIGNAL 1 32
 FT PROPEP 33 41
 FT CHAIN 42 196
 FT CHAIN 199 461
 FT PEPTIDE 199 212
 FT SITE 212 213
 FT DOMAIN 96 131
 FT DOMAIN 135 175
 FT DOMAIN 213 461
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 FT ACT_SITE 300 300
 FT ACT_SITE 402 402
 FT ACT_SITE 402 402
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 FT DISULFID 139 150
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 FT DISULFID 182 320
 FT DISULFID 239 255
 FT DISULFID 373 387
 FT DISULFID 398 426
 FT CARBOHYD 215 215
 FT CARBOHYD 291 291
 FT CARBOHYD 335 335
 SQ SEQUENCE 461 AA; 51912 MW; 8A4CF93664BDACD5 CRC64;
 Query Match 52.1%; Score 100; DB 1; Length 461;
 Best Local Similarity 45.5%; Pred. No. 3e-10;
 Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;
 Qy 1 ANAFLLXLRPGSLRXCKXXQCSFEXARXIFKDAKRLFWISY 44
 Db 42 ANSFLEEVRAAGSLERECMEELCEDEFAQDFQNVEDTLARWIK 85
 RESULT 11
 ID TMGL_HUMAN STANDARD: PRT: 218 AA.
 AC 014668:
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DE Transmembrane gamma-carboxyglutamic acid protein 1 precursor (Proline-
 DE rich Gla protein 1) (Proline-rich gamma-carboxyglutamic acid protein
 GN PRG1 OR TMGL OR PRG1.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97404347; Pubmed=9256434;
 RA Kildan J.D., Harris J.E., Haldeman B.A., Davie E.W.;
 RT "Primary structure and tissue distribution of two novel proline-rich
 gamma-carboxyglutamic acid proteins";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997).
 CC -1- PTMSE SPECIFICITY: Highly expressed in the spinal cord.
 CC -1- PTMSE: Gla residues are produced after subsequent posttranslational
 CC modifications of glutamic acid by a vitamin K-dependent gamma-
 CC carboxylase.
 CC -----
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 CC -----
 CC EMBL; AF009242; AAB67070.1; -.
 CC DR HSSP: 604428; -.
 CC DR MIM: 604428; -.
 CC DR HSSP: P00740; 1CFH
 CC DR InterPro: IPR000294; VitK_dep_GLA.
 CC DR InterPro: IPR002383; GLA_blood.
 CC DR Pfam: PF00594; gla; 1.
 CC DR PRINTS: PRO0001; GLABLOOD.
 CC DR SMART: SM00069; GLA; 1.
 CC DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
 CC KM Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
 CC FT PROPEP 1 20 POTENTIAL.
 CC FT CHAIN 21 218 TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
 CC FT FT 21 218 PROTEIN 1.
 CC FT DOMAIN 21 83 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 84 106 POTENTIAL.
 CC FT DOMAIN 107 218 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 24 61 GLA-RICH.
 CC FT DOMAIN 131 135 POLY-PRO.
 CC SQ SEQUENCE 218 AA; 24947 MW; 26538A61AB0AEB98 CRC64;
 OY 1 ANAFLLXLRPGSLRXKXKXQCSFXARXIFKDXARFKLEWISY 44
 DB 21 ANGFEFEIRGQNIERECKEFCFEAREAEENNEKTEWSTY 64
 Query Match 51.6%; Score 99; DB 1; Length 218;
 Best Local Similarity 40.9%; Pred. No. 2; Le-10;
 Matches 18; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

CC -1- FUNCTION: FACTOR XA IS A VITAMIN K-DEPENDENT GLYCOPROTEIN THAT
 CC CONVERTS PROTHROMBIN TO THROMBIN IN THE PRESENCE OF FACTOR VA,
 CC CA++ AND PHOSPHOLIPID DURING BLOOD CLOTTING.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-1-Thr and then
 CC Arg-1-Ile bonds in prothrombin to form thrombin.
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 CC MORE DISULFIDE BONDS.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM (BY SIMILARITY).
 CC -1- PTM: N- AND O-GLYCOSYLATED (BY SIMILARITY).
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IIX (IN THE
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY)
 CC (BY SIMILARITY).
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
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 CC -----
 CC EMBL; AF003200; AAB62542.1; -.
 CC DR HSSP: P00742; 1HCG.
 CC DR InterPro: IPR000152; Asx_hydroxyl.
 CC DR InterPro: IPR001314; Chymotrypsin.
 CC DR InterPro: IPR000561; EGF_1like.
 CC DR InterPro: IPR000742; EGF_2.
 CC DR InterPro: IPR001881; EGF_Ca.
 CC DR InterPro: IPR002383; GLA_blood.
 CC DR InterPro: IPR001254; Trypsin.
 CC DR InterPro: IPR000294; VitK_dep_GLA.
 CC DR Pfam: PF00008; EGF; 2.
 CC DR Pfam: PF00594; gla; 1.
 CC DR Pfam: PF00089; trypsin; 1.
 CC DR PRINTS: PRO0722; CHYMOTRYPSIN.
 CC DR PRINTS: PRO0001; GLABLOOD.
 CC DR SMART: SM00179; EGF_Ca; 1.
 CC DR SMART: SM00001; EGF_1like; 1.
 CC DR SMART: SM00069; GLA; 1.
 CC DR SMART: SM00020; TRYP_SPC; 1.
 CC DR PROSITE: PS00010; ASX_HYDROXYL; 1.
 CC DR PROSITE: PS00022; EGF_1; 1.
 CC DR PROSITE: PS01186; EGF_2; 2.
 CC DR PROSITE: PS01187; EGF_CA; 1.
 CC DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
 CC DR PROSITE: PS00240; TRYPsin_DOM; 1.
 CC DR PROSITE: PS00134; TRYPsin_SER; 1.
 CC DR PROSITE: PS00135; TRYPsin_HIS; 1.
 CC DR Glycoprotein; Hydrolyase; Serine protease; Plasma; Blood coagulation;
 CC Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 CC Signal; Zymogen; EGF-like domain; Repeat.
 CC FT SIGNAL 1 20 POTENTIAL.
 CC FT PROPEP 21 40 BY SIMILARITY.
 CC FT CHAIN 41 180 FACTOR X LIGHT CHAIN.
 CC FT CHAIN 184 490 FACTOR X HEAVY CHAIN.
 CC FT PROPEP 184 232 ACTIVATION PEPTIDE.
 CC FT CHAIN 233 490 ACTIVATED FACTOR XA, HEAVY CHAIN.
 CC FT DOMAIN 86 122 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
 CC FT DOMAIN 125 165 EGF-LIKE 2.
 CC FT DOMAIN 233 490 SERINE PROTEASE.
 CC FT MOD_RES 46 GAMMA-CARBOXYGLUTAMIC ACID (BY
 CC SIMILARITY).
 CC FT MOD_RES 47 GAMMA-CARBOXYGLUTAMIC ACID (BY
 CC SIMILARITY).
 CC FT MOD_RES 54 GAMMA-CARBOXYGLUTAMIC ACID (BY
 CC SIMILARITY).

FT	MOD_RES	56	56	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	59	59	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	60	60	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	65	65	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	66	66	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	69	69	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	72	72	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	75	75	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	79	79	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	103	103	HYDROXYLATION (BY SIMILARITY).
FT	ACT_SITE	274	274	CHARGE RELAY SYSTEM.
FT	ACT_SITE	320	320	CHARGE RELAY SYSTEM.
FT	ACT_SITE	417	417	CHARGE RELAY SYSTEM.
FT	DISULFID	90	101	BY SIMILARITY.
FT	DISULFID	95	110	BY SIMILARITY.
FT	DISULFID	112	121	BY SIMILARITY.
FT	DISULFID	129	140	BY SIMILARITY.
FT	DISULFID	136	149	BY SIMILARITY.
FT	DISULFID	151	164	BY SIMILARITY.
FT	DISULFID	172	340	INTERCHAIN (BY SIMILARITY).
FT	DISULFID	239	244	BY SIMILARITY.
FT	DISULFID	259	275	BY SIMILARITY.
FT	DISULFID	388	402	BY SIMILARITY.
FT	DISULFID	413	441	BY SIMILARITY.
FT	CAROHND	61	61	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CAROHND	187	187	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CAROHND	205	205	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	490 AA:	53965 MW;	3A59FA85AF2A6D11 CRC64;

Query Match 51.0%; Score 98; DB 1; Length 490;

Best Local Similarity 40.9%; Pred. No. 7.4e-10;

Matches 18; Conservative 7; Mismatches 19; Indels 0; Gaps 0

OY 1 ANAFELXLRPGSLKRXCKXXQCSFYXARYIFDAXTKLFWISY 44

DB 41 ANSFEELKKGKGLERECWENCSEAELEVFEDREKTNFWMKY 84

RESULT 13

PRTC_RABIT PRTC_RABIT STANDARD; PRT; 458 AA.

AC Q28661;

DT 15-DEC-1998 (Rel. 37, Last Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)

DE (Autoproteolysin IIR) (Anticoagulant protein C) (Blood coagulation factor XIV) (Fragment).

GN Oryctolagus cuniculus (Rabbit).

OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID=9986;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA Shen L., He X., Dahlback B.;

RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.

CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va

CC	and.viii.		
CC	-1 SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A TETRAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS STRONGLY PROMOTED BY THROMBOMODULIN.		
CC	-1 TISSUE SPECIFICITY: PLASMA: SYNTHESIZED IN THE LIVER.		
CC	-1 PTM: THE VITAMIN K-DEPENDENT ENZYMAIC CARBOXYLATION OF SOME GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.		
CC	-1 MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING SITE IS NECESSARY FOR THE RECOGNITION OF THE THROMBIN-THROMBOMODULIN COMPLEX.		
CC	-1 SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.		
CC	-1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or_send_an_email_to_license@sib-sib.ch).		
CC	-----		
DR	EMBL; U49933; AAA92956.1; -.		
DR	HSSP; P04070; 1PCU.		
DR	MEROPS; S01.218; -.		
DR	InterPro: IPR000152; Asx_hydroxyl.		
DR	InterPro: IPR000561; EGF-like.		
DR	InterPro: IPR001881; EGF-Ca.		
DR	InterPro: IPR001254; Trypsin.		
DR	InterPro: IPR000294; Vltk_dep_GLA.		
DR	Pfam; PF00008; EGF_2.		
DR	Pfam; PF00594; gla; 1.		
DR	Pfam; PF00083; trypsin; 1.		
DR	SMART; SM00181; EGF_2.		
DR	SMART; SM00069; GLA; 1.		
DR	SMART; SM00020; Tryp_spec; 1.		
DR	PROSITE: PS00010; ASX_HYDROXYL; 1.		
DR	PROSITE: PS00022; EGF_1; 1.		
DR	PROSITE; PS01187; EGF_2; 2.		
DR	PROSITE; PS01187; EGF_CA; 1.		
DR	PROSITE; PS00011; GLU_CARBOXYLATION; 1.		
DR	PROSITE; PS00240; TRYPSIN_DOM; 1.		
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.		
DR	PROSITE; PS00135; TRYPSIN_SER; 1.		
KW	Blood coagulation; Glycoprotein; Serine protease;		
KW	Gamma-carboxylglutamic acid; Calcium binding; Vitamin K; Hydroxylation;		
KW	EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.		
FT	NON_TER	1	27
FT	SIGNAL	<1	1
FT	PROPEP	28	36
FT	CHAIN	37	458
FT	CHAIN	37	192
FT	CHAIN	195	458
FT	PEPTIDE	195	209
FT	SITE	209	210
FT	DOMAIN	91	126
FT	DOMAIN	130	170
FT	DOMAIN	210	458
FT	MOD_RES	42	42
FT	MOD_RES	43	43
FT	MOD_RES	50	50
FT	MOD_RES	52	52
FT	MOD_RES	55	55
FT	MOD_RES	56	56

FT DISULFID 396 410 BY SIMILARITY.
 FT DISULFID 421 449 BY SIMILARITY.
 FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 475 AA; 53142 MW; 570BF84956C5C7AD CRC64;

Query Match 47.4%; Score 91; DB 1; Length 475;
 Best Local Similarity 38.6%; Pred. No. 1.3e-08;
 Matches 17; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRPGSLRXCKXKXOCSPFXAXRIFKDAKRTLFWISY 44
 Db 41 ANSFLKMKOGNIEKRECKNEKCSKEAREAFEDNKTETFWNITY 84

RESULT 16

TMG2_HUMAN STANDARD; PRT; 202 AA.
 AC 014669;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DE Transmembrane gamma-carboxyglutamic acid protein 2 precursor (Proline-rich Gla protein 2) (Proline-rich gamma-carboxyglutamic acid protein 2).
 GN PRKG2 OR TMG2 OR PRGP2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;

RM SEQUENCE FROM N.A.
 RA MEDLINE=97404347; PubMed=9256434;
 RX Kulman J.D., Harris J.E., Haldeman B.A., Davie E.W.;
 RT "Primary structure and tissue distribution of two novel proline-rich gamma-carboxyglutamic acid proteins";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Highly expressed in the thyroid.
 CC -1- PPM: Gla residues are produced after subsequent posttranslational modifications of glutamic acid by a vitamin K-dependent gamma-carboxylase.

CC -----
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 CC -----

DR EMBL: AF009243; AAB67071.1; -.
 DR MIM: 604429; -.
 DR HSSP: P00740; ICFH.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR000294; VltK_dep_GLA.
 DR Pfam: PF00594; gla; 1.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00069; GLA; 1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
 KW Gamma-carboxyglutamic acid; Vitamin K; Transmembrane; Signal.
 FT SIGNAL 1 23
 FT PROPEP 24 49
 FT CHAIN 50 202

FT TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
 FT PROTEIN 2.
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 110 109
 FT DOMAIN 133 202
 FT DOMAIN 54 91
 FT DOMAIN 161 173
 FT POLY-PRO.

FT DOMAIN 191 194 POLY-PRO.
 SO SEQUENCE 202 AA; 22393 MW; BC79400C98492060 CRC64;

Query Match 46.4%; Score 89; DB 1; Length 202;
 Best Local Similarity 45.0%; Pred. No. 1.3e-08;
 Matches 18; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

Oy 5 LXLRLPGSLRXCKXKXOCSPFXAXRIFKDAKRTLFWISY 44
 Db 55 LELLTPGNLERECLEERCSEWEAREYFEDNLTETFEWESY 94

RESULT 17

TMG3_HUMAN STANDARD; PRT; 231 AA.
 AC 098207;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DE Transmembrane gamma-carboxyglutamic acid protein 3 precursor.
 GN TMG3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;

RM SEQUENCE FROM N.A.
 RA TISSUE=Spinal cord;
 RX MEDLINE=21117044; PubMed=11171957;
 RA Kulman J.D., Harris J.E., Xie L., Davie E.W.;
 RT "Identification of two novel transmembrane gamma-carboxyglutamic acid proteins expressed broadly in fetal and adult tissues";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:1370-1375(2001).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed in brain, lung, kidney and heart.
 CC -1- PPM: Gla residues are produced after subsequent posttranslational modifications of glutamic acid by a vitamin K-dependent gamma-carboxylase.

CC -----
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 CC -----

DR EMBL: AF326350; AAK0955.1; -.
 DR HSSP: P00740; ICFH.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR000294; VltK_dep_GLA.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00069; GLA; 1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.

KW Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
 FT PROPEP 1 19
 FT CHAIN 20 231
 FT TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
 FT PROTEIN 3.
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 79 101
 FT DOMAIN 102 231
 FT DOMAIN 23 60
 FT DOMAIN 231 60
 FT GLA-RICH.
 SO SEQUENCE 231 AA; 25848 MW; BA373E4848490D81 CRC64;

Query Match 45.8%; Score 88; DB 1; Length 231;
 Best Local Similarity 36.4%; Pred. No. 2.2e-08;
 Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRPGSLRXCKXKXOCSPFXAXRIFKDAKRTLFWISY 44
 Db 20 ANEFLLELRQGTIERCKMEICSYEVKAEVENKKTETFEWNGY 63

RESULT	18			
ID	FA9_BOVIN	STANDARD;	PRT;	416 AA.
AC	P00741;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	30-MAY-2000 (Rel. 09, Last annotation update)			
DE	Coagulation factor IX (EC 3.4.21.22) (Christmas factor).			
GN	F9.			
OS	Bos taurus (Bovine).			
OC	Eumetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=60056619; PubMed=291916.			
RA	Katayama K., Ericsson L.H., Enfield D.L., Walsh K.A., Neurath H.,			
RA	David E.W., Titani K.;			
RT	"Comparison of amino acid sequence of bovine Coagulation Factor IX			
RT	(Christmas Factor) with that of other vitamin K-dependent plasma			
RT	proteins.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 76:4990-4994(1979).			
RN	[2]			
RP	REVISION TO 64.			
RX	MEDLINE=83308813; PubMed=6688526;			
RA	McMullen B.A., Fujikawa K., Kistel W.;			
RT	"The occurrence of beta-hydroxyaspartic acid in the vitamin			
RT	K-dependent blood coagulation zymogens.";			
RL	Biochem. Biophys. Res. Commun. 113:8-14(1983).			
RN	[3]			
RP	SEQUENCE OF 51-111 FROM N.A.			
RX	MEDLINE=82272386; PubMed=6287289;			
RA	Choo K.H., Gould K.G., Rees D.J.G., Brownlee G.G.;			
RT	"Molecular cloning of the gene for human anti-haemophilic factor IX.";			
RL	Nature 299:178-180(1982).			
RN	[4]			
RP	STRUCTURE OF CARBOHYDRATE ON SER-53.			
RX	MEDLINE=8921399; PubMed=9314937;			
RA	Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T.,			
RA	Miyata T., Iwanaga S., Takao T., Shimonishi Y., Ikenaka T.;			
RT	A new trisaccharide sugar chain linked to a serine residue in the			
RT	first EGF-like domain of clotting factors VII and IX and protein Z.";			
RL	Adv. Exp. Med. Biol. 281:121-131(1990).			
RN	[6]			
RP	STRUCTURE OF CARBOHYDRATE ON SER-53.			
RX	MEDLINE=90130422; PubMed=2105311;			
RA	Hase S., Nishimura H., Kawabata S., Iwanaga S., Ikenaka T.;			
RT	"The structure of (xylose)2glucose-O-serine 53 found in the first			
RT	epidermal growth factor-like domain of bovine blood clotting factor			
RT	IX.";			
RL	J. Biol. Chem. 265:1858-1861(1990).			
CC	-1- FUNCTION: FACTOR IX IS A VITAMIN K-DEPENDENT PLASMA PROTEIN THAT			
CC	PARTICIPATES IN THE INTRINSIC PATHWAY OF BLOOD COAGULATION BY			
CC	CONVERTING FACTOR X TO ITS ACTIVE FORM IN THE PRESENCE OF CA++			
CC	IONS, PHOSPHOLIPIDS, AND FACTOR VIIIa.			
CC	-1- CATALYTIC ACTIVITY: Hydrolyses one Arg-1-ile bond in factor X to			
CC	form factor Xa.			
CC	-1- SUBUNIT: FACTOR IX IS ACTIVATED BY FACTOR XIa, WHICH EXCISES THE			
CC	ACTIVATION PEPTIDE AND THUS PRODUCES A MOLECULE CONSISTING OF 2			
CC	CHAINS HELD TOGETHER BY ONE OR MORE DISULFIDE BONDS.			
CC	-1- MISCELLANEOUS: CALCIUM BINDS TO THE GAMMA-CARBOXYGLUTAMIC ACID			
CC	(GLA) RESIDUES AND, WITH STRONGER AFFINITY, TO ANOTHER SITE.			
CC	BEYOND THE GLA DOMAIN.			

CC	-1	SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC	-1	SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
CC		-----
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CC		-----
DR	EMBL; J00007; AAA30520.1; -.	
DR	PIR; A00923; KFB0.	
DR	HSSP; P00740; ICFH.	
DR	MEROPS; S01.214; -.	
DR	GlycositeDB; P00741; -.	
DR	InterPro; IPR000152; Asx_hydroxyl.	
DR	InterPro; IPR001314; Chymotrypsin.	
DR	InterPro; IPR000561; EGF-like.	
DR	InterPro; IPR000742; EGF_2.	
DR	InterPro; IPR001881; EGF_Ca.	
DR	InterPro; IPR001438; EGF_II.	
DR	InterPro; IPR002383; GLA_blood.	
DR	InterPro; IPR001254; Trypsin.	
DR	InterPro; IPR000294; Vltk_dep_GLA.	
DR	Pfam; PF00008; EGF; 2.	
DR	Pfam; PF00594; gla; 1.	
DR	Pfam; PF00089; trypsin; 1.	
DR	PRINTS; PR00722; CHYMOTRYPSIN.	
DR	PRINTS; PR00010; EGFBLD.	
DR	PRINTS; PR00001; GLABLOD.	
DR	SMART; SM00179; EGF_CA; 1.	
DR	SMART; SM00001; EGF-like; 1.	
DR	SMART; SM00069; GLA; 1.	
DR	SMART; SM00020; Tryp_spec; 1.	
DR	PROSITE; PS00010; ASX_HYDROXYL; 1.	
DR	PROSITE; PS00022; EGF_1; 1.	
DR	PROSITE; PS01186; EGF_2; 2.	
DR	PROSITE; PS01187; EGF_CA; 1.	
DR	PROSITE; PS00011; GLU_CARBOXYLATION; 1.	
DR	PROSITE; PS02040; TRYPSIN_DOM; 1.	
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.	
DR	PROSITE; PS00135; TRYPSIN_SER; 1.	
KW	Blood coagulation; Plasma; Serine protease; Calcium-binding; Hydroxylase; Glycoprotein; Vitamin K; Gamma-carboxyglutamic acid; Hemophilias; Hydroxylation; Zymogen; EGF-like domain.	
KW	Hemophilias; Hydroxylation; Zymogen; EGF-like domain.	
FT	CHAIN	1 146
FT	PROPEP	147 181
FT	CHAIN	182 416
FT	DOMAIN	47 83
FT	DOMAIN	84 125
FT	DOMAIN	182 416
FT	SITE	146 147
FT	SITE	181 182
FT	MOD_RES	7 7
FT	MOD_RES	8 8
FT	MOD_RES	15 15
FT	MOD_RES	17 17
FT	MOD_RES	20 20
FT	MOD_RES	21 21
FT	MOD_RES	26 26
FT	MOD_RES	27 27
FT	MOD_RES	30 30
FT	MOD_RES	33 33
FT	MOD_RES	36 36
FT	MOD_RES	40 40
FT	MOD_RES	64 64
FT	DISULFID	18 23
FT	DISULFID	51 62
FT	DISULFID	56 71
FT	DISULFID	73 82
FT	DISULFID	88 99

FT DISULFID 95 109 BY SIMILARITY.
 FT DISULFID 111 124 BY SIMILARITY.
 FT CARBOHYD 53 53 O-LINKED (GLC. . .).
 FT CARBOHYD 158 158 /FTID-CAR_000008.
 FT CARBOHYD 168 168 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .).
 FT ACT_SITE 222 222 CHARGE RELAY SYSTEM.
 FT ACT_SITE 270 270 CHARGE RELAY SYSTEM.
 FT ACT_SITE 366 366 CHARGE RELAY SYSTEM.
 FT VARIANT 64 64 D -> T (IN REF. 1).
 SQ SEQUENCE 416 AA; 46785 MW; 34A7DEF916330662 CRC64;

Query Match 44.88; Score 86; DB 1; Length 416;
 Best Local Similarity 44.18; Pred. No. 9.1e-08;
 Matches 15; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

OY 11 GLRXCKXXCSPFXARXIFKDXRTLEWISY 44
 DB 12 GNLEBECKEKECFEAEVEFTEKTEFEWKQY 45

RESULT 19
 PRTC_HUMAN STANDARD; PRT: 461 AA.
 AC P04070; Q16001; Q15190; Q15189;
 DT 01-NOV-1986 (Rel. 03, Created)
 DT 01-NOV-1986 (Rel. 03, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
 DE (Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation factor XIV).
 GN PROC.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85270390; PubMed=2991887;
 RA Foster D.C., Yoshitake S., Davie E.W.;
 RT "The nucleotide sequence of the gene for human protein C";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:4673-4677(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
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 RX MEDLINE=86120978; PubMed=3511471;
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 RL Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986).
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 RX MEDLINE=92184750; PubMed=1544894;
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 RX MEDLINE=93190290; PubMed=8446940;
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RP MOLECULAR PATHOLOGY OF HEMOPHILIA B.

Query Match 43.28; Score 83; DB 1; Length 461;
Best Local Similarity 44.18; Pred. No. 3.5e-07;
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DB 58 GNLERCEMEKCSFEERAREVFNTERITTEPMKOT 91
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AC P00734;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Prothrombin precursor (EC 3.4.21.5) (Coagulation factor II).
GN F2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN RP SEQUENCE FROM N.A.
RX MEDLINE=88077877; PubMed=2825773;
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RX MEDLINE=93043342; PubMed=1421398;
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RN RP VARIANT TOKUSHIMA.


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RL Biochemistry 26:1117-1122(1987).
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RT "Prothrombin Tokushima: characterization of dysfunctional thrombin
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RN [20]
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RX MEDLINE=92256895; PubMed=1349838;
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RX MEDLINE=83204687; PubMed=6405779;
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RT type 3 (157 Glu leads to Lys) and the localization of a third
RT thrombin cleavage site."
RL Br. J. Haematol. 54:245-254(1983).
CC -1- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS
CC FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,
CC AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: SYNTHESIZED IN THE LIVER; FOUND IN PLASMA.
CC -1- PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
CC RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MITOSOMAL
CC ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES
CC ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY
CC CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
CC OF PROTHROMBIN TO THROMBIN.
CC -1- DISEASE: DEFECTS IN F2 ARE THE CAUSE OF VARIOUS FORMS OF
CC DYSPROTHROMBINEMIA.
CC -1- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A
CC PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &
CC FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES
CC THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &
CC HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR
CC V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
CC THROMBIN.
CC -1- MISCELLANEOUS: IT IS NOT KNOWN WHETHER 1 OR 2 SMALLER ACTIVATION
CC PEPTIDES, WITH ADDITIONAL CLEAVAGE AFTER 314-ARG, ARE RELEASED IN
CC NATURAL BLOOD CLOTTING.
CC -1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL
CC PEPTIDE (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
CC BY FACTOR XA.
CC -1- MISCELLANEOUS: THE CLEAVAGE AFTER R-198, OBSERVED IN VITRO, DOES
CC NOT OCCUR IN PLASMA.
CC -1- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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Db 44 ANTFLEEVKGNLERECVEETCSYEAFEALESSPATDVFNPKY 87
RESULT 22
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DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21117044; PubMed=11171957;
RA Kulman J.D., Harris J.E., Xie L., Davie E.W.;
RT "Identification of two novel transmembrane gamma-carboxyglutamic acid
RT proteins expressed broadly in fetal and adult tissues."
RL Proc. Natl. Acad. Sci. U.S.A. 98:1370-1375(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in lung, liver, kidney, pancreas and
CC placenta.
CC -1- PTM: Glu residues are produced after subsequent posttranslational
CC modifications of glutamic acid by a vitamin K-dependent gamma-
CC carboxylase.
CC -----
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CC or send an email to license@sib.ch).
CC -----
DR EMBL: AF326351; AAK0956.1; -
DR EMBL: BC010052; AAH10052.1; -
DR HSSP: P00740; 1CFH.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR000294; Vltk_dep_GLA.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00069; GLA: 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
KW Gamma-carboxyglutamic acid; vitamin K; Transmembrane; Signal.
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FT PROPEP 18 49
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FT DOMAIN 50 113
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Matches 18; Conservative 4; Mismatches 21; Indels 1; Gaps 1;
Oy 2 NAF-LXXLRPGSLRXKCKXKXOCSEFXARXIFKDAKRTLFWISY 44
Db 53 NRFDELFTPGNLERECNEELCNYEAREIFVDEDKTIAFMOEY 96

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RESULT 23
THRB_RAT STANDARD; PRT; 617 AA.
AC 18292;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Prothrombin precursor (EC 3.4.21.5).
GN F2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
RX MEDLINE=90332426; PubMed=2377469;
RA Dhanich M., Monard D.;
RT "cDNA sequence of rat prothrombin.";
RL Nucleic Acids Res. 18:4251-4251(1990).
RN [2]
RP SEQUENCE OF 383-617 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92212913; PubMed=1557383;
RA Banfield D.K., Macgillivray R.T.;
RT "Partial characterization of vertebrate prothrombin cDNAs:
RT amplification and sequence analysis of the B chain of thrombin from
RT nine different species.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
CC -1- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS
CC FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,
CC AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.
CC -1- PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
CC RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL
CC ENZYME. THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES
CC ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY
CC CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
CC OF PROTHROMBIN TO THROMBIN.
CC -1- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A
CC PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &
CC FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES
CC THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &
CC HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR
CC V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
CC THROMBIN.
CC -1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL
CC FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
CC BY FACTOR XA.
CC -1- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL, outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X52835; CAA37017.1; -
DR EMBL: M81397; AAA42240.1; -
DR PIR: S10511; S10511.
DR HSSP: P00734; IUVS.
DR MEROPS: S01.217; -.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR003966; Prothrombin.
DR InterPro: IPR001254; Trypsin.
DR InterPro: IPR000294; Vitk_dep_GLA.
DR Pfam: PF00594; gla_1.
DR Pfam: PF00551; kringle_2.

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DR Pfam: PF00089; trypsin_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR PRINTS: PR00018; KRINGLE.
DR PRINTS: PR01505; PROTHROMBIN.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00130; KR; 2.
DR SMART: SM00020; TRYP_SPC; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00021; KRINGLE_1; 2.
DR PROSITE: PS50070; KRINGLE_2; 2.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR Blood coagulation; Plasma; Calcium-binding; Glycoprotein; Repeat;
KW Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver;
KW Hydrolyase; Serine protease; Kringle; Signal.
FT SIGNAL 1 24
FT PROPEP 25 43.
FT CHAIN 44 617
FT PEPTIDE 44 200
FT PEPTIDE 201 323
FT CHAIN 324 359
FT CHAIN 360 617
FT DOMAIN 109 187
FT DOMAIN 215 292
FT DOMAIN 360 617
FT SITE 323 324
FT SITE 323 324
FT SITE 359 360
FT ACT_SITE 402 402
FT ACT_SITE 458 458
FT ACT_SITE 564 564
FT MOD_RES 50 50
FT MOD_RES 51 51
FT MOD_RES 58 58
FT MOD_RES 60 60
FT MOD_RES 63 63
FT MOD_RES 64 64
FT MOD_RES 69 69
FT MOD_RES 70 70
FT MOD_RES 73 73
FT MOD_RES 76 76
FT CARBOHYD 120 120
FT CARBOHYD 144 144
FT CARBOHYD 412 412
FT CARBOHYD 552 552
FT DISULFID 61 66
FT DISULFID 91 104
FT DISULFID 109 170
FT DISULFID 130 187
FT DISULFID 158 182
FT DISULFID 215 292
FT DISULFID 236 275
FT DISULFID 264 287
FT DISULFID 332 478
FT DISULFID 387 403
FT DISULFID 532 546
FT DISULFID 560 590
SQ SEQUENCE 617 AA; 70411 MW; AD27D1B71445DB1D CRC64;

```

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Query Match 41.1%; Score 79; DB 1; Length 617;
Best Local Similarity 37.2%; Pred. No. 2.5e-06;
Matches 16; Conservative 5; Mismatches 22; Indels 0; Gaps 0;

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OY 2 NAFLXLRPGSLKRXKXXOCSEFXKXARXIFKDAKRTLEWISY 44
   : 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 46 SGFLEELRKNGKLERECVEECSEAEFALESPPDITVFAKRY 88

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RESULT 24
THRB_MOUSE

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Query Match      85.1%: Score 165; DB 1; Length 407;
Best Local Similarity 72.7%: Pred. No. 7.le-21;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Oy      1 ANGFLXLRPGSLKRXCRXXLCSEFXXAHXIFRNXXRTQFWVSX 44
      |||| | |||| | || | |||| | |||| | |||| | |||| |
Db      1 ANGFLLELLPGSLERECKREELCSFEFAHIFRNEERTQFWVSX 44

RESULT      2
146932
coagulation factor VII - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 12-Feb-1999
C:Accession: I46932
R:Brothers, A.B.; Clarke, B.J.; Sheffield, W.P.; Blajchman, M.A.
Thromb. Res. 69, 231-238, 1993
A:Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII
A:Reference number: I46932; MUID:93190306
A:Accession: I46932
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-443 <BRO>
A:Cross-references: GB:S56300; NID:g266294; PID:g266295
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology; F189-120/Domain: EGF homology <EG1>
F:189-120/Domain: EGF homology <EG1>
F:130-166/Domain: EGF homology <EG2>
F:192-425/Domain: trypsin homology <TRY>

Query Match      71.6%: Score 139; DB 2; Length 443;
Best Local Similarity 54.5%: Pred. No. 2.7e-16;
Matches 24; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

Oy      1 ANGFLXLRPGSLKRXCRXXLCSEFXXAHXIFRNXXRTQFWVSX 44
      |||| | |||| | || | |||| | |||| | |||| | |||| |
Db      40 ANSFLEELRPGSLERECKREELCSFEFAREVFQSTERTQFWITX 83

RESULT      3
KRNUT
coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1989 #sequence_revision 19-May-1994 #text_change 08-Dec-2000
C:Accession: A28322; A23819; A31186; B31186; S63524
R:O'Hara, P.J.; Grant, F.J.; Halldeman, B.A.; Gray, C.L.; Insley, M.Y.; Hagen, F.S.; Murray,
Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987
A:Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-dependent
A:Reference number: A28322; MUID:87260948
A:Accession: A28322
A:Molecule type: DNA
A:Residues: 1-466 <ONH>
A:Cross-references: J0502933; NID:g180333; PID:AAA51983.1; PID:g180334
R:Hagen, F.S.; Gray, C.L.; O'Hara, P.; Grant, F.J.; Saari, G.C.; Woodbury, R.G.; Hart, C.
Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986
A:Title: Characterization of a cDNA coding for human factor VII.
A:Reference number: A23819; MUID:86205965
A:Accession: A23819
A:Molecule type: mRNA
A:Residues: 1-466 <HAG>
A:Cross-references: GB:M13232; NID:g182799; PID:AAA88040.1; PID:g182801
R:Rithm, L.; Bjørn, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen, A.
Biochemistry 27, 7785-7793, 1988
A:Title: Amino acid sequence and posttranslational modifications of human factor VII-a
A:Reference number: A90539; MUID:89088153
A:Accession: A31186
A:Molecule type: protein
A:Residues: 61-212 <THI>
A:Accession: B31186
A:Molecule type: protein

```

A:Residues: 213-466 <TH2>
R:Bioern, S.; Foster, D.C.; Thim, L.; Wilderg, F.C.; Christensen, M.; Komiya, Y.; Pe
J. Biol. Chem. 266, 11051-11057, 1991
A:Title: Human plasma and recombinant factor VII. Characterization of O-glycosylation
A:Reference number: A40529; MUID:91250411
A:Contents: annotation: carbohydrate binding sites
R:Persson, E.; Petersen, L.C.
Eur. J. Biochem. 234, 293-300, 1995
A:Title: Structurally and functionally distinct Ca(2+) binding sites in the gamma-carb
A:Reference number: S63524; MUID:96096752
A:Accession: S63524
A:Molecule type: Protein
A:Residues: 61-65;99-103;105-109;213-217;308-312 <ER>
C:Genetics:
A:Gene: GDB:F7
A:Cross-references: GDB:119897; OMIM:227500
A:Map position: 13q34-13q34
A:Introns: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1
C:Function:
A:Description: catalyzes the proteolytic activation of coagulation factor X in the pr
agulation factor IX in the presence of calcium and tissue factor
A:Pathway: blood coagulation extrinsic pathway
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglut
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-60/Domain: propeptide #status predicted <PKO>
F:45-10/Domain: Gla domain homology <GLA>
F:61-212/Product: coagulation factor VIIa light chain #status experimental <MA1>
F:151-187/Domain: EGF homology <EG1>
F:213-466/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
F:213-447/Domain: trypsin homology <TRY>
F:66;67;74;76;80;85;86;89;95/Modified site: gamma-carboxyglutamic acid (Glu) #stat
F:77-82;110-121;115-130;132-141;151-162;158-172;174-187;195-222;219-224;238-254;
F:112;120/Binding site: carboxylate (Ser) (covalent) #status experimental
F:1123/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status absent
F:205;382/Binding site: carboxylate (Asn) (covalent) #status experimental
F:213-213/Cleavage site: Arg-11e (coagulation factor X1a) #status experimental
F:253;302;404/Active site: His, Asp, Ser #status predicted
F:350-351/Cleavage site: Arg-Gly (coagulation factor Xa) #status predicted

Query Match 67.5%; Score 131; DB 1; Length 466;
Best Local Similarity 54.5%; Pred. No. 7;le-15;
Matches 24; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Oy 1 ANGLXLLRPGSLXRCXRLCSFXAHXIFRNNXTRQFWNSY 44
Db 61 ANAFLEELRPGSLERECKEBOCSFEAREIRKDAERIKLEWISY 104

RESULT 4
JX0210
protein C (activated) (EC 3.4.21.69) precursor - mouse
N:Alternate names: vitamin K-dependent serine proteinase
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: JX0210
R:Tada, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.
J. Biochem. 111, 491-495, 1992
A:Title: Isolation and characterization of a mouse protein C cDNA.
A:Reference number: JX0210; MUID:92316897
A:Accession: JX0210
A:Molecule type: mRNA
A:Residues: 1-461 <TAD>
A:Cross-references: GB:D10445; NID:g220385; PIDN:BA01235.1; PID:g220386
A:Experimental source: liver
C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase thatb
s.
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglut
F:1-33/Domain: signal sequence #status predicted <SIG>
F:72-85/Domain: Gla domain homology <GLA>

F-61-212/Product: coagulation factor VIIa light chain #status experimental <MA1>
F-110-141/Domain: EGF homology <EG1>
F-151-187/Domain: EGF homology <EG2>
F-213-466/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
F-213-447/Domain: trypsin homology <TRY>
F-67-82, 71-76, 79, 80, 85, 86, 89, 95/Modified site: gamma-carboxyglutamic acid (Glu) #siteb
F-112-120/Binding site: carboxylate (Ser) (covalent) #status experimental
F-123/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status absent
F-205, 382/Binding site: carboxylate (Asn) (covalent) #status experimental
F-212-213/Cleavage site: Arg-Ile (coagulation factor XIa) #status experimental
F-253, 302, 404/Active site: His, Asp, Ser #status predicted
F-350-351/Cleavage site: Arg-Gly (coagulation factor XIa) #status predicted

```

Query Match          67.5%; Score 131; DB 1; Length 466;
Best Local Similarity 54.5%; Pred. No. 7; I.e-15;
Matches    24; Conservative    5; Mismatches   15; Indels      0; Gaps      0;

OY      1 ANGFLXLRPGSLKRXCRXXLCSEFYXAHXIFRNXXRTROFWVSY 44
        || || | ||||| | : || | | | : || : || : ||
Db       61 ANAFLEELRPGSLERECEQCSFEAREIRFDARTKLFIWISY 104

RESULT  4

JX0210
protein C (activated) (EC 3.4.21.69) precursor - mouse
N.Alternate names: vitamin K-dependent serine proteinase
C.Species: Mus musculus (house mouse)
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C.Accession: JX0210
R.Tada, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.
J. Biochem. 111, 491-495, 1992
A.Title: Isolation and characterization of a mouse protein C cDNA.
A.Reference number: JX0210; MUID:92316897
A.Accession: JX0210
A.Molecule type: mRNA
A.Residues: 1-461 <TAD>
A.Cross-references: GB:D10445; NID:g220385; PIDD:BAA01235.1; PID:g220386
A.Experimental source: liver
C.Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase thatb
s.
C.Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homolog;
C.Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamic
F.1-33/Domain: signal sequence #status predicted <SIG>
F.27-85/Domain: Gla domain homology <Gla>
```

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 30, 2002, 15:32:46 ; Search time 77.69 Seconds
(without alignments)
54,421 Million cell updates/sec

Title: US-09-302-239-4
Perfect score: 194
Sequence: 1 ANGFLXLRPGSLXRCRXX.....XXAHXIFRNXXRTQFWVSX 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : PIR_71:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	165	85.1	407	1 KFB07	coagulation factor
2	139	71.6	443	2 A46932	coagulation factor
3	131	67.5	466	1 KFH07	coagulation factor
4	115	59.3	461	1 JX0210	protein C (activat
5	106	54.6	461	1 S18994	protein C (activat
6	105	54.1	456	1 KXBO	coagulation factor
7	94	48.5	482	1 EXRT	coagulation factor
8	94	48.5	488	1 KXHU	coagulation factor
9	89	45.9	461	1 KXHU	protein C (activat
10	89	45.9	492	1 EXBO	coagulation factor
11	87	44.8	461	1 KFHU	coagulation factor
12	86	44.3	416	1 KFB0	coagulation factor
13	81	41.8	452	1 A30351	coagulation factor
14	81	41.8	459	2 J00419	coagulation factor
15	81	41.8	475	1 EXCH	coagulation factor
16	78	40.2	622	1 TBHU	thrombin (EC 3.4.2
17	75	38.7	617	2 S10511	thrombin (EC 3.4.2
18	74	38.7	618	2 A35827	thrombin (EC 3.4.2
19	74	38.1	642	2 S53433	plasma protein S p
20	70	36.1	675	1 KXBOS	plasma protein S p
21	69	35.6	625	1 TBBO	thrombin (EC 3.4.2
22	69	35.6	642	2 S53434	plasma protein S p
23	69	35.6	646	2 S38819	plasma protein S p
24	69	35.6	676	1 KXHU	plasma protein S p
25	67	34.5	675	1 KXRTS	plasma protein S p
26	66	34.0	422	1 KXHU	plasma protein Z p
27	62	32.0	396	1 KXBO	plasma protein Z p
28	60	30.9	675	1 KXMS	plasma protein S p
29	58	29.9	678	2 B48089	growth arrest-spec

30	57	29.4	673	2 A48089	growth arrest-spec
31	56.5	29.1	576	2 G96763	probable MAP kinase
32	55	28.4	674	2 I55476	growth potentiation
33	54.5	28.1	594	2 D84859	probable MAP kinase
34	54.5	28.1	603	2 C96575	probable MAP kinase
35	52	26.8	605	1 W1WLB	probable MAP kinase
36	52	26.8	620	1 W1WLB	probable MAP kinase
37	51	26.3	413	1 VHVNH	E1 protein - bovin
38	51	26.3	413	1 VHVNH	nucleoprotein - in
39	47.5	24.5	1123	2 T51517	protein kinase SUR
40	46	23.7	402	2 C72226	telomerase reverse
41	45	23.2	422	2 T39306	hypothetical prote
42	45	23.2	687	2 T08528	mitogen-activated
43	45	23.2	1275	2 T18556	probable DNA topoi
44	44.5	22.9	319	2 T15137	O-antigen biosynth
45	44	22.7	320	2 G84993	hypothetical prote
46	43.5	22.4	638	2 D86477	glutathione synth
47	43	22.2	292	2 T41028	protein P1504.27 l
48	43	22.2	529	2 A95423	short chain dehydr
49	43	22.2	555	2 F86487	probable ABC trans
50	42	21.6	133	2 G81710	unknown protein (I
					hypothetical prote

ALIGNMENTS

RESULT 1
KFB07
Coagulation factor VIIa (EC 3.4.21.21) - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 21-May-1990 #sequence: revision 23-Mar-1995 #text-change 16-Jul-1999
C:Accession: A31979; C20274
R:Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, S.
J. Biol. Chem. 263, 14868-14877, 1988
A:Title: Bovine factor VII. Its purification and complete amino acid sequence.
A:Reference number: A31979; MUID:8908362
A:Accession: A31979
A:Molecule type: protein
A:Residues: 1-407 <TAK>
R:McMullen, B. A.; Fujikawa, K.; Kisilev, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood
A:Reference number: A20274; MUID:83308813
A:Accession: C20274
A:Molecule type: protein
A:Residues: 58-62, 'X', 64-68 <MCW>
A>Note: the residue designated 'X' was determined to be hydroxyaspartic acid
R:Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga
J. Biochem. 104, 867-868, 1988
A:Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood c
A:Reference number: A44556; MUID:89213999
A:Contents: annotation
A>Note: structure and location of covalently bound carbohydrate
C:Function:
A:Description: catalyzes the proteolytic activation of coagulation factor X in the pr
A:Description: factor IX in the presence of calcium and tissue factor
A:Pathway: blood coagulation extrinsic pathway
C:Superfamily: coagulation factor X; EGF homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; Gla domain homology; calcium binding; carboxylu
F:1-152/Product: coagulation factor VIIa light chain #status experimental <MAI>
F:1-44/Domain: Gla domain homology (fragment) <GLA>
F:50-81/Domain: EGF homology <EG1>
F:91-127/Domain: EGF homology <EG2>
F:153-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
F:153-387/Domain: trypsin homology <TRY>
F:6,7,14,16,19,20,25,26,29,34,35/Modified site: gamma-carboxyglutamic acid (Glu) #sta
F:17-22,50-61,55-70,72-81,91-102,99-112,114-127,135-262,159-164,178-194,310-329,340-3
F:52/Binding site: carbohydrate (Ser) (covalent) #status experimental
F:63/Modified site: erythro-beta-hydroxyaspartic acid (Asp) (partial) #status experim
F:145,203/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:152-153/Cleavage site: Arg-11e (coagulation factor X1a) #status experimental
F:193,242,344/Active site: His, Asp, Ser #status predicted
F:290-291/Cleavage site: Arg-Gly (coagulation factor Xa) #status experimental

Query Match 45.9%; Score 89; DB 2; Length 419;
Best Local Similarity 46.3%; Pred. No. 1.2e-07;
Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

OY 1 ANGFLXLRPGSLXRCXRLCSFXXAHXIFPNXXRTROFW 41
DB 1 ANSFLELRHSSLRECEIEICDFEAKETIFQNVDDTLAFW 41

RESULT 49
PCT-US92-10242-1
Sequence 1, Application PC/TUS9210242
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Masters, Rolf
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESSEE: Research Institute
STREET: 10666 North Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10242
FILING DATE: 19921118
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRO472P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..157
OTHER INFORMATION: /note= "protein C Light Chain"
NAME/KEY: Region
LOCATION: 158..169
OTHER INFORMATION: /note= "protein C Activation
Peptide"
FEATURE:
NAME/KEY: Region
LOCATION: 170..419
OTHER INFORMATION: /note= "Protein C Heavy Chain"
PCT-US92-10242-1

Query Match 45.9%; Score 89; DB 5; Length 419;
Best Local Similarity 46.3%; Pred. No. 1.2e-07;
Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

OY 1 ANGFLXLRPGSLXRCXRLCSFXXAHXIFPNXXRTROFW 41
DB 1 ANSFLELRHSSLRECEIEICDFEAKETIFQNVDDTLAFW 41

RESULT 50
US-08-756-506-2
Sequence 2, Application US/08756506
Patent No. 5905185
GENERAL INFORMATION:
APPLICANT: Garner, Ian
APPLICANT: Cottingham, Ian R.
APPLICANT: Temperley, Simon M.
APPLICANT: Foster, Donald C.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Prunkard, Donna E.
TITLE OF INVENTION: PROTEIN C PRODUCTION IN TRANSGENIC
TITLE OF INVENTION: ANIMALS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,506
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 95-28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 460 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-756-506-2

Query Match 45.9%; Score 89; DB 2; Length 460;
Best Local Similarity 46.3%; Pred. No. 1.3e-07;
Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

OY 1 ANGFLXLRPGSLXRCXRLCSFXXAHXIFPNXXRTROFW 41
DB 43 ANSFLELRHSSLRECEIEICDFEAKETIFQNVDDTLAFW 83

Search completed: August 30, 2002, 15:31:15
Job time: 6240 sec


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US-08-745-254A-2
; Sequence 2, Application US/08745254A
; Patent No. 5837843
; GENERAL INFORMATION:
; APPLICANT: Smirnov, Mikhail, D.
; APPLICANT: Esmon, Charles T.
; TITLE OF INVENTION: Modified Protein C
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center, 1201 West Peachtree Street
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/745,254A
; FILING DATE: 8-NOV-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRF 165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-873-8794
; TELEFAX: (404)-873-8795
; INFORMATION FOR SEQ ID NO: 2:
; LENGTH: 42 amino acids
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY:
; LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29
; OTHER INFORMATION: /note="where xaa means gamma
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: /note="partial sequence of human protein C"
US-08-745-254A-2

Query Match 45.9%; Score 89; DB 2; Length 42;
Best Local Similarity 68.3%; Pred. No. 1.1e-08;
Matches 28; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANGFLXLRPGSLRXRCXXLCSPFXAHXIFRNXXRTQFW 41
Db 1 ANSFLXLRHSSLRXRCIXXICDPFXAKXIIFQNVDTLAFW 41

RESULT 45
US-08-955-636-1
; Sequence 1, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelstuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 44
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)..(0)
; OTHER INFORMATION: xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-1

Query Match 45.9%; Score 89; DB 3; Length 44;
Best Local Similarity 68.3%; Pred. No. 1.2e-08;
Matches 28; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANGFLXLRPGSLRXRCXXLCSPFXAHXIFRNXXRTQFW 41
Db 1 ANSFLXLRHSSLRXRCIXXICDPFXAKXIIFQNVDTLAFW 41

RESULT 46
US-08-965-832-2
; Sequence 2, Application US/08965832
; Patent No. 5847085
; GENERAL INFORMATION:
; APPLICANT: CHARLES T. ESMON AND MIKHAIL D. SMIRNOV
; TITLE OF INVENTION: Modified Protein C
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center, 1201 West
; STREET: Peachtree Street
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,832
; FILING DATE: 7-NOV-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/745,254
; FILING DATE: 8-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/053,768
; FILING DATE: 25-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRF 165/167
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-873-8794
; TELEFAX: (404)-873-8795
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY:
; LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29
; OTHER INFORMATION: /note="where xaa means gamma
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: /note="partial sequence of human protein C"
US-08-965-832-2
```



```
FEATURE:
NAME/KEY: Region
LOCATION: 143...448
OTHER INFORMATION: /note="Factor X Heavy Chain"
PCF-US92-10242-3
```

```
Query Match
Best Local Similarity 48.5%; Score 94; DB 5; Length 448;
Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;
```

```
QY 1 ANGFLXXLRPGSLXRCRXXCXLCSEFXAXHIFRNXXTROFW 44
DB 1 ANSFLEEMKKGHLRECMETCSYEAREVEFEDSDKTNEFWNKY 44
```

```
RESULT 41
US-08-955-636-24
Sequence 24, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Neissestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 24
LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-24
```

```
Query Match
Best Local Similarity 46.4%; Score 90; DB 3; Length 44;
Matches 28; Conservative 2; Mismatches 11; Indels 0; Gaps 0;
```

```
QY 1 ANGFLXXLRPGSLXRCRXXCXLCSEFXAXHIFRNXXTROFW 41
DB 1 ANSFLLXLRGSLXRCXCIXXCIDCFXAKXIFEDVDTLAFW 41
```

```
RESULT 42
US-08-955-636-35
Sequence 35, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Neissestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 35
LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-35
```

```
Query Match
Best Local Similarity 46.4%; Score 90; DB 3; Length 44;
Matches 28; Conservative 2; Mismatches 11; Indels 0; Gaps 0;
```

```
QY 1 ANGFLXXLRPGSLXRCRXXCXLCSEFXAXHIFRNXXTROFW 41
DB 1 ANSFLLXLRGSLXRCXCIXXCIDCFXAKXIFEDVDTLAFW 41
```

```
RESULT 43
US-08-229-280-5
Sequence 5, Application US/08229280
Patent No. 5516640
GENERAL INFORMATION:
APPLICANT: MATANABE, Keisuke
APPLICANT: NAKAKI, Toru
TITLE OF INVENTION: METHOD OF DETERMINATION OF
TITLE OF INVENTION: PIVKA OF EVERY KIND AND
TITLE OF INVENTION: REAGENT THEREFOR
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS, P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 MB storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: Wordperfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/229,280
FILING DATE:
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-130015
FILING DATE: MAY 7, 1993
APPLICATION NUMBER: JP 6-16348
FILING DATE: FEBRUARY 10, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Terryence F. Chapman
REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Futuya Case 1312
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homosapiens
FEATURE:
OTHER INFORMATION: Xaa in the sequence is
OTHER INFORMATION: -carboxyglutamic acid
US-08-229-280-5
```

```
Query Match
Best Local Similarity 45.9%; Score 89; DB 1; Length 41;
Matches 28; Conservative 2; Mismatches 11; Indels 0; Gaps 0;
```

```
QY 1 ANGFLXXLRPGSLXRCRXXCXLCSEFXAXHIFRNXXTROFW 41
DB 1 ANSFLLXLRHSLXRCXCIXXCIDCFXAKXIFQNVDTLAFW 41
```

RESULT 44

FEATURE:
NAME/KEY: Region
LOCATION: 140..142
OTHER INFORMATION: /note= "Factor X Connecting
OTHER INFORMATION: Tripeptide"
FEATURE:
NAME/KEY: Region
LOCATION: 143..448
OTHER INFORMATION: /note= "Factor X Heavy Chain"
US-08-955-471-3

Query Match 48.5%; Score 94; DB 2; Length 448;
Best Local Similarity 36.4%; Pred. No. 1.7e-08;
Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Oy 1 ANGFLXLRPGSLRXCRXXLCSPXAXHIFRNXXRTROFWVS 44
Db 1 ANSFLBEMKKGHLRECMETCTSYEARVFEEDSDKTNEFWNKY 44

RESULT 39
PCT-US92-10068-1
Sequence 1, Application PC/TUS9210068
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C
APPLICANT: Edgington, Thomas S
APPLICANT: Fair, Daryl S
TITLE OF INVENTION: Factor X-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Inflammation
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps
STREET: 10666 North Torrey Pines Road
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10068
CLASSIFICATION:
FILING DATE: 19921120
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/798,221
FILING DATE: 22-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: SCR1221P
REFERENCE/DOCKET NUMBER: 34,163
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: AMINO ACID
MOLECULE TYPE: linear
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..139
OTHER INFORMATION: /note= "Factor X Light Chain"
NAME/KEY: Region

LOCATION: 140..142
OTHER INFORMATION: /note= "Factor X Connecting
OTHER INFORMATION: Tripeptide"
FEATURE:
NAME/KEY: Region
LOCATION: 143..448
OTHER INFORMATION: /note= "Factor X Heavy Chain"
PCT-US92-10068-1

Query Match 48.5%; Score 94; DB 5; Length 448;
Best Local Similarity 36.4%; Pred. No. 1.7e-08;
Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Oy 1 ANGFLXLRPGSLRXCRXXLCSPXAXHIFRNXXRTROFWVS 44
Db 1 ANSFLBEMKKGHLRECMETCTSYEARVFEEDSDKTNEFWNKY 44

RESULT 40
PCT-US92-10242-3
Sequence 3, Application PC/TUS9210242
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Mesters, Rolf
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps
STREET: 10666 North Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10242
FILING DATE: 19921118
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR0472P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: AMINO ACID
MOLECULE TYPE: linear
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..139
OTHER INFORMATION: /note= "Factor X Light Chain"
NAME/KEY: Region
LOCATION: 140..142
OTHER INFORMATION: /note= "Factor X Connecting
OTHER INFORMATION: Tripeptide"

```

; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-23
```

```

Query Match          49.5%; Score 96; DB 3; Length 44;
Best Local Similarity 65.9%; Pred. No. 7.1e-10;
Matches 29; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
```

```
Oy      1 ANGFLXXLRPGSLRXCRXXLCSFXXAHXIFRNXXRTROFWSY 44
         |||||::|||::|||::|||::|||::|||::|||::|||
Db      1 ANSFLXXLRHGNVXRXCXXVCXFXXARXIFONTXDTMAFWSY 44
```

```

RESULT 37
US-08-295-411-3
; Sequence 3, Application US/08295411
; Patent No. 5679639
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Masters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,411
; FILING DATE: 22-AUG-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,989
; FILING DATE: 18-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSPR1263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..139
```

```

; OTHER INFORMATION: /note= "Factor X light Chain"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 140..142
; OTHER INFORMATION: /note= "Factor X Connecting
; OTHER INFORMATION: tripeptide"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 143..448
; OTHER INFORMATION: /note= "Factor X Heavy Chain"
US-08-295-411-3
```

```

Query Match          48.5%; Score 94; DB 1; Length 448;
Best Local Similarity 36.4%; Pred. No. 1.7e-08;
Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;
```

```
Oy      1 ANGFLXXLRPGSLRXCRXXLCSFXXAHXIFRNXXRTROFWSY 44
         |||||::|||::|||::|||::|||::|||::|||::|||
Db      1 ANSFLXMKKHLERCMEETCSYEAREVFEEDSDKTFEWNKY 44
```

```

RESULT 38
US-08-955-471-3
; Sequence 3, Application US/08955471
; Patent No. 5968751
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Masters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,471
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/295,411
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSPR1263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..139
; OTHER INFORMATION: /note= "Factor X light Chain"
```

LOCATION: 63
OTHER INFORMATION: /note= "An amino acid represented
OTHER INFORMATION: by the greek letter Beta"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 84
OTHER INFORMATION: /note= "Location of Intron D"
FEATURE:
NAME/KEY: Modified-site
LOCATION: (158,159)
OTHER INFORMATION: /note= "Location of Intron F"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 198
OTHER INFORMATION: /note= "Location of Intron G"
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: group(17..22,50..61, 55..70, 72..81, 89..100, 96
LOCATION: ..109, 111..124, 132..251, 150..155, 170..186,
LOCATION: 299..313, 324..352)
US-08-487-037-3

Query Match 51.0%; Score 99; DB 1; Length 437;
Best Local Similarity 36.4%; Pred. No. 2.3e-09;
Matches 16; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

Oy 1 ANGFLXXLRPGSLKRCRXXLCSPFXAHXIFRNXXRTQFWVSY 44
Db 41 ANSFLTMKKGHLRTCMTTCTCTTARTVFTSDSKTTFNNKY 84

RESULT 35

US-08-487-037-1

Sequence 1, Application US/08487037

Patent No. 5795863

GENERAL INFORMATION:

APPLICANT: Wolf, David L.

TITLE OF INVENTION: RECOMBINANT AGENTS AFFECTING THROMBOSIS

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 2000 Pennsylvania Avenue, NW

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20006-1812

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/487,037

FILING DATE: 07-JUN-1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Adler, Reid G.

REGISTRATION NUMBER: 30,988

REFERENCE/DOCKET NUMBER: 2803-0002.02

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500

TELEFAX: (202) 887-0763

TELEX: 90-4030

INFORMATION FOR SEQ. ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 488 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: both

FEATURE:

NAME/KEY: Modified-site

LOCATION: -17

OTHER INFORMATION: /note= "Location of Intron A"
FEATURE:
NAME/KEY: Modified-site
LOCATION: (37,38)
OTHER INFORMATION: /note= "Location of Intron B"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 46
OTHER INFORMATION: /note= "Location of Intron C"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 63
OTHER INFORMATION: /note= "Amino acid represented by
OTHER INFORMATION: the greek letter Beta"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 84
OTHER INFORMATION: /note= "Location of Intron D"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 128
OTHER INFORMATION: /note= "Location of Intron E"
FEATURE:
NAME/KEY: Modified-site
LOCATION: (209,210)
OTHER INFORMATION: /note= "Location of Intron F"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 249
OTHER INFORMATION: /note= "Location of Intron G"
FEATURE:
NAME/KEY: Peptide
LOCATION: -40..0
OTHER INFORMATION: /note= "Pre-Pro leader sequence"
FEATURE:
NAME/KEY: Protein
LOCATION: 1..139
OTHER INFORMATION: /note= "Factor Xa- light chain"
FEATURE:
NAME/KEY: Peptide
LOCATION: 143..194
OTHER INFORMATION: /note= "Activation Peptide"
FEATURE:
NAME/KEY: Protein
LOCATION: 195..448
OTHER INFORMATION: /note= "Factor Xa-Heavy Chain"
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: group(17..22, 50..61, 55..70, 72..81, 89..100, 96
LOCATION: ..109, 111..124, 132..302, 201..206, 221..237,
LOCATION: 350..364, 375..403)
US-08-487-037-1

Query Match 51.0%; Score 99; DB 1; Length 488;
Best Local Similarity 36.4%; Pred. No. 2.5e-09;
Matches 16; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

Oy 1 ANGFLXXLRPGSLKRCRXXLCSPFXAHXIFRNXXRTQFWVSY 44
Db 41 ANSFLTMKKGHLRTCMTTCTCTTARTVFTSDSKTTFNNKY 84

RESULT 36

US-08-955-636-23

Sequence 23, Application US/08955636A

Patent No. 6017882

GENERAL INFORMATION:

APPLICANT: Nelstuen, Gary

TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT

FILE REFERENCE: 09531/002001

CURRENT APPLICATION NUMBER: US/08/955,636A

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: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/487,037
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Adler, Reid G.
: REGISTRATION NUMBER: 30,988
: REFERENCE/DOCKET NUMBER: 2803-0002.02
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 887-1500
: TELEFAX: (202) 887-0763
: TELEX: 90-4030
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 437 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: both
: FEATURE:
: NAME/KEY: Protein
: LOCATION: 1..139
: OTHER INFORMATION: /note= "Factor Xa-Light Chain"
: FEATURE:
: NAME/KEY: Peptide
: LOCATION: -40..0
: OTHER INFORMATION: /note= "Pre-Pro leader sequence"
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: -17
: OTHER INFORMATION: /note= "Location of Intron A"
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: (37^38)
: OTHER INFORMATION: /note= "Location of Intron B"
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 46
: OTHER INFORMATION: /note= "Location of Intron C"
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 63
: OTHER INFORMATION: /note= "An amino acid represented
: OTHER INFORMATION: by the greek letter Beta"
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 84
: OTHER INFORMATION: /note= "Location of Intron D"
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 128
: OTHER INFORMATION: /note= "Location of Intron E"
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: (158^159)
: OTHER INFORMATION: /note= "Location of Intron F"
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 198
: OTHER INFORMATION: /note= "Location of Intron G"
: FEATURE:
: NAME/KEY: Disulfide-bond
: LOCATION: group(17..22, 50..61, 55..70, 72..81, 89..100, 96
: LOCATION: ..109, 111..124, 132..251, 150..155, 170..186,
: LOCATION: 299..313, 324..352)
: US-08-487-037-2

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Query Match

51.0%; Score 99; DB 1; length 437;

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Best Local Similarity 36.4%; Pred. No. 2,3e-09;
Matches 16; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

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QY 1 ANGFLLXLRPGSLXRCRXALCSFXAHXIFRXXXTROFVSY 44
Db 41 ANSFLTTMKKGLTRICMTTTCSTYTAHVFTSDXTNFWNRY 84

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RESULT 34

US-08-487-037-3

Sequence 3, Application US/08487037

Patent No. 5795863

GENERAL INFORMATION:

APPLICANT: Wolf, David L.

TITLE OF INVENTION: RECOMBINANT AGENTS AFFECTING THROMBOSIS

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FORSTER

STREET: 2000 Pennsylvania Avenue, NW

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20006-1812

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/487,037

FILING DATE: 07-JUN-1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Adler, Reid G.

REGISTRATION NUMBER: 30,988

REFERENCE/DOCKET NUMBER: 2803-0002.02

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500

TELEFAX: (202) 887-0763

TELEX: 90-4030

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 437 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: both

FEATURE:

NAME/KEY: Modified-site

LOCATION: -40..397

OTHER INFORMATION: /note= "Same features apply from

OTHER INFORMATION: SEQ ID NO:2"

FEATURE:

NAME/KEY: Protein

LOCATION: 1..139

OTHER INFORMATION: /note= "Factor Xa - Light Chain"

FEATURE:

NAME/KEY: Modified-site

LOCATION: -40..0

OTHER INFORMATION: /note= "Pre-Pro leader sequence"

FEATURE:

NAME/KEY: Modified-site

LOCATION: -17

OTHER INFORMATION: /note= "Location of Intron A"

FEATURE:

NAME/KEY: Modified-site

LOCATION: (37^38)

OTHER INFORMATION: /note= "Location of Intron B"

FEATURE:

NAME/KEY: Modified-site

LOCATION: 46

OTHER INFORMATION: /note= "Location of Intron C"

FEATURE:

NAME/KEY: Modified-site

```
TELEFAX: (202)822-0168
TELEX: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 17..22
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 50..61
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 55..70
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 72..81
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 89..100
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 96..109
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 111..124
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 132
OTHER INFORMATION: /note= "Disulfide linkage with
OTHER INFORMATION: residue 160 of SEQ ID NO:1, residue 108 of SEQ ID NO:3 or
OTHER INFORMATION: residue 108 of SEQ ID:4"
US-08-484-558-2

Query Match          51.0%; Score 99; DB 1; Length 139;
Best Local Similarity 36.4%; Pred. NO. 7e-10;
Matches 16; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

Oy 1 ANGFLXLRPGSLKRXRCRXHLCSEFXAHXIFRNXXRTROFWVS 44
Db 1 ANSFLTMKKGHLTRCMTTCSYTTARTVFTDSKDTWTFWVKY 44

RESULT 32
US-08-774-592-2
; Sequence 2, Application US/08774592
; Patent No. 5770699
; GENERAL INFORMATION:
; APPLICANT: King, Robert
; TITLE OF INVENTION: PROCESS FOR PRODUCTION OF INHIBITED
; NUMBER OF INVENTION: FORMS OF ACTIVATED BLOOD FACTORS
; CORRESPONDENCE ADDRESSES: 4
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/774,592
; FILING DATE: 30-Dec-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
```

```
APPLICATION NUMBER: US 08/330,978
FILING DATE: 28-OCT-1994
CLASSIFICATION: 530
APPLICATION NUMBER: US 08/484,558
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2803-0007.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)887-1500
TELEFAX: (202)822-0168
TELEX: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 17..22
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 50..61
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 55..70
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 72..81
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 89..100
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 96..109
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 111..124
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 132
OTHER INFORMATION: /note= "Disulfide linkage with
OTHER INFORMATION: residue 160 of SEQ ID NO:1, residue 108 of SEQ ID:4"
US-08-774-592-2

Query Match          51.0%; Score 99; DB 1; Length 139;
Best Local Similarity 36.4%; Pred. NO. 7e-10;
Matches 16; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

Oy 1 ANGFLXLRPGSLKRXRCRXHLCSEFXAHXIFRNXXRTROFWVS 44
Db 1 ANSFLTMKKGHLTRCMTTCSYTTARTVFTDSKDTWTFWVKY 44

RESULT 33
US-08-487-037-2
; Sequence 2, Application US/08487037
; Patent No. 5795863
; GENERAL INFORMATION:
; APPLICANT: Wolf, David L.
; TITLE OF INVENTION: RECOMBINANT AGENTS AFFECTING THROMBOSIS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES: 11
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
```

LOCATION: 50..61
FEATURE: NAME/KEY: Disulfide-bond
LOCATION: 55..70
FEATURE: NAME/KEY: Disulfide-bond
LOCATION: 72..81
FEATURE: NAME/KEY: Disulfide-bond
LOCATION: 89..100
FEATURE: NAME/KEY: Disulfide-bond
LOCATION: 96..109
FEATURE: NAME/KEY: Disulfide-bond
LOCATION: 111..124
FEATURE: NAME/KEY: Disulfide-bond
LOCATION: 132
OTHER INFORMATION: /note="Disulfide linkage with
OTHER INFORMATION: residue 160 of SEQ ID NO:1, residue 108 of SEQ ID NO:3 or
OTHER INFORMATION: residue 108 of SEQ ID:4"
US-08-330-978-2

Query Match 51.0%; Score 99; DB 1; Length 139;
Best Local Similarity 36.4%; Pred. No. 7e-10;
Matches 16; Conservative 6; Mismatches 22; Indels 0; Gaps 0;
OY 1 ANGFLXXLRPGSLXRCRXKXLCSPFXAHXIFRNXXRTROFWVSY 44
DB 1 ANSFLTTMKKGHLTRTCMTTTCSTYTRVFTDSDKNTFWNKY 44

RESULT 30
US-08-474-042-2
Sequence 2, Application US/08474042
Patent No. 5589572
GENERAL INFORMATION:
APPLICANT: King, Robert
TITLE OF INVENTION: PROCESS FOR PRODUCTION OF INHIBITED
TITLE OF INVENTION: FORMS OF ACTIVATED BLOOD FACTORS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
City: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474, 042
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484, 558
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2803-0007.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)887-1500
TELEFAX: (202)822-0168
TELEX: 90-4030 MRSNFOERSMSH
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Linear
FEATURE: NAME/KEY: Disulfide-bond
LOCATION: 17..22
FEATURE: NAME/KEY: Disulfide-bond
LOCATION: 50..61
FEATURE: NAME/KEY: Disulfide-bond
LOCATION: 55..70
FEATURE: NAME/KEY: Disulfide-bond
LOCATION: 72..81
FEATURE: NAME/KEY: Disulfide-bond
LOCATION: 89..100
FEATURE: NAME/KEY: Disulfide-bond
LOCATION: 96..109
FEATURE: NAME/KEY: Disulfide-bond
LOCATION: 111..124
FEATURE: NAME/KEY: Disulfide-bond
LOCATION: 132
OTHER INFORMATION: /note="Disulfide linkage with
OTHER INFORMATION: residue 160 of SEQ ID NO:1, residue 108 of SEQ ID NO:3 or
OTHER INFORMATION: residue 108 of SEQ ID:4"
US-08-474-042-2

Query Match 51.0%; Score 99; DB 1; Length 139;
Best Local Similarity 36.4%; Pred. No. 7e-10;
Matches 16; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

OY 1 ANGFLXXLRPGSLXRCRXKXLCSPFXAHXIFRNXXRTROFWVSY 44
DB 1 ANSFLTTMKKGHLTRTCMTTTCSTYTRVFTDSDKNTFWNKY 44

RESULT 31
US-08-484-558-2
Sequence 2, Application US/08484558
Patent No. 5602233
GENERAL INFORMATION:
APPLICANT: King, Robert
TITLE OF INVENTION: PROCESS FOR PRODUCTION OF INHIBITED
TITLE OF INVENTION: FORMS OF ACTIVATED BLOOD FACTORS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
City: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484, 558
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2803-0007.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)887-1500


```
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)..(0)
; OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid
US-08-955-636-28
```

```
Query Match
Best Local Similarity 67.0%; Score 130; DB 3; Length 44;
Best Local Similarity 77.3%; Pred. No. 8.9e-16;
Matches 34; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
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```
OY 1 ANGFLXXLRPGSLRXRCRXKXLCSEFXAXHXIFRNXXRTROFWASY 44
Db 1 ANAFLLXXLRPGSLRXRCCKXKXCSEFXAXAFXIFKDXAKRTKLFWISY 44
```

```
RESULT 23
US-08-955-636-29
; Sequence 29, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelisestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)..(0)
; OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid
US-08-955-636-29
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Query Match
Best Local Similarity 65.5%; Score 127; DB 3; Length 44;
Best Local Similarity 77.3%; Pred. No. 2.9e-15;
Matches 34; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
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```
OY 1 ANGFLXXLRPGSLRXRCRXKXLCSEFXAXHXIFRNXXRTROFWASY 44
Db 1 ANAFLLXXLRPGSLRXRCCKXKXCSEFXAXAKIFDAXKTKLFWISY 44
```

```
RESULT 24
US-08-955-636-26
; Sequence 26, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelisestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)..(0)
; OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid
US-08-955-636-26
```

```
Query Match
Best Local Similarity 63.4%; Score 123; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 1.5e-14;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
```

```
OY 1 ANGFLXXLRPGSLRXRCRXKXLCSEFXAXHXIFRNXXRTROFWASY 44
Db 1 ANAFLLXXLRPGSLRXRCCKXKXCSEFXAXAKIFKDXAKRTKLFWISY 44
```

```
RESULT 25
US-08-955-636-27
; Sequence 27, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelisestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)..(0)
; OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid
US-08-955-636-27
```

```
Query Match
Best Local Similarity 63.4%; Score 123; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 1.5e-14;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
```

```
OY 1 ANGFLXXLRPGSLRXRCRXKXLCSEFXAXHXIFRNXXRTROFWASY 44
Db 1 ANAFLLXXLRPGSLRXRCCKXKXCSEFXAXAKIFKDXAKRTKLFWISY 44
```

```
RESULT 26
US-08-955-636-30
; Sequence 30, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelisestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)..(0)
; OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid
US-08-955-636-30
```

```
Query Match
Best Local Similarity 62.4%; Score 121; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 3.2e-14;
Matches 33; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
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```
OY 1 ANGFLXXLRPGSLRXRCRXKXLCSEFXAXHXIFRNXXRTROFWASY 44
Db 1 ANAFLLXXLRPGSLRXRCCKXKXCSEFXAXAKIFKDXAKRTKLFWISY 44
```



```

1      STREET: 1201 Elm Street, Suite 4500
2      CITY: Dallas
3      STATE: Texas
4      COUNTRY: US
5      ZIP: 75270-2197
6
7      COMPUTER READABLE FORM:
8      MEDIUM TYPE: Floppy disk
9      COMPUTER: IBM PC compatible
10     OPERATING SYSTEM: PC-DOS/MS-DOS
11     SOFTWARE: Patent Release #1.0, Version #1.25
12
13     CURRENT APPLICATION DATA:
14     APPLICATION NUMBER: US/08/021,615A
15     FILING DATE: 19-FEB-1993
16     CLASSIFICATION: 514
17
18     PRIOR APPLICATION DATA:
19     APPLICATION NUMBER: US 07/882,202
20     FILING DATE: 13-MAY-1992
21
22     ATTORNEY/AGENT INFORMATION:
23     NAME: Hansen, Eugenia S.
24     REGISTRATION NUMBER: 31,966
25     REFERENCE/DOCKET NUMBER: OMRF B34290CIP
26
27     TELECOMMUNICATION INFORMATION:
28     TELEPHONE: 214-939-4500
29     TELEFAX: 214-939-4500
30
31     INFORMATION FOR SEQ ID NO: 4:
32     SEQUENCE CHARACTERISTICS:
33     LENGTH: 466 amino acids
34     TYPE: amino acid
35     TOPOLOGY: linear
36
37     MOLECULE TYPE: protein
38
39     US-08-021-615A-4

```

US-RSULT 18
Sequence 4, Application US/08321777
Patent No. 5504067
GENERAL INFORMATION:
APPLICANT: Morrissey, James H.
APPLICANT: Comp, Philip C.
TITLE OF INVENTION: Treatment of Bleeding with Modified
TITLE OF INVENTION: Tissue Factor in Combination with FVIIa
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Richards, Medlock & Andrews
STREET: 1201 Elm Street, Suite 4500
CITY: Dallas
STATE: Texas
COUNTRY: US
ZIP: 75270-2197
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321.777
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/882202
FILING DATE: 13-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hansen, Eugenia S.

```

?      REGISTRATION NUMBER: 31,966
?      REFERENCE/DOCKET NUMBER: OMRF B342900
?      TELECOMMUNICATION INFORMATION:
?      TELEPHONE: 214-939-4500
?      TELEFAX: 214-939-4600
?      INFORMATION FOR SEQ ID NO: 4:
?      SEQUENCE CHARACTERISTICS:
?      LENGTH: 466 amino acids
?      TYPE: amino acid
?      TOPOLOGY: linear
?      MOLECULE TYPE: protein
US-08-321-777-4

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/378,907
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/871,003
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 90-07C7
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-378-907-2

Query Match
Best Local Similarity 67.5%; Score 131; DB 4; Length 444;
Matches 24; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 1 ANGFLXLRPGSLRXRCRXKXLCSPFXAHXIFRNXXRTQFWVSY 44
Db 39 ANAFLEELRPGSLERCKECCSFPEARIEIFDAERTKLEWISY 82

RESULT 15
PCT-US94-05779-2
Sequence 2, Application PC/TUS9405779
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05779
FILING DATE: 23-MAY-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/065,725
FILING DATE: 21-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,920
FILING DATE: 28-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-1PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-05779-2

Query Match
Best Local Similarity 67.5%; Score 131; DB 5; Length 444;
Matches 24; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 1 ANGFLXLRPGSLRXRCRXKXLCSPFXAHXIFRNXXRTQFWVSY 44
Db 39 ANAFLEELRPGSLERCKECCSFPEARIEIFDAERTKLEWISY 82

RESULT 16
US-07-882-202A-4
Sequence 4, Application US/07882202A
Patent No. 5374617
GENERAL INFORMATION:
APPLICANT: Morrissey, James H.
TITLE OF INVENTION: Treatment of Bleeding with Modified
TITLE OF INVENTION: Tissue Factor In Combination with FVIIa
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richards, Medlock & Andrews
STREET: 1201 Elm Street, Suite 4500
CITY: Dallas
STATE: Texas
COUNTRY: US
ZIP: 75270-2197
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/882,202A
FILING DATE: 13-MAY-1992
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Hansen, Eugene S.
REGISTRATION NUMBER: 31,966
REFERENCE/DOCKET NUMBER: OMRF B34290
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4500
TELEFAX: 214-939-4600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 466 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-882-202A-4

Query Match
Best Local Similarity 67.5%; Score 131; DB 1; Length 466;
Matches 24; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 1 ANGFLXLRPGSLRXRCRXKXLCSPFXAHXIFRNXXRTQFWVSY 44
Db 61 ANAFLEELRPGSLERCKECCSFPEARIEIFDAERTKLEWISY 104

RESULT 17
US-08-021-615A-4
Sequence 4, Application US/08021615A
Patent No. 5504064
GENERAL INFORMATION:
APPLICANT: Morrissey, James H.
TITLE OF INVENTION: Treatment of Bleeding with Modified
TITLE OF INVENTION: Tissue Factor In Combination with an Activator of
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richards, Medlock & Andrews

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; Sequence 2, Application US/08464233
; Patent No. 6039944
; GENERAL INFORMATION:
; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hart, Charles E.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,233
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/327,690
; FILING DATE: 24-OCT-1994
; APPLICATION NUMBER: 08/065,725
; FILING DATE: 21-MAY-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-464-233-2

Query Match 67.5%; Score 131; DB 3; Length 444;
Best Local Similarity 54.5%; Pred. No. 6,4e-15;
Matches 24; Conservative 5; Mismatches 15; Indels 0; Gaps 0;
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QY 1 ANGFLXXLRPGSLXRXCRXXLCSEFXAHXIFRNXXTROFWY 44
  ||| ||||| | | | | | | | | | | | | | | | | | | |
Db 39 ANAFLELRPGSLRCKEBCSFEEAREIFKDAERTKLFWISY 82
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RESULT 13
; US-09-189-607-2
; Sequence 2, Application US/09189607
; Patent No. 6168789
; GENERAL INFORMATION:
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; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hart, Charles E.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
```

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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/189,607
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/660,289
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/327,690
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/065,725
; FILING DATE: 21-MAY-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-189-607-2

Query Match 67.5%; Score 131; DB 4; Length 444;
Best Local Similarity 54.5%; Pred. No. 6,4e-15;
Matches 24; Conservative 5; Mismatches 15; Indels 0; Gaps 0;
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QY 1 ANGFLXXLRPGSLXRXCRXXLCSEFXAHXIFRNXXTROFWY 44
  ||| ||||| | | | | | | | | | | | | | | | | | | |
Db 39 ANAFLELRPGSLRCKEBCSFEEAREIFKDAERTKLFWISY 82
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RESULT 14
; US-09-378-907-2
; Sequence 2, Application US/09378907
; Patent No. 6183743
; GENERAL INFORMATION:
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; APPLICANT: Hart, Charles E.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hedner, Ulla
; APPLICANT: Rasmussen, Mirella E.
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
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APPLICATION NUMBER: US/08/660,289
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/475,845
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 08/327,690
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-660-289-2

Query Match 67.5%; Score 131; DB 2; Length 444;
Best Local Similarity 54.5%; Pred. No. 6.4e-15;
Matches 24; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

OY 1 ANGFLXLRPGSLXRXCRXXLCSFXXAHXIFRNXXRTROFWVS 44
Db 39 ANAFLELRPGSLERCKECCSFEEAREIFKDAERTKLFWISY 82

RESULT 10
US-08-537-807-2
Sequence 2, Application US/08537807
Patent No. 5861374
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/537,807
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05779
FILING DATE: 23-MAY-1994
APPLICATION NUMBER: US 08/065,725
FILING DATE: 21-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,920
FILING DATE: 28-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-1PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-537-807-2

Query Match 67.5%; Score 131; DB 2; Length 444;
Best Local Similarity 54.5%; Pred. No. 6.4e-15;
Matches 24; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

OY 1 ANGFLXLRPGSLXRXCRXXLCSFXXAHXIFRNXXRTROFWVS 44
Db 39 ANAFLELRPGSLERCKECCSFEEAREIFKDAERTKLFWISY 82

RESULT 11
US-08-871-003-2
Sequence 2, Application US/08871003
Patent No. 597864
GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
APPLICANT: Petersen, Lars C.
APPLICANT: Hedner, Ulla
APPLICANT: Rasmussen, Mirella E.
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,003
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A.
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 90-07C7
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-871-003-2

Query Match 67.5%; Score 131; DB 2; Length 444;
Best Local Similarity 54.5%; Pred. No. 6.4e-15;
Matches 24; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

OY 1 ANGFLXLRPGSLXRXCRXXLCSFXXAHXIFRNXXRTROFWVS 44
Db 39 ANAFLELRPGSLERCKECCSFEEAREIFKDAERTKLFWISY 82

RESULT 12
US-08-464-233-2

APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend Kourlie and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,845
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/327,690
FILING DATE: 24-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-475-845-2

Query Match 67.5%; Score 131; DB 1; Length 444;
Best Local Similarity 54.5%; Pred. No. 6.4e-15;
Matches 24; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 1 ANGFLXLRPGSLRXRCRXHLCFFXXAHXIFRNXXRTQFWWSY 44
Db 39 ANAFLELRPGSLERCKEKCQCSFEARERIFKDAERTKLFWISY 82

RESULT 8
US-08-327-690-2
Sequence 2, Application US/08327690
Patent No. 5817788
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Townsend and Townsend Kourlie and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/327,690
FILING DATE: 24-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-327-690-2

Query Match 67.5%; Score 131; DB 2; Length 444;
Best Local Similarity 54.5%; Pred. No. 6.4e-15;
Matches 24; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 1 ANGFLXLRPGSLRXRCRXHLCFFXXAHXIFRNXXRTQFWWSY 44
Db 39 ANAFLELRPGSLERCKEKCQCSFEARERIFKDAERTKLFWISY 82

RESULT 9
US-08-660-289-2
Sequence 2, Application US/08660289
Patent No. 5833982
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend Kourlie and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.24
CURRENT APPLICATION DATA:

Query Match 67.5%; Score 131; DB 1; Length 406;
Best Local Similarity 54.5%; Pred. No. 5.8e-15;
Matches 24; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 1 ANGFLXXLRPGSLRXCRXXLCSPFXAHXIFRNXXRTROFWVSY 44
Db 1 ANAFLEELRPGSLRECKECCSFEEAREIFKDAERTKLEWISY 44

RESULT 5
US-08-955-471-5
; Sequence 5, Application US/08955471
; Patent No. 5968751
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Masters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,471
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/295,411
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..152
; OTHER INFORMATION: /note= "Factor VII Light Chain"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 153..406
; OTHER INFORMATION: /note= "Factor VII Heavy Chain"
; US-08-955-471-5

Query Match 67.5%; Score 131; DB 2; Length 406;
Best Local Similarity 54.5%; Pred. No. 5.8e-15;
Matches 24; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 1 ANGFLXXLRPGSLRXCRXXLCSPFXAHXIFRNXXRTROFWVSY 44
Db 1 ANAFLEELRPGSLRECKECCSFEEAREIFKDAERTKLEWISY 44

Db 1 ANAFLEELRPGSLRECKECCSFEEAREIFKDAERTKLEWISY 44

RESULT 6
PCT-US92-10242-5
; Sequence 5, Application PC/TUS9210242
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Masters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 North Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10242
; FILING DATE: 19921118
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,989
; FILING DATE: 18-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRO472P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..152
; OTHER INFORMATION: /note= "Factor VII Light Chain"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 153..406
; OTHER INFORMATION: /note= "Factor VII Heavy Chain"
; PCT-US92-10242-5

Query Match 67.5%; Score 131; DB 5; Length 406;
Best Local Similarity 54.5%; Pred. No. 5.8e-15;
Matches 24; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 1 ANGFLXXLRPGSLRXCRXXLCSPFXAHXIFRNXXRTROFWVSY 44
Db 1 ANAFLEELRPGSLRECKECCSFEEAREIFKDAERTKLEWISY 44

RESULT 7
US-08-475-845-2
; Sequence 2, Application US/08475845
; Patent No. 5788965
; GENERAL INFORMATION:

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 30, 2002, 15:31:14 ; Search time 39.72 Seconds
(without alignments)
27.058 Million cell updates/sec

Title: US-09-302-239-4

Perfect score: 194
Sequence: 1 ANGFLXLRPGSLRXRCRXX.....XXAHXIFRNXXRTQFWWSY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :
1: Issued_Patents_AA:*
2: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	172	88.7	44	3	US-08-955-636-4
2	131	67.5	44	3	US-08-955-636-3
3	131	67.5	406	1	US-08-293-778-24
4	131	67.5	406	1	US-08-295-411-5
5	131	67.5	406	2	US-08-955-471-5
6	131	67.5	406	5	PCT-US92-10242-5
7	131	67.5	444	1	US-08-475-845-2
8	131	67.5	444	2	US-08-327-690-2
9	131	67.5	444	2	US-08-660-289-2
10	131	67.5	444	2	US-08-537-807-2
11	131	67.5	444	2	US-08-871-003-2
12	131	67.5	444	3	US-08-464-233-2
13	131	67.5	444	4	US-09-189-607-2
14	131	67.5	444	4	US-09-378-907-2
15	131	67.5	444	5	PCT-US94-05779-2
16	131	67.5	466	1	US-07-882-202A-4
17	131	67.5	466	1	US-08-021-615A-4
18	131	67.5	466	1	US-08-331-777-4
19	131	67.5	466	4	US-09-009-217-14
20	131	67.5	466	4	US-09-009-656-14
21	131	67.5	466	5	PCT-US93-04493-4
22	130	67.0	44	3	US-08-955-636-28
23	127	65.5	44	3	US-08-955-636-26
24	123	63.4	44	3	US-08-955-636-29
25	123	63.4	44	3	US-08-955-636-27
26	121	62.4	44	3	US-08-955-636-30
27	117	60.3	41	1	US-08-229-280-4

28	105	54.1	44	3	US-08-955-636-2	Sequence 2, Appl1
29	99	51.0	139	1	US-08-330-978-2	Sequence 2, Appl1
30	99	51.0	139	1	US-08-474-042-2	Sequence 2, Appl1
31	99	51.0	139	1	US-08-484-558-2	Sequence 2, Appl1
32	99	51.0	139	1	US-08-774-592-2	Sequence 2, Appl1
33	99	51.0	437	1	US-08-487-037-2	Sequence 2, Appl1
34	99	51.0	437	1	US-08-487-037-3	Sequence 3, Appl1
35	99	51.0	488	1	US-08-487-037-1	Sequence 3, Appl1
36	96	49.5	44	3	US-08-955-636-23	Sequence 23, Appl1
37	94	48.5	448	1	US-08-295-411-3	Sequence 3, Appl1
38	94	48.5	448	2	US-08-955-471-1	Sequence 3, Appl1
39	94	48.5	448	5	PCT-US92-10068-1	Sequence 3, Appl1
40	94	48.5	448	5	PCT-US92-10242-3	Sequence 3, Appl1
41	90	46.4	44	3	US-08-955-636-24	Sequence 35, Appl1
42	89	45.9	44	3	US-08-955-636-35	Sequence 35, Appl1
43	89	45.9	41	1	US-08-229-280-5	Sequence 5, Appl1
44	89	45.9	42	2	US-08-745-254A-2	Sequence 2, Appl1
45	89	45.9	44	3	US-08-955-636-1	Sequence 1, Appl1
46	89	45.9	45	2	US-08-965-832-2	Sequence 1, Appl1
47	89	45.9	419	1	US-08-295-411-1	Sequence 1, Appl1
48	89	45.9	419	2	US-08-955-471-1	Sequence 1, Appl1
49	89	45.9	419	5	PCT-US92-10242-1	Sequence 1, Appl1
50	89	45.9	460	2	US-08-756-506-2	Sequence 2, Appl1

ALIGNMENTS

```
RESULT 1
US-08-955-636-4
; Sequence 4, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelstuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955, 636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)..(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-4

Query Match      88.7%: Score 172; DB 3; Length 44;
Best Local Similarity 100.0%: Pred. No. 4.5e-23;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ANGFLXLRPGSLRXRCRXXLCSPFXAHXIFRNXXRTQFWWSY 44
Db 1 ANGFLXLRPGSLRXRCRXXLCSPFXAHXIFRNXXRTQFWWSY 44

RESULT 2
US-08-955-636-3
; Sequence 3, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelstuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955, 636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
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Query Match 48.5%; Score 94; DB 14; Length 448;
Best Local Similarity 36.4%; Pred. No. 6.8e-08;
Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;
QY 1 ANGFLXXLRPGSLRXCRXXLCSSFXXAHXIFRNXXRTRQFWVSY 44
|| || :: | | | | | | | | : | : | | |
Db 1 ansfleemkghlerecmeetsyeearevfedsdktnefwnky 44

Search completed: August 30, 2002, 15:30:22
Job time: 6272 sec

ID	AAR35762 standard; protein; 448 AA.
XX	
AC	AAR35762;
XX	
DT	24-SEP-1993 (first entry)
XX	
DE	Factor X (X).
XX	
KW	PC; protein C; IX; Factor IX; X; Factor X; PT; prothrombin; VII;
KM	Factor VII; CT; chymotrypsinogen; SP; serine protease; binding;
XX	exosite; catalytic activity.
XX	
OS	Homo sapiens.
XX	
FH	Location/Qualifiers
FT	Region
FT	/note= "Factor X light chain"
FT	Region
FT	/note= "Factor X activation"
FT	Region
FT	/note= "Factor X heavy chain"
FT	Peptide
FT	/note= "exosite 1"
FT	Peptide
FT	/note= "exosite 2"
FT	Peptide
FT	/note= "Pref. PC polypeptide; claim 2, page 136"
FT	Peptide
FT	/note= "Pref. PC polypeptide; claim 2, page 136"
FT	Peptide
FT	/note= "Pref. PC polypeptide; claim 2, page 136"
FT	Peptide
FT	/note= "note= "claim 7, page 138 describes an antibody that reacts with Factor X; fragments 330-344, 404..418 and 415-429 but not with fragment 285-306"
PN	MO9309804 -A.
PD	27-MAY-1993.
PP	18-NOV-1992; 92WO-US10242.
PR	18-NOV-1991; 91US-0793989.
PA	(SCRI) SCRIPPS RES INST.
PJ	Griffin JH, Masters RM; WPI; 1993-182244/22.
PT	Serine protease derived-polypeptide(s) and anti-peptide antibodies - for inhibiting coagulation and assaying for the presence of serine protease in fluid samples
PS	Disclosure; Page 128-130; 149pp; English.
CC	The PC polypeptides indicated in the Features Table inhibit coagulation (they prevent binding of serine protease to natural substrates), esp. when admin. to give an intravascular blood concn. of 0.1-100 (pref. 0.5-10) microm. NB: Sequences corresp. to SEQ ID NO 6, 7, 8 and 9 are described in the specification but have not yet been added to the SEQUENCE LISTING.
Sequence	448 AA;

Query Match	48.5%	Score 94;	DB 14;	Length 448;
Best Local Similarity	36.4%;	Pred. No. 6.8e-08;		
Matches 16;	Conservative	7;	Mismatches 21;	Indels 0;
Gaps 0;				
0y	1	ANGFLXLRPGSLARXCRRXXLCSPYXAHXIFPNXXRTQFWNTS	44	

```

Db      1  ansfleemkqghlercmeetsyearevfedsdktnefwnky 44
          || || :: | | | | ||: | :| : :| :|| |

```

RESULT	50
AAR37402	ID AAR37402 standard; protein: 448 AA.
XX	
AC	AAR37402:
XX	
DT	15-SEP-1993 (first entry)
XX	
DE	Factor X.
XX	
KW	Mac-1; macrophage-monocyte adhesive receptor; procoagulant;
KW	inflammation; thrombosis; atherosclerosis; septic shock;
KW	disseminated vascular coagulation; delayed hypersensitivity;
KW	haemostasis; angiogenesis; leucocyte recruitment; adhesion.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Region
FT	/note= "Factor X light chain"
FT	140..142
FT	/note= "Factor X connecting tripeptide"
FT	143..448
FT	/note= "Factor X heavy chain"
FT	238..246
FT	/note= "recognition site for Mac-1 binding"
FT	366..373
FT	/note= "recognition site for Mac-1 binding"
FT	423..430
FT	/note= "recognition site for Mac-1 binding"
XX	
PN	WO9309803-A.
PD	27-MAY-1993.
XX	
PF	20-NOV-1992; 92WO-US10068.
XX	
PR	22-NOV-1991; 91US-0798221.
XX	
PA	(SCHM.) SCHAEFER S C.
PA	(SCTR) SCRIPPS RES INST.
XX	
PI	Alteri DC, Edgington TS;
DR	WPI: 1993-182243/22.
XX	
PT	Factor X-derived polypeptide(s) inhibit binding of factor X to
PT	Mac-1 - useful for treating thrombosis, atherosclerosis,
PT	disseminated intravascular coagulation, septic shock etc.
PS	Disclosure: Page 101-103; 122pp; English.
XX	
CC	The sequence shown represents the complete amino acid sequence of
CC	human Factor X. Fragments of this sequence corresp. to the Mac-1
CC	(macrophage-monocyte adhesive receptor) recognition sites (see
CC	features) of 10-25 amino acid residues may be used to inhibit Factor
CC	Xa monocyte procoagulant activity, specifically inflammation. The
CC	same effect may be achieved with antibodies raised to such fragments.
CC	Typical applications include treatment of patients at risk of thrombosis
CC	or atherosclerosis before surgery, disseminated intravascular
CC	coagulation, septic shock, inflammation caused by infection (esp. by
CC	herpes simplex) or autoimmune diseases, delayed hypersensitivity, etc.
CC	The fragments also inhibit leucocyte/endothelial cell interaction and
CC	this regulate responses such as leucocyte recruitment, adhesion and
CC	extravasation, haematopoiesis, antigen presentation, angiogenesis,
CC	synlytal formation and haemostasis.
CC	See also AAR37403-20.
XX	
SQ	Sequence 448 AA;

Oy 2 NGFLXLRPGSLXRCXRXLCSEFXAHXIFRNXXRTQFWWSY 44
Db 49 sgkleeefvgnlerecmeekcsfeearvfeenterkifwisy 91

RESULT 47

AAR13675
ID AAR13675 standard; Protein: 250 AA.
AC AAR13675;
DT 09-OCT-1991 (first entry)
DE Factor X-LACI hybrid protein.
KW Kunitz domain; blood; coagulation; inhibitor; Factor X;
KM tissue factor; TF; Lipoprotein-Associated Coagulation Inhibitor.
XX
FH Key Location/Qualifiers
FT Protein 1..171
FT Peptide /label= XLC
FT 1..40
FT Domain /label= prepro_leader
FT 55..64
FT Domain /label= GLA_domain
FT 89..150
FT Domain /label= growth_factor_domains
FT 172..250
FT Domain /label= kunitz_domain
FT 57..62
FT Disulfide-bond 90..101
FT Disulfide-bond 95..110
FT Disulfide-bond 112..121
FT Disulfide-bond 129..140
FT Disulfide-bond 136..149
FT Disulfide-bond 151..164
FT Disulfide-bond 186..236
FT Disulfide-bond 195..219
FT Disulfide-bond 211..232
XX
PN EP439442-A.
XX
PD 31-JUL-1991.
XX
PF 21-JAN-1991; 91EP-0870008.
XX
PR 25-JAN-1990; 90US-0470289.
XX
PA (UNIW) UNIV OF WASHINGTON.
XX
PI Girard TJ, Broze GJ;
XX
DR WPI, 1991-224839/31.
XX
DR N-PSDB; AAQ12776.
XX
PT New factor X-LACI hybrid protein - comprises light chain of
XX factor X and LACI's first kunitz domain for use as anticoagulant
XX
PS Disclosure; Page 12-14; 17pp; English.
XX
XX The protein is used as a blood coagulation inhibitor in mammals. It
XX is believed to mimic the Xa/LACI complex in binding to and
XX inhibiting VIIa/tissue factor. LACI inhibits via a novel feedback
XX mechanism regulating generation of Xa (a prod. of VIIa/TF activity);
XX XIcLACIKI inhibits VIIa/TF activity directly.
XX The DNA allows prodn. of XIcLACIKI by introduction of the gene into
XX cells suitable for expression, e.g. E. coli or CHO cells.
SQ Sequence 250 AA;

Query Match 48.5%; Score 94; DB 12; Length 250;
Best Local Similarity 36.4%; Pred. No. 3.8e-08;

Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;
Oy 1 ANGFLXLRPGSLXRCXRXLCSEFXAHXIFRNXXRTQFWWSY 44
Db 41 ansfleemkghlerecmeetsyeearevfedsdktnefwky 84

RESULT 48

AAR22513
ID AAR22513 standard; Protein: 436 AA.
AC AAR22513;
DT 28-JUL-1992 (first entry)
DE Truncated precursor of human Factor Xa1.
KW Mutant; prothrombinase complex; proteolytic; precursor; thrombosis;
KM inflammation; restenosis; transplantation; haemophilia; antibodies.
XX Homo sapiens.
XX OS
XX PN W09204378-A.
XX PD 19-MAR-1992.
XX PF 04-SEP-1991; 91WO-US06337.
XX PR 04-SEP-1990; 90US-0578646.
XX (CORT-) COR THERAPEUTICS IN.
XX Wolf D;
XX WPI: 1992-114303/14.
XX
XX The full length cDNA of human factor X (Mp19X) was converted to
XX encode a truncated form of human Factor X, designated rx', by deletion
XX of the activation peptide by oligonucleotide site directed mutagenesis.
XX An oligonucleotide was used to align Arg 142 following the
XX C-terminus of the Factor X light chain with Ile 53 of the Factor X
XX activation peptide (1st residue of the heavy chain). When expressed
XX in CHO cells the truncated peptide was cleaved endogenously.
XX Modified Factor Xa was further produced by acylation e.g. with the
XX p-nitrophenyl ester of p-toluoylic acid. Factor rx' is used to
XX treat or prevent thrombosis; inflammation; restenosis or complications
XX of transplantation. It is also used in treatment of adult respiratory
XX distress syndrome and haemophilia. The modified Factor X has no
XX proteolytic activity and interferes with the ability of endogenous
XX factor Xa to convert prothrombin to thrombin. Antibodies reactive
XX with Factor rx' are passive therapeutic agents and used for diagnosis.
XX See also AAR22512.
XX
SQ Sequence 436 AA;

Query Match 48.5%; Score 94; DB 13; Length 436;
Best Local Similarity 36.4%; Pred. No. 6.6e-08;
Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Oy 1 ANGFLXLRPGSLXRCXRXLCSEFXAHXIFRNXXRTQFWWSY 44
Db 41 ansfleemkghlerecmeetsyeearevfedsdktnefwky 84

RESULT 49
AAR35762

DR	N-PSDB:AAK94153.
XX	
PT	830 Primers useful for synthesizing full length cDNA clones and their
PT	use in genetic manipulation -
XX	
PS	
XX	
CC	Claim 8; SEQ ID NO 2675; 1380bp + sequence listing; English.
CC	The invention relates to primers for synthesising full length cDNA
CC	clones, 830 cDNA molecules encoding a human protein have been
CC	isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
CC	molecules have been determined. Primers for synthesising the full length
CC	cDNA are useful for clarifying the function of the protein encoded by
CC	the cDNA. The full length clones were obtained by construction of full
CC	length enriched cDNA libraries that were synthesised by the oligo-capping
CC	method. The primers enable the production of the full length cDNA easily
CC	without any special methods. The present sequence is a polypeptide
CC	encoded by a full length human cDNA of the invention.
CC	Note: The sequence data for this patent did not form part of the printed
CC	specification, but was obtained in CD-ROM format directly from EPO.
XX	
SQ	Sequence 231 AA;
OY	
Db	Query Match 51.0%; Score 99; DB 22; Length 231; Best Local Similarity 38.6%; Pred. No. 4.8e-09; Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0; 1 ANGFLXLRPGSLXRXCRRXLCSFYXAHXIFRNXXRTROFWVS Y 44 : : : : : : : : : : : 20 anefleelrvgtlirecmeelecsyeavxevfenkexkfwmkyg 63
RESULT 45	
ID AAY18308	
ID AAY18308 standard; peptide: 44 AA.	
XX AAY18308;	
AC	
XX 17-AUG-1999 (first entry)	
DT	
DE Modified GLA domain of vitamin K-dependent protein.	
XX	
KW GLA domain; muteln; vitamin K-dependent protein; clotting disorder;	
KW therapy.	
XX	
OS Bos taurus.	
OS OS	
XX Synthetic.	
FH Key	Location/Qualifiers
FT Misc-difference 1..44	
FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic	
FT acid"	
FN WO9920767-A1.	
PN	
PD 29-APR-1999.	
XX	
PF 20-OCT-1998; 98WO-US22152.	
XX	
PR 23-OCT-1997; 97US-0955636.	
XX	
PA (MINU) UNIV MINNESOTA.	
XX	
PI Neisestuen GI;	
XX	
DR WPI; 1999-288309/24.	
XX	
PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic	
PT acid domain, useful for treating clotting disorders	
XX	
PS Disclosure; Page 79; 86pp; English.	
XX	
CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)	

CC	domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the CC GLA domain results in a protein which has enhanced membrane binding CC affinity as compared to the native protein.
XX	Sequence 44 AA:
SO	
Query Match	49.5%; Score 96; DB 20; Length 44;
Best Local Similarity	65.9%; Pred. No. 3.1e-09;
Matches 29; Conservative	4; Mismatches 11; Indels 0; Gaps 0;
OY	1 ANGELXLRPGSLAKXCXXLCSFYAHXIFPNXXKRTQFWSY 44 : Db 1 ansfixxlrhgvnxrxscxxvcfxaxrxiqtxdtmawfsfy 44
RESULT 46	
AAP60057	ID AAP60057 standard; protein; 453 AA.
AC	AAP60057;
XX	
DT	23-MAY-1991 (first entry)
DE	Factor IX/Factor VII fusion peptide.
XX	Factor VII; Factor IX; fusion peptide.
KW	EP200421-A.
PN	10-DEC-1986.
PD	
XX	16-APR-1986; 86EP-0302855.
Pf	
XX	16-DEC-1985; 85US-0810002.
PR	17-APR-1985; 85US-0724311.
XX	(ZYMO-) ZYMOGENETICS INC.
PA	Hagen FS, Murry MJ, Berkner KL, Insley MY, Woodbury RG; PI Gray CL;
PI	
XX	WPI: 1986-326899/50.
DR	N-PSDB; AAN60065.
DR	
XX	DNA construct used to transfect hosts - to produce protein which PT activates to give factor VIIA
PT	
XX	Disclosure: Fig. 7; 55pp; English.
PS	
XX	The peptide is encoded by a Factor IX/Factor VII fusion cDNA. CC cDNA encoding Factor VIIcan be used in a DNA construct which contains CC a nucleotide sequence encoding a protein which, on activation, has the CC same biological activity for blood coagulation as Factor IIA. The CC nucleotide codes at least partially for Factor VII and comprises sequence CC encoding a calcium binding domain joined to second sequence downstream of CC this encoding a catalytic domain for serine protease activity of Factor CC VIIA. Calcium binding domain comprises a gene encoding Factor VII, IX, CC X, Protein C, prothrombin or Protein S. The construct is used to CC transfect host cells to produce the protein which, on activation, CC yields Factor VIIA.
CC	
XX	Sequence 453 AA:
SQ	
Query Match	49.0%; Score 95; DB 7; Length 453;
Best Local Similarity	41.9%; Pred. No. 4.6e-08;
Matches 18; Conservative	5; Mismatches 20; Indels 0; Gaps 0;

FT	Modified-site	/note="gamma-carboxyglutamic acid"
FT	Modified-site	19
FT	Modified-site	/label="OTHER
FT	Modified-site	/note="gamma-carboxyglutamic acid"
FT	Modified-site	20
FT	Modified-site	/label="OTHER
FT	Modified-site	/note="gamma-carboxyglutamic acid"
FT	Modified-site	25
FT	Modified-site	/label="OTHER
FT	Modified-site	/note="gamma-carboxyglutamic acid"
FT	Modified-site	26
FT	Modified-site	/label="OTHER
FT	Modified-site	/note="gamma-carboxyglutamic acid"
FT	Modified-site	29
FT	Modified-site	/label="OTHER
FT	Modified-site	/note="gamma-carboxyglutamic acid"
FT	Modified-site	35
FT	Modified-site	/label="OTHER
FT	Modified-site	/note="gamma-carboxyglutamic acid"

PN	CA2121927-A.
XX	
PD	08-NOV-1994.
XX	
PE	22-APR-1994; 94CA-2121927.
XX	
PR	07-MAY-1993; 93JP-0130015.
XX	10-FEB-1994; 94JP-0016348.
PA	(EISA) EISAI CO LTD.
PI	
XX	Iwasaki Y, Naraki T, Watanabe K.
RR	WPI; 1995-052669/08.

PT Determination of protein induced by vitamin-K absence (PIVKA) - by
PT using an anti-PIVKA antibody, useful as vitamin-K deficiency marker
XX
PS Disclosure: Page 10; 34pp; English.

CC AAM11907.M11907 represent Glu regions of vitamin K dependent plasma
CC proteins. This sequence is the Glu region of Factor VII. The Glu
CC region is the N-terminal region of the protein, and contains 10 glutamic
CC acid residues which are gamma-carboxylated. These 10 residues are
CC uncarboxylated in the precursor form, and require the presence of
CC vitamin K and a carboxylase to be converted into an active form. These
CC proteins suffer incomplete carboxylation when a state of protein induced
CC vitamin K absence (PIVKA) occurs. Various PIVKAs have been found to be
CC produced in the blood as a result of hepatocellular carcinoma. These
CC sequences are all epitopes for the anti-PIVKA-II monoclonal antibody.
CC The anti-PIVKA-II antibody (such as MW-3) specifically recognises the
CC prothrombin Glu region (see AAM11901), but has also been found to
CC recognise the rest of these Glu regions. The antibody can be used in the
CC method of the invention for the determination of PIVKA in a specimen.
CC The determination of PIVKA is clinically useful, as PIVKA is produced in
CC blood as a result of incomplete gamma-carboxylation in a state of
CC vitamin K deficiency or suppression. The determination of PIVKA can
CC therefore be used as a marker of the state of vitamin K deficiency or
CC suppression.

Sequence 41 AA:

Query Match	60.3%	Score 117;	DB 16;	Length 41;
Best Local Similarity	78.0%	Pred. No. 6.8e-13;		
Matches 32; Conservative	4;	Mismatches 5;	Indels 0;	Gaps 0;

```
Qy 1 ANGELXXLRPGSLXRRCXXLCSFXXAHXIFRNNXXRTQFM 41
    || ||||| |||||: || ||||| |||||: |||: |||: ||
Db 1 anafllxlrpgslxrccxxqcsfxaxarxifkdxarhlfw 41
```

RESULT 39

AAU02959
ID AAU02959 standard; Protein; 345 AA.

AC AAU02959;

DT 12-SEP-2001 (first entry)

Angiotensin converting enzyme (ACEV) splice variant protein #59.

Angiotensin converting enzyme splice variant; ACEV; interleukin 6;

platelet-derived endothelial cell growth factor; cardiovascular disease; KW

vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;

diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; KW

nonaroidotic pulmonary granulomatous disease; endothelial abnormality;

[illegible]XX 8
: 70 800

	XX	Z
	X	C
	X	B
	X	G
	X	H
	X	D
	X	E
	X	F
	X	A

XX

XX

PR 10-DEC-1999; 99IL-0133455.

PA (COMP-) COMPUGEN LTD.

PI Levine Z, David A, Azar I, Khosravi R, Bernstein J;

DR WPI; 2001-336004/35.

XX

PT converting enzyme (ACEV), useful in identifying candidate compounds

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	52
--	---	---	---	---	---	---	---	---	---	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----

PS Claim 4; Fig 59; 519pp; English.

The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen p53, and vasoactive intestinal polypeptide receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonrheumatic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial abnormality such as deep vein thrombosis.

SQ Sequence 345 AA;

Query Match	58.88;	Score 114;	DB 22;	Length 345;
Best Local Similarity	50.08;	Pred. No. 1.8e-11;		
Matches 22; Conservative	4;	Mismatches 18;	Indels 0;	Gaps 0;

QY 1 ANGFLXXLRPGSLXRXCRRXXLCSEFXAHXIFRNXRXRTQFWWSY 44
 11 1 1 1111 1 111 1 11:: 11:111: 1
 Db 42 ansllleelwpslrecneeqscfeearelfkspertkqfwivy 85

42 ans i ree l w p s i r e c n e e q s i r e a d e l i k s p e r t k q i w i y 83

[illegible]

FT	Misc-difference 1..44
FT	/note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"
FT	
XX	
PN	WO9920767-A1.
PD	29-APR-1999.
XX	
Pf	20-OCT-1998; 98WO-US22152.
XX	
PR	23-OCT-1997; 97US-0955636.
PA	(MINU) UNIV MINNESOTA.
PI	Nelstuen GL:
XX	
DR	WPI: 1999-288309/24.
XX	
PT	Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders
PS	Claim 11; Page 81; 86pp: English.
XX	
CC	This sequence represents a modified GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the GLA domain results in a protein which has enhanced membrane binding affinity as compared to the native protein.
CC	
CC	
SO	Sequence 44 AA:
OY	Query Match 62.4%; Score 121; DB 20; Length 44; Best Local Similarity 75.0%; Pred. No. 1.5e-13; Matches 33; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
Dd	1 ANGFLXLRLPGSLMXCRXXLCSPFXALXITRNXXRTQEFVSY 44 : : 1 anaflxlrlpgslmxcrxxlcspfxalxitrnxxrtqefvlsy 44
RESULT 38	
AAM11904	ID AAM11904 standard; peptide: 41 AA.
XX	
AC	AAM11904;
XX	
DT	01-APR-1997 (first entry)
XX	
DE	Factor VII Gla region.
XX	
KM	Prothrombin; PIKA; Gla region; Vitamin K dependent plasma protein;
KM	Factor X; Factor IX; Factor VII; Protein C; Protein S; Protein Z;
KM	protein induced vitamin K absence; vitamin K deficiency; vitamin K;
XX	hepatocellular carcinoma; gamma-carboxylase; anti-PIKA-II antibody.
OS	Homo sapiens.
PH	
Key	Location/Qualifiers
FT	Modified-site 6 /label= OTHER
FT	/note= "gamma-carboxyglutamic acid"
FT	Modified-site 7 /label= OTHER
FT	/note= "gamma-carboxyglutamic acid"
FT	Modified-site 14 /label= OTHER
FT	/label= OTHER
FT	/note= "gamma-carboxyglutamic acid"
FT	Modified-site 16 /label= OTHER

```

FT Disulfide-bond 55..70
FT Modified-site 63
FT /label= OTHER
FT /note= "beta-hydroxy-aspartic acid"
FT Disulfide-bond 72..81
FT Disulfide-bond 91..102
FT Disulfide-bond 98..112
FT Disulfide-bond 114..127
FT Disulfide-bond 135..162
FT Cleavage-site 143..144
FT /note= "proteolytic site"
FT Modified-site 145
FT /note= "glycosylation site"
FT Disulfide-bond 159..164
FT Disulfide-bond 178..194
FT Active-site 193
FT Active-site 242
FT Active-site 344
FT Cleavage-site 290..291
FT /note= "proteolytic site"
FT Disulfide-bond 310..329
FT Cleavage-site 315..316
FT /note= "proteolytic site"
FT Modified-site 322
FT /note= "glycosylation site"
FT Disulfide-bond 340..368
FT Cleavage-site 341..342
FT /note= "proteolytic site"
FT Cleavage-site 392..393
FT /note= "proteolytic site"
FT Cleavage-site 396..397
FT /note= "proteolytic site"
FT Cleavage-site 402..403
FT /note= "proteolytic site"
XX
XX US560560-A.
XX
XX 03-DEC-1996.
XX
XX 13-NOV-1989; 89US-0434149.
XX
XX 09-AUG-1993; 93US-0104509.
XX 13-NOV-1989; 89US-0434149.
XX 12-JUN-1992; 92US-0898248.
XX 22-AUG-1994; 94US-0293778.
XX
XX (NOVO ) NOVO-NORDISK AS.
XX
XX Bjorn SE, Nicolaisen EM, Wiberg FC, Woodbury R;
XX
XX WPI; 1997-033523/03.
XX
XX Mutated human factor VII or VIIa proteins - with amino acid
XX substitutions to improve proteolytic stability
XX
XX Claim 8; Page -: 28pp; English.
XX
XX Modified human factor VII or VIIa proteins are stabilised against
XX proteolytic cleavage by substitution of one of the residues Lys32,
XX Lys38, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and
XX Lys341 by an amino acid that provides a proteolytically more stable
XX peptide bond, provided that Lys32 is replaced by Gln, Glu, His,
XX Gly, Thr, Ala or Ser. The modified proteins are useful for treating
XX bleeding disorders such as thrombocytopenia and von Willebrand's
XX disease. They are also suitable for addition to plasma substitutes.
XX The present sequence is a specific example of a modified factor VII
XX protein.
XX
XX Sequence 406 AA;

```

Query Match 65.5%; Score 127; DB 18; Length 406;
 Best Local Similarity 54.5%; Pred. No. 1.2e-13;

```

Matches 24; Conservative 4; Mismatches 16; Indels 0; Gaps 0;
QY 1 ANGFLXXLRPGSLXRXCRXXLCSPXXAHXIFRNXXRRPQWVS 44
Db 1 anafllelrpgslereckeegsfearlelfgaertlflwisy 44

RESULT 35
AA18310
ID AA18310 standard; peptide; 44 AA.
AC
AC AA18310;
DT 17-AUG-1999 (first entry)
XX
DE Modified GLA domain of vitamin K-dependent protein.
XX
XX GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
XX therapy.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
FT Misc-difference 1..44 /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
FT acid"
XX
XX WO9920767-A1.
XX
XX 29-APR-1999.
XX
XX 20-OCT-1998; 98WO-US22152.
XX
XX 23-OCT-1997; 97US-0955636.
XX
XX (MINU ) UNIV MINNESOTA.
XX
XX Nelsestuen GL;
XX
XX WPI; 1999-288309/24.
XX
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
XX acid domain, useful for treating clotting disorders
XX
XX Disclosure; Page 80; 86pp; English.
XX
XX This sequence represents a modified GLA (gamma-carboxyglutamic acid)
XX domain. The invention relates to a vitamin K-dependent polypeptide
XX comprising a modified GLA domain containing an amino acid substitution
XX which enhances membrane binding of the modified polypeptide as compared
XX to the native polypeptide. The polypeptide is used to treat a clotting
XX disorder by decreasing or increasing clot formation. Modification of the
XX GLA domain results in a protein which has enhanced membrane binding
XX affinity as compared to the native protein.
XX
XX Sequence 44 AA;

```

Query Match 63.4%; Score 123; DB 20; Length 44;
 Best Local Similarity 75.0%; Pred. No. 6.7e-14;
 Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 ANGFLXXLRPGSLXRXCRXXLCSPXXAHXIFRNXXRRPQWVS 44
 ID AA18311 standard; peptide; 44 AA.
 AC AA18311;

CC Lys341 by an amino acid that provides a proteolytically more stable
CC peptide bond, provided that Lys32 is replaced by Gln, Glu, His,
CC Gly, Thr, Ala or Ser. The modified proteins are useful for treating
CC bleeding disorders such as thrombocytopenia and von Willebrand's
CC disease. They are also suitable for addition to plasma substitutes.
CC The present sequence is a specific example of a modified factor VII
CC protein.

XX
SQ Sequence 406 AA;

Query Match

Best Local Similarity 54.5%; Score 128; DB 18; Length 406;

Matches 24; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

OY 1 ANGFLXXLRPGSLXRXCRXXLCSPFXAHXIFPNXXRTQFWWSY 44
Db 1 anaflxlrpgslxrxcrxxlcsfpxahxifpnxxrtqfwwsy 44

RESULT 33

AAV18313
ID AAV18313 standard; peptide: 44 AA.

AC AAV18313;

DT 17-AUG-1999 (first entry)

XX Modified GLA domain of vitamin K-dependent protein.

KW GLA domain; muteln; vitamin K-dependent protein; clotting disorder;

KM therapy.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1..44

FT "Xaa" gamma-carboxyglutamic acid, or glutamic

FT acid"

FN M09920767-A1.

XX 29-APR-1999.

PF 20-OCT-1998; 98WO-US22152.

PR 23-OCT-1997; 97US-0955636.

XX (MINU) UNIV MINNESOTA.

PI Neisestuen GL;

DR WPI: 1999-288309/24.

XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic

PT acid domain, useful for treating clotting disorders

XX Disclosure: Page 81; 86pp; English.

CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)
CC domain. The invention relates to a vitamin K-dependent polypeptide
CC comprising a modified GLA domain containing an amino acid substitution
CC which enhances membrane binding of the modified polypeptide as compared
CC to the native polypeptide. The polypeptide is used to treat a clotting
CC disorder by decreasing or increasing clot formation. Modification of the
CC GLA domain results in a protein which has enhanced membrane binding
CC affinity as compared to the native protein.

XX Sequence 44 AA;

Query Match

Best Local Similarity 54.5%; Score 127; DB 20; Length 44;

Best Local Similarity 77.3%; Pred. No. 1.4e-14;
Matches 34; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 ANGFLXXLRPGSLXRXCRXXLCSPFXAHXIFPNXXRTQFWWSY 44
Db 1 anaflxlrpgslxrxcrxxlcsfpxahxifpnxxrtqfwwsy 44

RESULT 34

AAW14511
ID AAW14511 standard; protein: 406 AA.

AC AAW14511;

DT 14-MAY-1997 (first entry)

XX Modified blood coagulation Factor VII (K32Q + K38T).

KW Blood coagulation; factor 7; muteln; mutation; modification;

KM thrombocytopenia; von Willebrand's disease; plasma substitute.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 6

FT "Label" OTHER

FT "note" "gamma-carboxyglutamic acid"

FT Modified-site 7

FT "Label" OTHER

FT "note" "gamma-carboxyglutamic acid"

FT Modified-site 14

FT "Label" OTHER

FT "note" "gamma-carboxyglutamic acid"

FT Modified-site 16

FT "Label" OTHER

FT "note" "gamma-carboxyglutamic acid"

FT Modified-site 19

FT "Label" OTHER

FT "note" "gamma-carboxyglutamic acid"

FT Modified-site 20

FT "Label" OTHER

FT "note" "gamma-carboxyglutamic acid"

FT Modified-site 26

FT "Label" OTHER

FT "note" "gamma-carboxyglutamic acid"

FT Modified-site 29

FT "Label" OTHER

FT "note" "gamma-carboxyglutamic acid"

FT Modified-site 32

FT "Label" OTHER

FT "note" "gamma-carboxyglutamic acid"

FT Modified-site 35

FT "Label" OTHER

FT "note" "gamma-carboxyglutamic acid"

FT Modified-site 38..39

FT "Label" OTHER

FT "note" "proteolytic site in unmodified factor VII"

FT Modified-site 42..43

FT "Label" OTHER

FT "note" "proteolytic site"

FT Modified-site 44..45

FT "Label" OTHER

FT "note" "proteolytic site"

FT Modified-site 50..61

FT "Label" OTHER

FT "note" "proteolytic site"

PI	Nelstestuen GL;
XX	
DR	WPI; 1999-288309/24.
XX	
PT	Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders
XX	
PS	Disclosure: Page 80; 86pp; English.
CC	
XX	This sequence represents a modified GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the CC GLA domain results in a protein which has enhanced membrane binding affinity as compared to the native protein.
CC	
XX	
SQ	Sequence 44 AA;
	Query Match 67.0%; Score 130; DB 20; Length 44; Best Local Similarity 77.3%; Pred. No.: 4,le-15; Matches 34; Conservative 5; Mismatches 5; Indels 0; Gaps 0.
OY	1 ANGFLXLRPGSLRXCRXXLCSFYXAHXIFRNXXRTQFWVS Y 44 : : : Db 1 anaflxxlrpgslrxcrxxxqcsfxxafkifdxartklfwisy 44
	RESULT 31
AAM14507	
ID	AAM14507 standard; protein; 406 AA.
XX	
AC	AAM14507;
XX	
DT	14-MAY-1997 (first entry)
XX	
DE	Modified blood coagulation Factor VII (K320).
XX	
KM	Blood coagulation; factor 7; muten; mutation; modification; thrombocytopenia; von Willebrand's disease; plasma substitute.
XX	
OS	Homo sapiens.
XX	
OS	Synthetic.
PH	
FT	Key
FT	Modified-site
FT	Location/Qualifiers
FT	/label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	7
FT	Modified-site
FT	/label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	14
FT	Modified-site
FT	/label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	16
FT	Modified-site
FT	/label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	19
FT	Modified-site
FT	/label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	20
FT	Modified-site
FT	/label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	17..22
FT	Modified-site
FT	/label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	26
FT	Modified-site
FT	/label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	29
FT	Modified-site
FT	/label= OTHER
FT	/note= "gamma-carboxylutamic acid"

FT	/label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	32..33
FT	/note= "proteolytic site in unmodified fac
FT	32
FT	/note= "native Lys32 has been substituted t
FT	32
FT	provide a proteolytically more stab
FT	bond"
FT	35
FT	/label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	38..39
FT	/note= "proteolytic site"
FT	42..43
FT	/note= "proteolytic site"
FT	44..45
FT	/note= "proteolytic site"
FT	50..61
FT	55..70
FT	63
FT	/label= OTHER
FT	/note= "beta-hydroxy-aspartic acid"
FT	72..81
FT	91..102
FT	98..112
FT	114..127
FT	135..162
FT	143..144
FT	/note= "proteolytic site"
FT	145
FT	/note= "glycosylation site"
FT	159..164
FT	178..194
FT	193
FT	242
FT	344
FT	290..291
FT	/note= "proteolytic site"
FT	310..329
FT	315..316
FT	/note= "proteolytic site"
FT	322
FT	/note= "glycosylation site"
FT	340..368
FT	341..342
FT	/note= "proteolytic site"
FT	392..393
FT	/note= "proteolytic site"
FT	396..397
FT	/note= "proteolytic site"
FT	402..403
FT	/note= "proteolytic site"
PN	US5580560-A.
PD	03-DEC-1996.
PE	13-NOV-1989;
PR	89US-0434149.
PR	09-AUG-1993;
PR	93US-0104509.
PR	13-NOV-1989;
PR	89US-0434149.
PR	12-JUN-1992;
PR	92US-0896248.
PR	22-AUG-1994;
PR	94US-0293778.
PA	(NOVO) NOVO-NORDISK AS.
PI	Bjorn SE, Nicolaisen EM, Wiberg FC, Woodbury R;
PI	WPI: 1997-033523/03.
DR	
XX	Mutated human factor VII or VIIa proteins - with amino acid
XX	substitutions to improve proteolytic stability


```

XX DE Human Factor VII polypeptide.
XX
XX Factor VIIa; thrombus; vascular patency; blood coagulation; Factor X;
KM plasma factor; Factor IX; myocardial injury; human; Factor VII.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..38
FT /note= "signal peptide"
FT Protein 39..444
FT /note= "mature peptide"
FT Misc-difference 10
FT /note= "indicated incorrectly as Trp under sequence
FT listing ID 2"
XX
XX US6183743-B1.
XX
XX 06-FEB-2001.
XX
XX 20-AUG-1999; 99US-0378907.
XX
XX 06-JUN-1997; 97US-0871003.
XX 28-FEB-1991; 91US-062920.
XX 28-FEB-1992; 92WO-US01636.
XX 21-MAY-1993; 93US-0065725.
XX 23-MAY-1994; 94WO-US05779.
XX 24-OCT-1994; 94US-0327690.
XX 07-JUN-1995; 95US-0475845.
XX 07-JUN-1996; 96US-0660289.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX (NOVO ) NOVO NORDISK AS.
XX
XX Hart CE, Petersen LC, Hedner U, Rasmussen ME;
XX WPI; 2001-201993/20.
XX N-PSDB; AAF57099.
XX
XX Use of modified human factor VIIa with a covalent modification in its
XX catalytic center, to inhibit thrombus formation or to maintain vascular
XX patency -
XX
XX Example; Columns 43-48; 34pp; English.
XX
XX The invention relates to the use of modified human Factor VIIa for
XX inhibiting thrombus formation, or maintaining or improving vascular
XX patency in a patient. The modified factor VIIa comprises a covalent
XX modification in its catalytic center which effectively interrupts the
XX blood coagulation cascade. The modifications render Factor VIIa
XX substantially unable to activate plasma factor IX or X. The modified
XX Factor VIIa can be used for preventing or treating myocardial injury
XX associated with post-ischemic reperfusion, for improving regional
XX myocardial blood flow during reperfusion and maintaining or improving
XX vascular patency in a patient. The present sequence represents the
XX human Factor VII polypeptide.
XX
XX Sequence 444 AA:
XX
XX Query Match 67.5%; Score 131; DB 22; Length 444;
XX Best Local Similarity 54.5%; Pred. No. 2.6e-14;
XX Matches 24; Conservative 5; Mismatches 15; Indels 0; Gaps 0;
XX
XX 1 ANGFLXLRPGSLKRXCRXXLCSPFXAHXIFRNXXRTQEFVSY 44
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX Db 39 anafllelrpgslereckeegcsfeaearejfkdaertklfwisy 82
XX
XX RESULT 27
XX AAP60056
XX ID AAP60056 standard; protein; 466 AA.

```

```

XX AAP60056;
XX
XX 23-MAY-1991 (first entry)
XX
XX Factor VII peptide encoded by cDNA clone lambda VII2463.
XX
XX Factor VII; Factor VIIa; DNA construct;
XX
XX EP200421-A.
XX
XX 10-DEC-1986.
XX
XX 16-APR-1986; 86EP-0302855.
XX
XX 16-DEC-1985; 85US-0810002.
XX 17-APR-1985; 85US-0724311.
XX
XX (ZYMO-) ZYMOGENETICS INC.
XX
XX Hagen FS, Murry MJ, Berkner KL, Insley MY, Woodbury RG;
XX PI Gray CL;
XX
XX WPI; 1986-326899/50.
XX N-PSDB; AAN60064.
XX
XX DNA construct used to transfect hosts - to produce protein which
XX activates to give factor VIIa
XX
XX Disclosure; Fig. 1b; 55pp; English.
XX
XX The partial factor VII cDNA sequence encoding the peptide is from
XX cDNA clone lambda VII2463. It is used in a DNA construct which contains
XX a nucleotide sequence encoding a protein which, on activation, has the
XX same biological activity for blood coagulation as Factor VIIa. The
XX nucleotide codes at least partially for Factor VII and comprises a
XX sequence encoding a calcium binding domain joined to a second sequence
XX downstream of this encoding a catalytic domain for the serine protease
XX activity of Factor VIIa. The calcium binding domain comprises a gene
XX encoding Factor VII, IX, X, protein C, prothrombin or protein S. The
XX construct is used to transfect host cells to produce the protein which,
XX on activation, yields Factor VIIa.
XX
XX Sequence 466 AA:
XX
XX Query Match 67.5%; Score 131; DB 7; Length 466;
XX Best Local Similarity 54.5%; Pred. No. 2.8e-14;
XX Matches 24; Conservative 5; Mismatches 15; Indels 0; Gaps 0;
XX
XX 1 ANGFLXLRPGSLKRXCRXXLCSPFXAHXIFRNXXRTQEFVSY 44
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX Db 61 anafllelrpgslereckeegcsfeaearejfkdaertklfwisy 104
XX
XX RESULT 28
XX AAR52562
XX ID AAR52562 standard; protein; 466 AA.
XX
XX AAR52562;
XX
XX 27-MAY-1994 (first entry)
XX
XX Factor VIII.
XX
XX Truncated tissue factor; tTF; factor VIIa; FVIIa; activator;
XX bleeding disorder; haemophilia; liver cirrhosis; coagulation;
XX transmembrane domain; extracellular domain; soluble.
XX
XX Homo sapiens.
XX
XX WO9323074-A.
XX

```

KW Factor VII; modified; Ser344Ala mutant; vascular patency;
 KW prevention; myocardial injury; blood flow; angioplasty; trauma;
 KW initial hyperplasia; restenosis; deep vein thrombosis; treatment;
 KW pulmonary embolism; stroke; disseminated intravascular coagulation;
 KW fibrin deposition; endotoxaemia; myocardial infarction;
 KW anticoagulant.
 XX
 OS Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 344 /note="Ser344Ala mutated"
 XX
 XX WO9747651-A1.
 XX
 PD 18-DEC-1997.
 XX
 PF 06-JUN-1997; 97WO-DK00251.
 XX
 PR 07-JUN-1996; 96US-0660289.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 XX (ZYMO) ZYMOGENETICS.
 PI Hart CE, Hedner U, Petersen LC, Rasmussen ME;
 XX
 DR MPI: 1998-052245/05.
 XX N-PSDB; AA02230.
 DR
 PT Inhibiting thrombus formation by topical administration of modified
 PT factor VII - also used to maintain vascular patency, prevent
 PT myocardial injury and improve regional myocardial blood flow
 XX
 PS Example 1; Pages 74-76; 97pp: English.
 XX
 CC The sequence is that of a Ser344Ala modified factor VII which
 CC can be used as part of a method for inhibiting thrombus formation.
 CC The method is used to maintain or improve vascular patency,
 CC to prevent or minimise myocardial injury associated with
 CC post-ischaemic reperfusion and to improve regional myocardial blood
 CC flow during post-ischaemic reperfusion. The method is particularly
 CC used where the site of thrombus or reduced patency is associated with
 CC (micro)surgery, angioplasty or trauma or where the myocardial injury
 CC is myocardial necrosis. Particular applications are in treatment or
 CC prevention of intimal hyperplasia or restenosis caused by acute (e.g.
 CC mechanical) injury; deep vein thrombosis; pulmonary embolism; stroke;
 CC disseminated intravascular coagulation; fibrin deposition associated
 CC with endotoxaemia and myocardial infarction. When used in conjunction
 CC with tissue plasminogen activator or streptokinase, it can also be
 CC used to treat acute closure of a coronary artery. It effectively
 CC interrupts the coagulation cascade; is active at relatively low doses
 CC and lacks the side effects of known anticoagulants (particularly it
 CC is more selective than heparin, does not destroy other coagulation
 CC proteins and is less likely to cause bleeding complications). It
 CC acts specifically at the site of injury and binds to tissue factor,
 CC preventing coagulation induced by this. It may also have a
 CC longer plasma half-life than other anticoagulants.
 XX
 SQ Sequence 444 AA;

Query Match 67.5%; Score 131; DB 19; Length 444;
 Best Local Similarity 54.5%; Pred. No. 2,6e-14;
 Matches 24; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 1 ANGFLXXLRPGSLRXCRXXLCSEFXAHXIFRXXXTROFWASY 44
 Db 39 anafllelrpgslrxcrrxlcsefxahxifrrxxxtrofwasy 82

RESULT 25
 AAY67967
 ID AAY67967 standard; Protein; 444 AA.

XX
 AC AAY67967;
 XX
 DT 05-APR-2000 (first entry)
 XX
 XX Factor VII SEQ ID NO:2.
 DE
 XX
 KW Factor VII; catalytic active site; blood coagulation; plasma;
 KW Factor X; Factor IX; vasotropic; antithrombotic; anticoagulant;
 KW myocardial injury; post-ischaemic reperfusion; platelet deposition;
 KW thrombus formation; vascular patency.
 XX
 OS Unidentified.
 XX
 PN US5997864-A.
 XX
 PD 07-DEC-1999.
 XX
 PF 06-JUN-1997; 97US-0871003.
 XX
 PR 28-FEB-1993; 91US-0662920.
 PR 21-MAY-1993; 93US-0065725.
 PR 23-MAY-1994; 94WO-0505779.
 PR 24-OCT-1994; 94US-0327690.
 PR 07-JUN-1995; 95US-0475845.
 PR 07-JUN-1996; 96US-0660289.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Hart CE, Petersen LC, Hedner U, Rasmussen ME;
 XX
 DR MPI: 2000-104599/09.
 XX N-PSDB; AA57385.
 DR
 PT Inhibition or minimization of myocardial injury associated with
 PT post-ischaemic reperfusion -
 XX
 PS Disclosure: Column 47-50; 34pp; English.
 XX
 CC The present invention describes a method for the inhibition or
 CC minimisation of myocardial injury associated with post-ischaemic
 CC reperfusion by administering factor VII, which has at least 1
 CC modification in its catalytic triad (therefore inhibiting the ability
 CC of factor VII to activate plasma factor X or IX). The method can be
 CC used for inhibiting or minimising myocardial injury and for imparting
 CC regional myocardial blood flow associated with post-ischaemic
 CC reperfusion. It can also be used for inhibiting blood coagulation,
 CC platelet deposition, thrombus formation and maintaining or improving
 CC vascular patency. Factor VII can be administered at relatively low
 CC doses and does not produce undesirable side effects. Further it acts
 CC specifically at sites of injury. The present sequence represents
 CC Factor VII.
 XX
 SQ Sequence 444 AA;

Query Match 67.5%; Score 131; DB 21; Length 444;
 Best Local Similarity 54.5%; Pred. No. 2,6e-14;
 Matches 24; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 1 ANGFLXXLRPGSLRXCRXXLCSEFXAHXIFRXXXTROFWASY 44
 Db 39 anafllelrpgslrxcrrxlcsefxahxifrrxxxtrofwasy 82

RESULT 26
 AAB61992
 ID AAB61992 standard; Protein; 444 AA.
 AC AAB61992;
 XX
 DT 14-MAY-2001 (first entry)

Db	1	anaflxalrpgslxrxcxxxqcsfxkxarxlfdkdxrtklfwisy	44
RESULT	18		
ID	AAM52187		
XX	AAM52187	standard; Protein; 406 AA.	
AC	AAM52187;		
XX			
DT	07-FEB-2002	(first entry)	
XX			
DE	Human FVII mutant K143N/N145T/R315N/V317T.		
XX			
KW	Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;		
KW	cardiant; hepatocytic; cerebroprotective; haemophilia; liver disease;		
KW	myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;		
XX	muten.		
XX			
OS	Homo sapiens.		
OS	Synthetic.		
XX			
XX	Key	Location/Qualifiers	
FT	Misc-difference	6	
FT		/label= GLU, OTHER	
FT		/note= "OTHER = gamma carboxyglutamic acid"	
FT	Misc-difference	7	
FT		/label= GLU, OTHER	
FT		/note= "OTHER = gamma carboxyglutamic acid"	
FT	Misc-difference	14	
FT		/label= GLU, OTHER	
FT		/note= "OTHER = gamma carboxyglutamic acid"	
FT	Misc-difference	16	
FT		/label= GLU, OTHER	
FT		/note= "OTHER = gamma carboxyglutamic acid"	
FT	Misc-difference	19	
FT		/label= GLU, OTHER	
FT		/note= "OTHER = gamma carboxyglutamic acid"	
FT	Misc-difference	20	
FT		/label= GLU, OTHER	
FT		/note= "OTHER = gamma carboxyglutamic acid"	
FT	Misc-difference	25	
FT		/label= GLU, OTHER	
FT		/note= "OTHER = gamma carboxyglutamic acid"	
FT	Misc-difference	26	
FT		/label= GLU, OTHER	
FT		/note= "OTHER = gamma carboxyglutamic acid"	
FT	Misc-difference	29	
FT		/label= GLU, OTHER	
FT		/note= "OTHER = gamma carboxyglutamic acid"	
FT	Misc-difference	35	
FT		/label= GLU, OTHER	
FT		/note= "OTHER = gamma carboxyglutamic acid"	
FT	Modified-site	52	
FT		/note= "O-glycosylated"	
FT	Modified-site	60	
FT		/note= "O-glycosylated"	
FT	Misc-difference	143	
FT		/note= "Wild-type Lys substituted by Asn"	
FT	Misc-difference	145	
FT		/note= "Wild-type Asn substituted by Thr"	
FT	Cleavage-site	152..153	
FT		/note= "proteolytic cleavage site converting FVII zymogen to an activated form, comprising two chains linked by a single disulphide bridge"	
FT	Misc-difference	315	
FT		/note= "Wild-type Arg substituted by Asn"	
FT	Misc-difference	317	
FT		/note= "Wild-type Val substituted by Thr"	
FT	Modified-site	322	
FT		/note= "N-glycosylated"	
XX			
XX	WO200158935-A2.		

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PD      16-AUG-2001.
XX
PF      12-FEB-2001; 2001WO-DK00094.
XX
PR      11-FEB-2000; 2000DK-0000218.
XX
PR      18-OCT-2000; 2000DK-0001558.
XX
PA      (MAXY-) MAXGEN APS.
XX
PI      Andersen KV, Pedersen AH, Bornaes C;
XX
XX      WPI: 2001-581807/65.
XX
PT      New conjugate, useful for treating Factor VIIa related diseases or
XX      disorders such as haemophilia, liver disease, myocardial infarction and
XX      deep-vein thrombosis, comprises non-polypeptide group covalently
XX      attached to polypeptide group -
XX
XX      Example 3; Page -: 89pp; English.
XX
PS      The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
CC      polypeptide conjugates, comprising at least one non-polypeptide group
CC      covalently attached to a polypeptide, where the amino acid sequence of
CC      polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
CC      least one amino acid residue containing an attachment group for the
CC      non-polypeptide group has been introduced or removed. The FVIIa
CC      conjugates have haemostatic, thrombolytic, cardiac, hepatotrophic and
CC      cerebroprotective activity and are useful for treating FVIIa/VF-related
CC      diseases or disorders such as haemophilia, liver disease, myocardial
CC      infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
CC      have increased functional in vivo half life and/or increased plasma half
CC      life, increased bioavailability and/or reduced sensitivity to proteolytic
CC      degradation. Consequently medical treatment using the conjugates has a
CC      number of advantages over currently available such as longer duration
CC      between injections. The present sequence is that of a human FVII mutant,
CC      having an addition in vivo glycosylation site and tested for its
CC      amidolytic activity.
CC      Note: The present sequence is not shown in the specification but is
CC      derived from the human wild-type FVII sequence shown in SEQ ID NO 1
CC      (AAM52171).
XX
SQ      Sequence    406 AA;

Query Match          67.5%; Score 131; DB 22; Length 406;
Best Local Similarity 77.3%; Pred. No. 2.4e-14;
Matches   34; Conservative    5; Mismatches    5; Indels    0; Gaps    0;

QY      1 ANGFLXLLRPGSLRXRCRXLLCSFFXAHHIFPNMXRTROFWNSV 44
        |||||||
Db       1 anaflxllrpgslrxrcrkxxqgsfxaxrlfhdartkllfwlasy 44

RESULT 19
ID      AAB84866 standard; Protein: 406 AA.
XX
AC      AAB84866;
XX
DT      31-JUL-2001 (first entry)
XX
DE      Wild-type human blood coagulant factor VII (FVII).
XX
KW      Human; haemostatic; blood coagulant factor VII; FVII; haemophilia.
XX
OS      Homo sapiens.
XX
FH      Key Location/Qualifiers
FT      Disulfide-bond 159..164
XX
XX      JP2001061479-A.

```

CC non-polypeptide group has been introduced or removed. The FVIIa
CC conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and
CC cerebroprotective activity and are useful for treating FVIIa/TF-related
CC diseases or disorders such as haemophilia, liver disease, myocardial
CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
CC have increased bioavailability in vivo half life and/or increased plasma half
CC life, increased bioavailability and or reduced sensitivity to proteolytic
CC degradation. Consequently medical treatment using the conjugates has a
CC number of advantages over currently available such as longer duration
CC between injections. The present sequence is that of a human FVII mutant,
CC having an addition in vivo glycosylation site and tested for its
CC amidolytic activity.
CC Note: The present sequence is not shown in the specification but is
CC derived from the human wild-type FVII sequence shown in SEQ ID NO 1
CC (AAM52171).
XX
SQ Sequence 406 AA;

Query Match 67.5%; Score 131; DB 22; Length 406;
Best Local Similarity 77.3%; Pred. No. 2.4e-14;
Matches 34; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 1 ANGFLXXLRPGSLRXRCRXHLCSPFXAHXIFRNXXRTROFWWSY 44
II |||||
Db 1 anaflxxlrpgslrxrcrxhlcspfxahxifrnxxrtrofwwsy 44

RESULT 17
AAM52186
ID AAM52186 standard; Protein; 406 AA.
XX
AC AAM52186;
XX
DT 07-FEB-2002 (first entry)
XX
XX
DE Human FVII mutant R315N/V317T.
XX
XX
KW Factor VII: FVII: Factor VIIa: FVIIa: haemostatic; thrombolytic;
KW cardiant; hepatotrophic; cerebroprotective; haemophilia; liver disease;
KW myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;
KW mutlein.
XX
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT 6
FT MISC-difference 6 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT 7
FT MISC-difference 7 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT 14
FT MISC-difference 14 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT 16
FT MISC-difference 16 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT 19
FT MISC-difference 19 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT 20
FT MISC-difference 20 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT 25
FT MISC-difference 25 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT 26
FT MISC-difference 26 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT 29
FT MISC-difference 29 /label= Glu, OTHER

FT /note= "OTHER = gamma carboxyglutamic acid"
FT 35
FT MISC-difference 35 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT 52
FT Modified-site 52 /note= "O-glycosylated"
FT 60
FT Modified-site 60 /note= "O-glycosylated"
FT 145
FT Modified-site 145 /note= "O-glycosylated"
FT 152..153
FT Cleavage-site 152..153 /note= "proteolytic cleavage site converting FVII zymogen
to an activated form, comprising two chains
linked by a single disulphide bridge"
FT
FT MISC-difference 315 /note= "Wild-type Arg substituted by Asn"
FT 317
FT MISC-difference 317 /note= "Wild-type Val substituted by Thr"
FT 322
FT Modified-site 322 /note= "N-glycosylated"
XX
PN WO200158935-A2.
XX
PD 16-AUG-2001.
XX
XX
PF 12-FEB-2001; 2001WO-DK00094.
XX
PR 11-FEB-2000; 2000DK-0000218.
XX 18-OCT-2000; 2000DK-0001558.
XX
XX (MAXY-) MAXYGEN APS.
XX
PI Andersen KV, Pedersen AH, Bornaes C;
XX WPI; 2001-581807/65.
XX
XX
XX New conjugate, useful for treating Factor VIIa related diseases or
PT disorders such as haemophilia, liver disease, myocardial infarction and
PT deep-vein thrombosis, comprises non-polypeptide group covalently
PT attached to polypeptide group -
XX
XX
XX Example 3; Page -: 89pp; English.
XX
XX The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
CC polypeptide conjugates, comprising at least one non-polypeptide group
CC covalently attached to a polypeptide, where the amino acid sequence of
CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
CC least one amino acid residue containing an attachment group for the
CC non-polypeptide group has been introduced or removed. The FVIIa
CC conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and
CC cerebroprotective activity and are useful for treating FVIIa/TF-related
CC diseases or disorders such as haemophilia, liver disease, myocardial
CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
CC have increased bioavailability in vivo half life and/or increased plasma half
CC life, increased bioavailability and or reduced sensitivity to proteolytic
CC degradation. Consequently medical treatment using the conjugates has a
CC number of advantages over currently available such as longer duration
CC between injections. The present sequence is that of a human FVII mutant,
CC having an addition in vivo glycosylation site and tested for its
CC amidolytic activity.
CC Note: The present sequence is not shown in the specification but is
CC derived from the human wild-type FVII sequence shown in SEQ ID NO 1
CC (AAM52171).
XX
SQ Sequence 406 AA;

Query Match 67.5%; Score 131; DB 22; Length 406;
Best Local Similarity 77.3%; Pred. No. 2.4e-14;
Matches 34; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 1 ANGFLXXLRPGSLRXRCRXHLCSPFXAHXIFRNXXRTROFWWSY 44
II |||||

KW		myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;
KX		mucin.
XX		
OS	Homo sapiens .	
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	Misc-difference	6
FT	/label= Glu, OTHER	
FT	/note= "OTHER = gamma carboxyglutamic acid"	
FT	Misc-difference	7
FT	/label= Glu, OTHER	
FT	/note= "OTHER = gamma carboxyglutamic acid"	
FT	Misc-difference	14
FT	/label= Glu, OTHER	
FT	/note= "OTHER = gamma carboxyglutamic acid"	
FT	Misc-difference	16
FT	/label= Glu, OTHER	
FT	/note= "OTHER = gamma carboxyglutamic acid"	
FT	Misc-difference	19
FT	/label= Glu, OTHER	
FT	/note= "OTHER = gamma carboxyglutamic acid"	
FT	Misc-difference	20
FT	/label= Glu, OTHER	
FT	/note= "OTHER = gamma carboxyglutamic acid"	
FT	Misc-difference	25
FT	/label= Glu, OTHER	
FT	/note= "OTHER = gamma carboxyglutamic acid"	
FT	Misc-difference	26
FT	/label= Glu, OTHER	
FT	/note= "OTHER = gamma carboxyglutamic acid"	
FT	Misc-difference	29
FT	/label= Glu, OTHER	
FT	/note= "OTHER = gamma carboxyglutamic acid"	
FT	Misc-difference	35
FT	/label= Glu, OTHER	
FT	/note= "OTHER = gamma carboxyglutamic acid"	
FT	Misc-difference	52
FT	/note= "O-glycosylated"	
FT	Modified-site	60
FT	/note= "O-glycosylated"	
FT	Misc-difference	143
FT	/note= "Wild-type Lys substituted by Asn"	
FT	Misc-difference	145
FT	/note= "Wild-type Asn substituted by Thr"	
FT	Cleavage-site	152..153
FT	/note= "proteolytic cleavage site converting FVII zymogen to an activated form, comprising two chains linked by a single disulphide bridge"	
FT	Modified-site	322
FT	/note= "N-glycosylated"	
XX		
PN	WO200158935-A2.	
XX		
PD	16-AUG-2001.	
XX		
PE	12-FEB-2001; 2001WO-DK00094.	
XX		
PR	11-FEB-2000; 2000DK-0000218. 18-OCT-2000; 2000DK-0001558.	
XX		
PA	(MAXY-) MAXGEN APS.	
XX		
PI	Andersen KV, Pedersen AH, Bornaes C;	
DR	WPI: 2001-581807/65.	
XX		
PT	New conjugate, useful for treating Factor VIIa related diseases or disorders such as haemophilia, liver disease, myocardial infarction and deep-vein thrombosis, comprises non-polypeptide group covalently attached to polypeptide group -	
XX		
PS	Example 3; Page -: 89pp; English.	

[illegible]

FT	Misc-difference	/note= "OTHER = gamma carboxyglutamic acid"
FT		20
FT		/label= GLU, OTHER
FT	Misc-difference	/note= "OTHER = gamma carboxyglutamic acid"
FT		25
FT		/label= GLU, OTHER
FT	Misc-difference	/note= "OTHER = gamma carboxyglutamic acid"
FT		26
FT		/label= GLU, OTHER
FT	Misc-difference	/note= "OTHER = gamma carboxyglutamic acid"
FT		29
FT		/label= GLU, OTHER
FT	Misc-difference	/note= "OTHER = gamma carboxyglutamic acid"
FT		35
FT		/label= GLU, OTHER
FT	Modified-site	/note= "OTHER = gamma carboxyglutamic acid"
FT		52
FT		/note= "O-glycosylated"
FT	Modified-site	/note= "O-glycosylated"
FT		60
FT		/note= "N-glycosylated"
FT	Modified-site	/note= "N-glycosylated"
FT		145
FT		/note= "N-glycosylated"
FT	Cleavage-site	152..153
FT		/note= "proteolytic cleavage site converting FVII zymogen to an activated form, comprising two chains linked by a single disulphide bridge"
FT	Modified-site	322
FT		/note= "N-glycosylated"
PN		WO200158935-A2.
PD		16-AUG-2001.
PE		12-FEB-2001; 2001WO-DK00094.
PR		11-FEB-2000; 2000DK-0000218.
PR		18-OCT-2000; 2000DK-0001558.
PA	(MAXY-) MAXGEN APS.	
PI	Andersen KV, Pedersen AH, Bornaaes C;	
DR	WPI: 2001-581807/65.	
XX	N-PSDB: AA199982.	
PT	New conjugate, useful for treating Factor VIIa related diseases or disorders such as haemophilia, liver disease, myocardial infarction and deep-vein thrombosis, comprises non-polypeptide group covalently attached to polypeptide group -	
PS	Claim 1; Page 81-83; 89pp: English.	
XX	The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa) polypeptide conjugates, comprising at least one non-polypeptide group covalently attached to a polypeptide, where the amino acid sequence of polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at least one amino acid residue containing an attachment group for the non-polypeptide group has been introduced or removed. The FVIIa conjugates have haemostatic, thrombolytic, cardiant, hepatotropic and cerebroprotective activity and are useful for treating FVIIa/VF-related diseases or disorders such as haemophilia, liver disease, myocardial infarction, thrombotic stroke and deep-vein thrombosis. The conjugates have increased functional in vivo half life and/or increased plasma half life, increased bioavailability and/or reduced sensitivity to proteolytic degradation. Consequently medical treatment using the conjugates has a number of advantages over currently available such as longer duration between injections.	
SQ	Sequence 406 AA:	

Query Match 67.5%; Score 131; DB 22; Length 406;
 Best Local Similarity 77.3%; Pred No. 2,4e-14;

	Matches	34;	Conservative	5;	Mismatches	5;	Indels	0;	Gaps	0;
Qy	1	ANGFLXLRPGSLXRXCRXXLCSPXXAHXIFPNXXRTROFWNSV	44							
	11									
Db	1	anaflxlrpgslxrckxxgcxfxxarxrlfidxartrkflfwlsy	44							
RESULT 11										
AAM52172										
ID	AAM52172	standard; Protein; 406 AA.								
XX	AAM52172;									
AC										
XX										
DT	07-FEB-2002	(first entry)								
XX										
DE		Mammalian expressed human FVII SEQ ID NO 3.								
XX										
KM	Factor VII; FVII; Factor VIIa; FVIIa; hemostatic; thrombolytic;									
KW	cardiant; hepatotrophic; cerebroprotective; haemophilia; liver disease;									
XX	myocardial infarction; thrombotic stroke; deep-vein thrombosis.									
OS	Homo sapiens.									
XX										
PH	Key	Location/Qualifiers								
FT	Modified-site	52								
FT		/note= "O-glycosylated"								
FT	Modified-site	60								
FT		/note= "O-glycosylated"								
FT	Modified-site	145								
FT		/note= "N-glycosylated"								
FT	Cleavage-site	152..153								
FT		/note= "proteolytic cleavage site converting FVII zymogen								
FT		to an activated form, comprising two chains								
FT		linked by a single disulphide bridge"								
FT	Modified-site	322								
FT		/note= "N-glycosylated"								
XX										
PN	WO200158935-A2.									
XX										
PD	16-AUG-2001.									
XX										
PF	12-FEB-2001; 2001WO-DK00094.									
XX										
PR	11-FEB-2000; 2000DK-0000218.									
PR	18-OCT-2000; 2000DK-0001558.									
XX										
PA	(MAXY-) MAXYGEN APS.									
XX										
PI	Andersen KV, Pedersen AH, Bornaes C;									
XX										
DR	WPI: 2001-581807/65.									
XX										
PT	N-PSDB; AAI99983.									
XX										
PT	New conjugate, useful for treating Factor VIIa related diseases or									
PT	disorders such as haemophilia, liver disease, myocardial infarction and									
PT	deep-vein thrombosis, comprises non-polypeptide group covalently									
PT	attached to polypeptide group -									
XX										
PS	Disclosure: Page 85-86; 89pp; English.									
XX										
CC	The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)									
CC	polypeptide conjugates, comprising at least one non-polypeptide group									
CC	covalently attached to a polypeptide, where the amino acid sequence of									
CC	polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at									
CC	least one amino acid residue containing an attachment group for the									
CC	non-polypeptide group has been introduced or removed. The FVIIa									
CC	conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and									
CC	cerebroprotective activity and are useful for treating FVIIa/TF-related									
CC	diseases or disorders such as haemophilia, liver disease, myocardial									
CC	infarction, thrombotic stroke and deep-vein thrombosis. The conjugates									
CC	have increased functional in vivo half life and/or increased plasma half									
CC	life, increased bioavailability and/or reduced sensitivity to proteolytic									
CC	degradation. Consequently medical treatment using the conjugates has a									

```

FT Modified-site 16 /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 19 /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 20 /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Disulfide-bond 25 /label= OTHER
FT Modified-site 26 /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 26 /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 29 /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Cleavage-site 32..33 /note= "proteolytic site"
FT Modified-site 35 /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Cleavage-site 38..39 /note= "proteolytic site"
FT Cleavage-site 42..43 /note= "proteolytic site"
FT Cleavage-site 44..45 /note= "proteolytic site"
FT Disulfide-bond 50..61 /note= "proteolytic site"
FT Disulfide-bond 55..70 /label= OTHER
FT /note= "beta-hydroxy-aspartic acid"
FT Disulfide-bond 72..81 /label= OTHER
FT Disulfide-bond 91..102 /label= OTHER
FT Disulfide-bond 98..112 /label= OTHER
FT Disulfide-bond 114..127 /label= OTHER
FT Disulfide-bond 135..162 /label= OTHER
FT Cleavage-site 143..144 /note= "proteolytic site"
FT Modified-site 145 /note= "glycosylation site"
FT Disulfide-bond 159..164 /note= "glycosylation site"
FT Disulfide-bond 178..194 /label= OTHER
FT Active-site 193 /label= OTHER
FT Active-site 242 /label= OTHER
FT Active-site 290..291 /note= "proteolytic site"
FT Cleavage-site 310..329 /note= "proteolytic site"
FT Disulfide-bond 315..316 /note= "proteolytic site in unmodified factor VII"
FT Cleavage-site 315 /note= "proteolytic site in unmodified factor VII"
FT Misc-difference /note= "native Arg315 has been substituted by Ser to
FT provide a proteolytically more stable peptide
FT bond"
FT Modified-site 322 /note= "glycosylation site"
FT Disulfide-bond 340..368 /note= "proteolytic site"
FT Cleavage-site 341..342 /note= "proteolytic site"
FT Cleavage-site 392..393 /note= "proteolytic site"
FT Cleavage-site 396..397 /note= "proteolytic site"
FT Cleavage-site 402..403 /note= "proteolytic site"
FT Cleavage-site 402..403 /note= "proteolytic site"
XX US5580560-A.
XX 03-DEC-1996.
PD

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XX 13-NOV-1989; 89US-0434149.
XX 09-AUG-1993; 93US-0104509.
XX 13-NOV-1989; 89US-0434149.
XX 12-JUN-1992; 92US-0898248.
XX 22-AUG-1994; 94US-0293778.
XX (NOVO ) NOVO-NORDISK AS.
XX Bjorn SE, Nicolaisen EM, Wiberg FC, Woodbury R;
XX WPI; 1997-033523/03.
XX Mutated human factor VII or VIIa proteins - with amino acid
XX substitutions to improve proteolytic stability
XX Example 4; Page -: 28pp; English.
XX Modified human factor VII or VIIa proteins are stabilised against
XX proteolytic cleavage by substitution of one of the residues Lys32,
XX Lys38, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and
XX Lys341 by an amino acid that provides a proteolytically more stable
XX peptide bond, provided that Lys32 is replaced by Gln, Glu, His,
XX Gly, Thr, Ala or Ser. The modified proteins are useful for treating
XX bleeding disorders such as thrombocytopenia and von Willebrand's
XX disease. They are also suitable for addition to plasma substitutes.
XX The present sequence is a specific example of a modified factor VII
XX protein.
XX Sequence 406 AA:
SQ

```

Query Match 67.5%; Score 131; DB 18; Length 406;
 Best Local Similarity 54.5%; Pred. No. 2.4e-14;
 Matches 24; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

```

QY 1 ANGELXXLRPGSLRXRCRXKXLCSEFXAHXFRFXXXTXRGQFWXSY 44
Db 1 anafllellrpsireckeegcsfeaearelfxkaertklitwisy 44

```

```

RESULT 10
AAM52171
ID AAM52171 standard; Protein; 406 AA.
XX AC
XX AAM52171;
XX 07-FEB-2002 (first entry)
XX DE Human FVII SEQ ID NO 1.
XX Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
XX cardiant; hepatotropic; cerebroprotective; haemophilia; liver disease;
XX myocardial infarction; thrombotic stroke; deep-vein thrombosis.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Misc-difference 6 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 7 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 14 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 16 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 19 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 19 /label= Glu, OTHER

```


OS	Homo sapiens.
OS	Synthetic.
XX	
FH	Key
FT	Misc-difference 235..239
FT	/note= "Wild-type Val-Pro-Gly-Thr-Thr substituted by Asp-Arg-Lys-Thr-Leu"
FT	Misc-difference 311..317
FT	/note= "Wild-type Leu-Gln-Ser-Arg-Lys-Val-Gly-Asp -Ser-Pro-Asn substituted by Gln-Ala-Ser-Tyr-Pro-Gly-Lys"
XX	
PN	JP2001061479-A.
XX	
PD	13-MAR-2001.
XX	
PE	24-AUG-1999; 99JP-0237610.
PR	24-AUG-1999; 99JP-0237610.
XX	
PA	(KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
DR	WPI; 2001-310677/33.
DR	N-PSDB; AAH19464.
XX	
PT	Mutant of blood coagulant factor VII, used for substitution therapy in the treatment of hemophilia .
XX	
PS	Claim 16; Page 23-24; 29pp; Japanese.
XX	
CC	The present invention relates to mutants of blood coagulant factor VII (FVII) or activated blood coagulant factor VII (FVIIa). The present sequence is one such mutant FVII: VII-39. The mutants can be used as an agent for the substitution therapy of haemophilia inhibitor patients.
CC	
XX	
SQ	Sequence 401 AA;
Oy	1 ANGFLXLRPGSLRXCRXILCSFXAXHXIFPNXXRTQFWWSY 44 : : : : Db 1 anaflaelrpqslereckeegcsfearellfkdaertklfwisy 44
RESULT 7	
ID AAR35764	
XX AAR35764 standard; protein: 406 AA.	
AC	
XX AAR35764;	
DT 24-SEP-1993 (first entry)	
DE Factor VII (VII).	
XX	
KW PC; protein C; IX; Factor IX; X; Factor X; PT; prothrombin; VII; Factor VII; CT; chymotrypsinogen; SP; serine protease; binding; exosite; catalytic activity.	
XX Homo sapiens.	
XX	
FH Key	Location/Qualifiers
FT Region	1..152
FT	/note= "Factor VII light chain"
FT Region	153..406
FT	/note= "Factor VII heavy chain"
FT Peptide	374..388
FT	/note= "exosite 1"
FT Peptide	290..310
FT	/note= "exosite 2"
FT	290..310
FT	/note= "pref. PC polypeptide; claim 2, page 136"

FT	Peptide	374..388
FT	/note= "pref. PC polypeptide; claim 2, page 136"	
FT	Pep tide	289...304
FT	/note= "pref. PC polypeptide; claim 4, page 137"	
FT	Pep tide	290...304
FT	/note= "pref. PC polypeptide; claim 4, page 137"	
FT	Peptide	245..266
FT	/note= "claim 9, page 138-139 describes an antibody that reacts with Factor VII; fragments 289-304, 290-304, 290-310, 374-388 and 400-414 but not with fragment 245-266"	
XX		
PN	WO9309804,A.	
XX		
PD	27-MAY-1993.	
XX		
PE	18-NOV-1992;	92MO-US10242.
XX		
PR	18-NOV-1991;	91US-0793989.
XX		
PA	(SCRI) SCRIPPS RES INST.	
XX		
PI	Griffin JH, Masters RM;	
DR	WPI; 1993-182244/22.	
XX		
PT	Serine protease derived-polypeptide(s) and anti-peptide antibodies - for inhibiting coagulation and assaying for the presence of serine protease in fluid samples	
PT		
PS	Disclosure; Page 133-135; 149pp; English.	
XX		
CC	The PC polypeptides indicated in the Features Table inhibit coagulation (they prevent binding of serine protease to natural substrates), esp. when admin. to give an intravascular blood concn. of 0.1-100 (pref. 0.5-10) microM. NB: Sequences corresp. to SEQ ID NO's 6, 7, 8 and 9 are described in the specification but have not yet been added to the SEQUENCE LISTING.	
CC		
CC		
XX		
SQ	Sequence 406 AA:	
Query Match 67.5%; Score 131; DB 14; Length 406; Best Local Similarity 54.5%; Pred. No. 2,4e-14; Matches 24; Conservative 5; Mismatches 15; Indels 0; Gaps 0;		
OY	1 ANGFLXILRPGSLRXRCRRXXLCSPFXAHXIFRNXXRTROFWVS 44 : : : : : Db 1 anafllelrpgslereckeegcsfeearelfkdaertklkfvisy 44	
RESULT 8		
AAM14509		
ID AAM14509	standard; protein; 406 AA.	
AC AAM14509;		
XX		
DT	14-MAY-1997 (first entry)	
XX		
DE	Modified blood coagulation Factor VII (R290S).	
XX		
KW	Blood coagulation; factor 7; muteln; mutation; modification; thrombocytopenia; von Willebrand's disease; plasma substitute.	
XX		
OS	Homo sapiens.	
XX		
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	Modified-site	6
FT	//label= OTHER	
FT	/note= "gamma-carboxyglutamic acid"	
FT	Modified-site	7

QY 1 ANGELXLRPGSLXRXCXRLCSFXXAHXIFRNXXRTREQWVSY 44

XX

XX
PI Nelsestuen GL;
XX
DR WPI; 1999-288309/24.
XX
PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
XX acid domain, useful for treating clotting disorders
PS Disclosure; Page 15; 86pp; English.
XX
CC This sequence is the factor VII GLA (gamma-carboxyglutamic acid)
CC domain. The invention relates to a vitamin K-dependent polypeptide
CC comprising a modified GLA domain containing an amino acid substitution
CC which enhances membrane binding of the modified polypeptide as compared
CC to the native polypeptide. The polypeptide is used to treat a clotting
CC disorder by decreasing or increasing clot formation. Modification of the
CC GLA domain results in a protein which has enhanced membrane binding
CC affinity as compared to the native protein.
XX
SQ Sequence 44 AA;

Query Match 88.7%; Score 172; DB 20; Length 44;
Best Local Similarity 100.0%; Pred. No. 2.2e-22;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANGFLXXLRPGSLXRRCRXXLCSPXXAHXIFRRXXRPROFWXY 44
DB 1 angflxxlirpsslxrcrxxlcsfxahxifrrxxrtlrqfwxy 44
|||||

RESULT 2
AAB36396
ID AAB36396 standard; peptide; 44 AA.
AC AAB36396;
XX
XX 27-FEB-2001 (first entry)
DT
XX
DE Bovine factor VII gamma-carboxyglutamic acid domain SEQ ID NO:4.
XX
XX Vitamin K-dependent protein; factor VII; protein C; GLA domain;
XX gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
XX factor X; prothrombin; enhanced membrane binding affinity;
XX clot formation; thrombolytic; haemostatic; bleeding disorder;
XX thrombosis; clotting disorder; haemophilia A; haemophilia B;
XX liver disease.
XX
XX Bos taurus.
XX
XX WO200066753-A2.
XX
XX 09-NOV-2000.
PD
XX
XX 28-APR-2000; 2000WO-US11416.
XX
XX 29-APR-1999; 99US-0302239.
XX
XX (MIND) UNIV MINNESOTA.
XX
XX Nelsestuen GL;
XX
XX WPI; 2001-007226/01.
XX
XX
XX Novel vitamin K-dependent polypeptide useful for treating clotting
XX disorders such as thrombosis and hemophilia, comprises modified
XX gamma-carboxy glutamic acid domain that enhances membrane binding
XX affinity -
XX
XX Disclosure; Page 12; 81pp; English.
XX
XX The present invention describes a vitamin K-dependent polypeptide (1)
XX comprising a modified gamma-carboxy glutamic acid (GLA) domain having

CC at least one amino acid substitution, that enhances membrane binding
CC affinity and the activity of the polypeptide relative to a corresponding
CC native vitamin K-dependent polypeptide and inhibits clot formation.
CC (1) can have thrombolytic and haemostatic activities, and can be used
CC as an inhibitor of clot formation. (1) is useful for decreasing clot
CC formation in a mammal, a factor VII or factor IX containing a modified
CC GLA domain is useful for increasing clot formation and for treating a
CC bleeding disorder. Including thrombosis and clotting disorders such as
CC haemophilia A, haemophilia B and liver disease. The present sequence
CC represents a wild type bovine factor VII GLA domain sequence, given in
CC the exemplification of the present invention.
XX
SQ Sequence 44 AA;

Query Match 88.7%; Score 172; DB 22; Length 44;
Best Local Similarity 100.0%; Pred. No. 2.2e-22;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANGFLXXLRPGSLXRRCRXXLCSPXXAHXIFRRXXRPROFWXY 44
DB 1 angflxxlirpsslxrcrxxlcsfxahxifrrxxrtlrqfwxy 44
|||||

RESULT 3
AA18305
ID AA18305 standard; peptide; 44 AA.
AC AA18305;
XX
XX 17-AUG-1999 (first entry)
DT
XX
DE Human factor VII GLA domain.
XX
XX GLA domain; vitamin K-dependent protein; clotting disorder;
XX therapy.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX MISC-difference 1..44 /note="Xaa=gamma-carboxyglutamic acid, or glutamic
XX acid"
XX
XX WO9920767-A1.
XX
XX 29-APR-1999.
PD
XX
XX 20-OCT-1998; 98WO-US22152.
XX
XX 23-OCT-1997; 97US-0955636.
XX
XX (MIND) UNIV MINNESOTA.
XX
XX Nelsestuen GL;
XX
XX WPI; 1999-288309/24.
XX
XX
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
XX acid domain, useful for treating clotting disorders
XX
XX Disclosure; Page 15; 86pp; English.
XX
XX
XX This sequence is the factor VII GLA (gamma-carboxyglutamic acid)
XX domain. The invention relates to a vitamin K-dependent polypeptide
XX comprising a modified GLA domain containing an amino acid substitution
XX which enhances membrane binding of the modified polypeptide as compared
XX to the native polypeptide. The polypeptide is used to treat a clotting
XX disorder by decreasing or increasing clot formation. Modification of the
XX GLA domain results in a protein which has enhanced membrane binding
XX affinity as compared to the native protein.
XX
XX Sequence 44 AA;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 30, 2002, 15:30:21 ; Search time 102.92 seconds
(without alignments)
47.486 Million cell updates/sec

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Perfect score: 194
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

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16: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	172	88.7	44	20	AAV18306
2	172	88.7	44	20	AAB36396
3	131	67.5	44	20	AAV18305
4	131	67.5	44	22	AAB36395
5	131	67.5	401	22	AAB84870
6	131	67.5	401	22	AAB84871
7	131	67.5	406	14	AAV35764
8	131	67.5	406	18	AAW14509
9	131	67.5	406	18	AAW14510
10	131	67.5	406	22	AAW52171
11	131	67.5	406	22	AAW52172

12	131	67.5	406	22	AAW52181	Human FVII mutant
13	131	67.5	406	22	AAW52182	Human FVII mutant
14	131	67.5	406	22	AAW52183	Human FVII mutant
15	131	67.5	406	22	AAW52184	Human FVII mutant
16	131	67.5	406	22	AAW52185	Human FVII mutant
17	131	67.5	406	22	AAW52186	Human FVII mutant
18	131	67.5	406	22	AAW52187	Human FVII mutant
19	131	67.5	406	22	AAB84866	Wild-type human b1
20	131	67.5	406	22	AAB84867	Mutant blood coagu
21	131	67.5	406	22	AAB84868	Mutant blood coagu
22	131	67.5	406	22	AAB84869	Mutant blood coagu
23	131	67.5	444	16	AAW64205	Factor VII - modif
24	131	67.5	444	19	AAW31687	Homo sapiens Ser34
25	131	67.5	444	21	AAV67967	Factor VII SEQ ID
26	131	67.5	444	22	AAB61992	Human Factor VII p
27	131	67.5	466	7	AAV60056	Factor VII peptide
28	131	67.5	466	14	AAV52562	Factor VII. Homo
29	131	67.5	466	19	AAW69606	Human Factor VIIa.
30	130	67.0	44	20	AAV18312	Modified GLA domain
31	130	67.0	406	18	AAW14507	Modified blood coa
32	128	66.0	406	18	AAW14508	Modified blood coa
33	127	65.5	44	20	AAV18313	Modified GLA domain
34	127	65.5	406	18	AAW14511	Modified blood coa
35	123	63.4	44	20	AAV18310	Modified GLA domain
36	123	63.4	44	20	AAV18311	Modified GLA domain
37	121	62.4	44	20	AAV18302	Modified GLA domain
38	117	60.3	41	16	AAW11904	Factor VII Gla reg
39	114	58.8	345	22	AAU02959	Angiotensin convert
40	114	58.8	406	18	AAW14506	Modified blood coa
41	105	54.1	44	20	AAV18304	Bovine protein C g
42	105	54.1	44	22	AAB36403	Bovine protein C g
43	99	51.0	139	17	AAV95596	Factor X light cha
44	99	51.0	231	22	AAV93243	Human polypeptide,
45	96	49.5	44	20	AAV18308	Modified GLA domain
46	95	49.0	453	7	AAV60057	Factor IX/Factor V
47	94	48.5	250	12	AAV13675	Factor X-Lact hybr
48	94	48.5	436	13	AAV22513	Truncated Precurso
49	94	48.5	448	14	AAV35762	Factor X (X). Hom
50	94	48.5	448	14	AAV37402	Factor X. Homo sa

ALIGNMENTS

RESULT 1	
AAV18306	standard; peptide; 44 AA.
AC	AAV18306;
XX	
17-AUG-1999	(first entry)
DT	
XX	
DE	Bovine factor VII GLA domain.
XX	
XX	GLA domain; vitamin K-dependent protein; clotting disorder;
KW	therapy.
XX	
OS	Bos taurus.
XX	
Key	Location/Qualifiers
FT	Misc-difference 1..44
FT	/note= "Xaa" gamma-carboxyglutamic acid, or glutamic acid"
FN	
XX	
W09920767-A1.	
PD	29-APR-1999.
XX	
PF	20-OCT-1998; 98WO-US22152.
XX	
PR	23-OCT-1997; 97US-0955636.
XX	
PA	(MINU) UNIV MINNESOTA.

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AC Q9QVH6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE FACTOR X LIGHT CHAIN.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=92041742; PubMed=1718949;
RA Enjyoji K., Miyazaki K., Kato H.;
RT "Characterization of rat factors X and Xa: demonstration of factor Xa
RT in rat plasma.";
RL J. Biochem. 109:890-898(1991).
DR HSP: P00740; ICFH
DR InterPro: IPR002383; GLA_blood.
DR PRINTS: PR00001; GLABLOOD.
SQ SEQUENCE 25 AA; 2932 MW; 657A6E9B57BEE56B CRC64;

Query Match 27.6%; Score 53; DB 11; Length 25;
Best Local Similarity 45.8%; Pred. NO. 0.02;
Matches 11; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 ANAFLLXLRPGSLXRCCKXXCSEF 24
||:|::|:| | | | | | | | | |
Db 1 ANSFEEIKKGNLFRECVXEICSEF 24

Search completed: August 30, 2002, 15:44:05
Job time: 820 sec

OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxId=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
 clone: P0707D10.";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP002910; BAB40147.1; -.
 DR HSSP; P27703; 2ERK.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003527; MAP_kin.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR SMART; SM01351; MARK; UNKNOWN_1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW ATP-binding; Transferase.
 SQ SEQUENCE 568 AA; 64753 MW; 5A702ED740DC2098 CRC64;

Query Match 29.9%; Score 57.5; DB 10; Length 568;
 Best Local Similarity 32.6%; Pred. No. 0.081;
 Matches 15; Conservative 6; Mismatches 22; Indels 3; Gaps 2;

OY 1 ANAFLXLRPGSL-XRCKXXCSPFXARXIFKDXARTKLFWISY 44
 Db 233 ASVFHRLKPKNLANADCKVKICDGLARVSPFD-TPSAIFWTDY 277

RESULT 48
 ID 061592 PRELIMINARY; PRT; 673 AA.
 AC 061592;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE GAS6 PROTEIN.
 GN GAS6 OR GAS6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mantiolelli G., Brancolini C., Bordo D., Phillips L., Schneider C.;
 RT "Growth-arrest is associated with a negative control element in the
 RT blood coagulation pathway.";
 RL Mol. Cell. Biol. 13:0-0(1993).
 DR EMBL; X59846; CAA42507.1; -.
 DR HSSP; P00740; 1CFH.
 DR MGD; MGI:95660; Gas6.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001791; Laminin_G.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 4.
 DR Pfam; PF00594; gla; 1.
 DR Pfam; PF00054; laminin_G; 2.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 3.
 DR SMART; SM00001; EGF_Like; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00282; LamG; 2.

DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS01187; EGF_CA; 3.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
 SQ SEQUENCE 673 AA; 74512 MW; 6A49B3F004F92815 CRC64;

Query Match 28.6%; Score 55; DB 11; Length 673;
 Best Local Similarity 33.3%; Pred. No. 0.27;
 Matches 12; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

OY 9 RPSLXRXCKXXCSPFXARXIFKDXARTKLFWISY 44
 Db 54 KOCHLERECVEEYCSKEARREVFENDPEYFYPRY 89

RESULT 49
 ID 099K57 PRELIMINARY; PRT; 674 AA.
 AC 099K57;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE GROWTH ARREST SPECIFIC 6.
 GN GAS6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC005444; AAH05444.1; -.
 DR HSSP; P00740; 1CFH.
 DR MGD; MGI:95660; Gas6.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001791; Laminin_G.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 4.
 DR Pfam; PF00594; gla; 1.
 DR Pfam; PF00054; laminin_G; 2.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00181; EGF; 4.
 DR SMART; SM00179; EGF_CA; 4.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00282; LamG; 2.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS01187; EGF_CA; 3.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
 SQ SEQUENCE 674 AA; 74609 MW; 7C41F7693903F401 CRC64;

Query Match 28.6%; Score 55; DB 11; Length 674;
 Best Local Similarity 33.3%; Pred. No. 0.27;
 Matches 12; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

OY 9 RPSLXRXCKXXCSPFXARXIFKDXARTKLFWISY 44
 Db 54 KOCHLERECVEEYCSKEARREVFENDPEYFYPRY 89

RESULT 50
 ID 09QVH6 PRELIMINARY; PRT; 25 AA.
 OY 09QVH6

QY 1 ANAELXLRPGSL--XRXCKXXOCSEFXARXIFKDAKRTKLFWISY 44
DB 145 ANYVHRDLKPKNLIANANCKLKVCDFGLARVAFND-PTTTFWMDY 189

RESULT 45

Q9PTW7 PRELIMINARY; PRT; 608 AA.
AC Q9PTW7;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE PROTHROMBIN.
GN OSPT.
OS Struthio camelus (Ostrich).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Palaeognathae; Struthioniformes; Struthionidae;
OC Struthio.
OX NCBI_TaxID=8801;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER.
RX MEDLINE=20579470; PubMed=11137455;
RA Frost C., Naude R., Oelofsen W., Muramoto K., Naganuma T., Ogawa T.;
RT "Purification and characterization of ostrich prothrombin.";
RL Int. J. Biochem. Cell Biol. 32:1151-1159(2000).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
DR EMBL: AB028871; BAA89046.1; -.
DR HSSP: P00734; IUVS.
DR MEROPS: S01.217; -.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR001254; Trypsin.
DR InterPro: IPR000294; VltK_dep_GLA.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00051; kringle; 2.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PRO0722; CHYMOTRYPSIN.
DR PRINTS: PRO0001; GLABLOOD.
DR PRINTS: PRO0018; KRINGLE.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00130; KR; 2.
DR SMART: SM00020; TRYP_SPE; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00021; KRINGLE_1; 2.
DR PROSITE: PS00070; KRINGLE_2; 2.
DR PROSITE: PS0240; TRYPsin_DOM; 1.
DR PROSITE: PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
KW Hydrolase; Serine protease.
SO SEQUENCE 608 AA; 69392 MW; 11B974B9AE54EA2 CRC64;

Query Match 31.8%; Score 61; DB 13; Length 608;
Best Local Similarity 31.7%; Pred. No. 0.02;

Matches 13; Conservative 5; Mismatches 23; Indels 0; Gaps 0;

QY 4 FLXALRPGSLRCKKXXOCSEFXARXIFKDAKRTKLFWISY 44
DB 48 FLEEMIKGNLRECLIEICIEYEAFEALESTARTEEFWSKY 88

RESULT 46

Q91001 PRELIMINARY; PRT; 607 AA.
AC Q91001;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE THROMBIN.
OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER.
RX MEDLINE=92212913; PubMed=1557383;
RA Banfield D.K., Macgillivray R.T.;
RT "Partial characterization of vertebrate prothrombin cDNAs:
RT amplification and sequence analysis of the B chain of thrombin from
RT nine different species.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER.
RX MEDLINE=94223694; PubMed=7513365;
RA Banfield D.K., Irwin D.M., Walz D.A., Macgillivray R.T.;
RT "Evolution of prothrombin: isolation and characterization of the cDNAs
RT encoding chicken and hagfish prothrombin.";
RL J. Mol. Evol. 38:177-187(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER.
RA Banfield D.K.;
RL Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.
DR EMBL: M81391; AAA21619.1; -.
DR HSSP: P00734; IUVS.
DR MEROPS: S01.217; -.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR003966; Prothrombin.
DR InterPro: IPR001254; Trypsin.
DR InterPro: IPR000294; VltK_dep_GLA.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00051; kringle; 2.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PRO0722; CHYMOTRYPSIN.
DR PRINTS: PRO0001; GLABLOOD.
DR PRINTS: PRO0018; KRINGLE.
DR PRINTS: PRO1505; PROTHROMBIN.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00130; KR; 2.
DR SMART: SM00020; TRYP_SPE; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00021; KRINGLE_1; 2.
DR PROSITE: PS00070; KRINGLE_2; 2.
DR PROSITE: PS0240; TRYPsin_DOM; 1.
DR PROSITE: PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
KW Hydrolase; Serine protease.
SO SEQUENCE 607 AA; 69110 MW; 002F3606EA36270F CRC64;

Query Match 30.2%; Score 58; DB 13; Length 607;
Best Local Similarity 29.3%; Pred. No. 0.07;

Matches 12; Conservative 5; Mismatches 24; Indels 0; Gaps 0;

QY 4 FLXALRPGSLRCKKXXOCSEFXARXIFKDAKRTKLFWISY 44
DB 48 FLEEMIKGNLRECLIEICIEYEAFEALESTVVDPAFWAKY 88

RESULT 47

Q9ASC3 PRELIMINARY; PRT; 568 AA.
AC Q9ASC3;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE P0707D10.3 PROTEIN.
GN P0707D10.3.

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DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE PROTEIN S PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Wydro R., Cohen E., Dackowski W., Stenflo J., Lundvall A.,
RA Dahlback B.;
RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL: X12892; CA31383.1; -.
DR HSSP: P00740; 1CFH.
DR InterPro: IPR000152; ASX_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001791; Laminin_G.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00054; laminin_G_1.
DR PRINTS: PR0001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 3.
DR SMART: SM00282; Lamg; 2.
DR PROSITE: PS00010; ASX_HYDROXYL; 3.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 3.
DR PROSITE: PS01187; EGF_CA; 2.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat;
KW Signal.
FT SIGNAL.
FT CHAIN.
FT SIGNAL.
SQ SEQUENCE 650 AA; 72480 MW; C67345CE8645174 CRC64;

Query Match
Best Local Similarity 33.3%; Score 64; DB 4; Length 650;
Matches 14; Conservative 8; Mismatches 22; Indels 0; Gaps 0;

QY 1 ANAFLLXLRPGSLRXKCKXXQCSFXXARKIFKDXAKRTKLFMISY 44
DB 16 ANSLLEETKQGNLERCIELCKNEAREYFENDPETDYFYPRY 59

RESULT 43
ID 016519 PRELIMINARY; PRT; 650 AA.
AC 016519;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE PROTEIN S PRECURSOR (FRAGMENT).
GN PROS1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=86313649; Pubmed=2944113;
RA Lundvall A., Dackowski W., Cohen E., Shaffer M., Mahr A., Dahlback B.,
RA Stenflo J., Wydro R.;
RL "Isolation and sequence of the cDNA for human protein S, a regulator
of blood coagulation.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:6716-6720(1986).
DR EMBL: M14338; AAA60181.1; -.
DR HSSP: P00740; 1CFH.
DR InterPro: IPR000152; ASX_hydroxyl.
DR InterPro: IPR000561; EGF-like.
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DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001791; Laminin_G.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF; 4.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00054; laminin_G; 1.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 3.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00282; Lamg; 2.
DR PROSITE: PS00010; ASX_HYDROXYL; 3.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 3.
DR PROSITE: PS01187; EGF_CA; 2.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat;
KW Signal.
FT SIGNAL.
FT NON_TER.
FT SIGNAL.
FT CHAIN.
FT SIGNAL.
SQ SEQUENCE 650 AA; 72462 MW; 9A8C044C503BF474 CRC64;
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Query Match
Best Local Similarity 33.3%; Score 64; DB 4; Length 650;
Matches 14; Conservative 8; Mismatches 22; Indels 0; Gaps 0;

QY 1 ANAFLLXLRPGSLRXKCKXXQCSFXXARKIFKDXAKRTKLFMISY 44
DB 16 ANSLLEETKQGNLERCIELCKNEAREYFENDPETDYFYPRY 59
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RESULT 44
ID 09XF36 PRELIMINARY; PRT; 608 AA.
AC 09XF36;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOGUE.
GN TDY1.
OS Medicago sativa (Alfalfa).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.
OX NCBI_TaxID=3879;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=99446225; Pubmed=10517028;
RA Schoenbeck M.A., Samac D.A., Fedorova M., Gregerson R.G., Gantt J.S.,
RA Vance C.P.;
RL "The alfalfa (Medicago sativa) TDY1 gene encodes a mitogen-activated
protein kinase homolog.";
RL Mol. Plant Microbe Interact. 12:882-893(1999).
DR EMBL: AF129087; AAD28617.1; -.
DR HSSP: P27703; 1ERK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_Kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS01351; MAPK; UNKNOWN_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 608 AA; 68903 MW; E5FD33A74BD5A8E6 CRC64;
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Query Match
Best Local Similarity 33.1%; Score 63.5; DB 10; Length 608;
Matches 16; Conservative 4; Mismatches 23; Indels 3; Gaps 2;
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```
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_Taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shin P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
RA Kim C., Altafi H., Bel O., Chin C., Chlou J., Choi E., Conn L.,
RA Conway A., Gonzales A., Hansen N., Howling B., Koo T., Lam B., Lee J.,
RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharasy N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA Ecker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC T10022 from chromosome
RT I.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC069551; AAF78388.1; -
DR HSSP: P24941; 1HCL.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS01351; MARK; UNKNOWN_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR ATP-binding; Transferase.
KW SEQUENCE 588 AA; 66220 MW; AE680FDBAF77CC3B CRC64;

Query Match 34.1%; Score 65.5; DB 10; Length 588;
Best Local Similarity 39.5%; Pred. No. 0.0031;
Matches 17; Conservative 4; Mismatches 19; Indels 3; Gaps 2;

OY 1 ANAFLLXLRPGSL--XRCKXXCSPFXRXRIFKDXRRTKLFV 44
DB 224 ANYFHDLPKRNLANADCKLKICDGLARVAFND-TPPTITWTDY 265

RESULT 37
O9SJG9 PRELIMINARY; PRT; 594 AA.
AC O9SJG9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PUTATIVE MAP KINASE.
GN AT2G42880.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_Taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Bentle M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., Vanaken S.E., Unayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhagen G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX Lin X.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC006931; AAD21721.1; -
DR HSSP: P24941; 1B38.
DR InterPro: IPR000719; Euk_pkinase.
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DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS01351; MARK; UNKNOWN_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 594 AA; 67275 MW; AEC31D4F90EE871E CRC64;

Query Match 34.1%; Score 65.5; DB 10; Length 594;
Best Local Similarity 34.8%; Pred. No. 0.0031;
Matches 16; Conservative 5; Mismatches 22; Indels 3; Gaps 2;

OY 1 ANAFLLXLRPGSL--XRCKXXCSPFXRXRIFKDXRRTKLFV 44
DB 133 ANYFHDLPKRNLANADCKLKICDGLARVAFND-TPPTITWTDY 177

RESULT 38
O9LP67 PRELIMINARY; PRT; 603 AA.
AC O9LP67;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE TF320.17 PROTEIN (MAP KINASE ATMPK9, PUTATIVE).
GN TF320.17 OR F22G10.12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OX eucosids II; Brassicales; Brassicaceae; Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Araujo R., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Egu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultzer L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kutz D.B., Kwan A., Lam B.,
RA Landin-Hopfer S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Malet R., Marshall A.,
RA Millscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shin P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:816-820(2000).
DR EMBL: AC018748; AAF78438.1; -
DR EMBL: AC024260; AAG51978.1; -
DR HSSP: P24941; 1HCL.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_kin.
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SQ SEQUENCE 510 AA; 58440 MW; 496BF0F657F53C97 CRC64;
 Query Match 35.2%; Score 67.5; DB 10; Length 510;
 Best Local Similarity 37.0%; Pred. No. 0.0011;
 Matches 17; Conservative 5; Mismatches 21; Indels 3; Gaps 2;
 QY 1 ANAFLLXLRPGSL--XRXCKXXQCSFXXARXIFKDXARTKLEWISY 44
 DB 143 ANVHFRLDKPKNILANSCKLKICDFGLARVSFNDA-PSAIFWTDY 187
 RESULT 34
 Q9LV37 PRELIMINARY; PRT; 619 AA.
 AC Q9LV37;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MAP KINASE.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RA Kaneo T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
 RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=20363099; Pubmed=10907853;
 RA Nakamura Y.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
 RT Sequence features of the regions of 4,251,695 bp covered by ninety P1,
 RT TAC and BAC clones.";
 RL DNA Res. 7:217-221(2000).
 DR EMBL: AB020749; BAB02016.1; -
 DR HSSP: P24941; IHCL
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003527; MAP_kin.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PS01351; MAPK; UNKNOWN_1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW ATP-binding; Kinase; Transferase.
 SQ SEQUENCE 619 AA; 70770 MW; 9AB2B461058ED2DB CRC64;
 Query Match 35.2%; Score 67.5; DB 10; Length 619;
 Best Local Similarity 37.0%; Pred. No. 0.0014;
 Matches 17; Conservative 5; Mismatches 21; Indels 3; Gaps 2;
 QY 1 ANAFLLXLRPGSL--XRXCKXXQCSFXXARXIFKDXARTKLEWISY 44
 DB 252 ANVHFRLDKPKNILANSCKLKICDFGLARVSFNDA-PSAIFWTDY 296
 RESULT 35
 Q9CWM3 PRELIMINARY; PRT; 399 AA.
 AC Q9CWM3;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE 1300015B06RIK PROTEIN.
 GN 1300015B06RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=STOMACH, AND LIVER;
 RX MEDLINE=21085660; Pubmed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King C., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Mang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyshak-Boris A., Yoshida K., Hasegawa T., Kawai H., Kontsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE
 TRYPSIN FAMILY
 CC EMBL: AK008819; BAB25912.1; -
 DR EMBL: AK005011; BAB23744.1; -
 DR HSSP: P00740; ICFH.
 DR MGD: MGI:1914151; 1300015B06RIK.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000742; EGF_2.
 DR InterPro: IPR001881; EGF_CA.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Trypsin.
 DR InterPro: IPR000294; Vitk_dep_GLA.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00181; EGF; 2.
 DR SMART: SM00179; EGF_CA; 2.
 DR SMART: SM00069; GLA; 1.
 DR SMART: SM00020; TYP-Spec; 1.
 DR PROSITE: PS00107; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 KW Hydrolyase; Serine protease.
 SQ SEQUENCE 399 AA; 44304 MW; 4FC85C9598F27E03 CRC64;
 Query Match 34.4%; Score 66; DB 11; Length 399;
 Best Local Similarity 31.7%; Pred. No. 0.0016;
 Matches 13; Conservative 8; Mismatches 20; Indels 0; Gaps 0;
 QY 4 FLXLLRPGSLXRXCKXXQCSFXXARXIFKDXARTKLEWISY 44
 DB 45 FLEIFQGNLEKECYEVCNFEAREVENDYITDEFWROY 85
 RESULT 36
 Q9LM33 PRELIMINARY; PRT; 588 AA.
 AC Q9LM33;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE T10022.12.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC Lycopodiophyta; Isoetopsida; Selaginellales; Selaginellaceae;
OX Selaginella.
RN NCBL_TaxID=59777;
RP [1]
RA SEQUENCE FROM N.A.
RL Choi D.-W., Close T.J., Iturriaga G.;
Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U96716; AAB57843.1; -.
DR HSSP: P27703; 1ERK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_kin.
DR Pfam: PF00069; pkinase; 1.
DR PROSITE: PS01351; MARK; UNKNOWN_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Transferase.
FT NON_TER 196
SQ SEQUENCE ~ 196 AA; 22852 MW; 11417FA4E31CF72D CRC64;

Query Match 35.7%; Score 68.5; DB 10; Length 196;
Best Local Similarity 37.0%; Pred. No. 0.00074;
Matches 17; Conservative 4; Mismatches 21; Indels 3; Gaps 2;

OY 2 ANFLXLLRPGSL--XRXCXXXCSEFYXARXIFKDXARTKLFWISY 44
DB 133 ANFHRLDKPKNILANAYCKLKICDFGLARAFNDA-PSAIFWTDY 180

RESULT 31
ID 09SPFO PRELIMINARY; PRT; 506 AA.

AC 09SPFO: 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE BLAST AND WOUNDING INDUCED MITOGEN-ACTIVATED PROTEIN KINASE.
GN BMMK1.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBL_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20089141; PubMed=10624015;
RA He C., Fong S.H., Yang D., Wang G.L.;
RT "BMMK1, a novel MAP kinase induced by fungal infection and mechanical
wounding in rice.";
RL MOL. Plant Microbe Interact. 12:1064-1073(1999).
DR EMBL: AF177392; AAD52659.1; -.
DR HSSP: P24941; 1HCL.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS01351; MARK; UNKNOWN_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 506 AA; 57955 MW; 0CB538FDEB171F0B CRC64;

Query Match 35.7%; Score 68.5; DB 10; Length 506;
Best Local Similarity 37.0%; Pred. No. 0.00074;
Matches 17; Conservative 5; Mismatches 21; Indels 3; Gaps 2;

OY 1 ANFLXLLRPGSL--XRXCXXXCSEFYXARXIFKDXARTKLFWISY 44
DB 133 ANFHRLDKPKNILANS DCKLKICDFGLARAFNDA-PSAIFWTDY 177

RESULT 32
ID 09SE23 PRELIMINARY; PRT; 506 AA.
AC 09SE23: 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MAP KINASE HOMOLOG.
GN MAPK1.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBL_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Cheong Y.H., Moon B.C., Kim J.K., Cho M.J.;
RT "Novel plant MAP kinases phosphorylate defense-related transcription
factors.";
RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF194415; AAF23902.1; -.
DR HSSP: P24941; 1HCL.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS01351; MARK; UNKNOWN_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 506 AA; 57945 MW; B05509010B2673C4 CRC64;

Query Match 35.7%; Score 68.5; DB 10; Length 506;
Best Local Similarity 37.0%; Pred. No. 0.00074;
Matches 17; Conservative 5; Mismatches 21; Indels 3; Gaps 2;

OY 1 ANFLXLLRPGSL--XRXCXXXCSEFYXARXIFKDXARTKLFWISY 44
DB 133 ANFHRLDKPKNILANS DCKLKICDFGLARAFNDA-PSAIFWTDY 177

RESULT 33
ID 09MB22 PRELIMINARY; PRT; 510 AA.
AC 09MB22: 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ATRMPK9.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBL_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Mizoguchi T., Ichimura K., Shinozaki K.;
RT "Arabidopsis thaliana mRNA for MAP kinase.";
RL Submitted (Feb-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB038694; BAA92223.1; -.
DR HSSP: P27703; 1ERK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS01351; MARK; UNKNOWN_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Transferase.

RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Pham P.K., Banh J., Dale J.M., Goldsmith A.D.,
RA Jiang P.X., Lee J.M., Onodera C.S., Quach H.L., Tang C., Tociunt M.,
RA Yamamura Y., Yu G., Yu S., Bowser L., Carlincl P., Chen H., Cheuk R.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Kim C., Koeseema E., Lam B., Lin J., Meyers M.C., Miranda M.,
RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
RA Shinn P., Southwick A., Tracy S.E., Shinzaki K., Davis R.W.,
RA Ecker J.R., Theologis A.;
RT "Full length cDNA of gene T10P20.15 (GI:9719729).";
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AC034107; AAF97831.1; -;
DR EMBL: AY045931; AAK76605.1; -;
DR HSSP: P24941; 1HCL.
DR InterPro: IPR000719; Euk_kinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_Chr_kinase.
DR Pfam: PF00069; kinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS01351; MAPK; UNKNOWN_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Transferase.
SQ SEQUENCE 589 AA; 66231 MW; 96769BA5E164BD74 CRC64;

Query Match 37.2%; Score 71.5; DB 10; Length 589;
Best Local Similarity 39.1%; Pred. No. 0.00025;
Matches 18; Conservative 4; Mismatches 21; Indels 3; Gaps 2;

OY 1 ANAFLLXLRPGSL--XRCKXXQCSFXXARXIFKDAKRTKLEWISY 44
Db 224 ANVFHRDLKPKNLIANADCKLKICDFGLARVSFND-PTALFMTDY 268

RESULT 28
Q9SE22 PRELIMINARY; PRT; 459 AA.
ID Q9SE22
AC Q9SE22;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MAP KINASE HOMOLOG.
GN MAPK2.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Eumariotidae; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Erihartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Cheong Y.H., Moon B.C., Kim J.K., Cho M.J.;
RT "Novel plant MAP kinases phosphorylate defense-related transcription
RT factors";
RL Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF194416; AAF23903.1; -;
DR HSSP: P24941; 1HCL.
DR InterPro: IPR000719; Euk_kinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_Chr_kinase.
DR Pfam: PF00069; kinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS01351; MAPK; UNKNOWN_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 459 AA; 53308 MW; E4B944437373057F CRC64;

Query Match 36.2%; Score 69.5; DB 10; Length 459;
Best Local Similarity 37.0%; Pred. No. 0.00044;
Matches 17; Conservative 5; Mismatches 21; Indels 3; Gaps 2;

OY 1 ANAFLLXLRPGSL--XRCKXXQCSFXXARXIFKDAKRTKLEWISY 44
Db 133 ANVFHRDLKPKNLIANADCKLKICDFGLARVSFND-PTALFMTDY 177

RESULT 29
Q29094 PRELIMINARY; PRT; 648 AA.
ID Q29094
AC Q29094;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE PROTEIN S (FRAGMENT).
GN PROS.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=95134217; PubMed=7832752;
RA Greengard J.S., Fernandez J.A., Radtke K.P., Griffin J.H.;
RT "Identification of candidate residues for interaction of protein S
RT with C4b binding protein and activated protein C.";
RL Biochem. J. 305:397-403(1995).
DR EMBL: L31379; AAA70382.1; -;
DR HSSP: P00740; 1CFH.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR002383; GFA_blood.
DR InterPro: IPR001791; laminin_G.
DR InterPro: IPR000294; VltK_dep_GLA.
DR Pfam: PF00008; EGF; 4.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00054; laminin_G; 1.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 3.
DR SMART: SM00001; EGF_like; 1.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00282; LamG; 2.
DR PROSITE: PS00010; ASX_HYDROXYL; 4.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 3.
DR PROSITE: PS01187; EGF_CA; 3.
DR PROSITE: PS00011; GLU_CARBOXYLATON; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
FT NON-TER 1
SQ SEQUENCE 648 AA; 71914 MW; 4BDFA8B13872136 CRC64;

Query Match 35.9%; Score 69; DB 6; Length 648;
Best Local Similarity 34.1%; Pred. No. 0.00078;
Matches 15; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

OY 1 ANAFLLXLRPGSLXRXCKXXQCSFXXARXIFKDAKRTKLEWISY 44
Db 15 ANSMLEKRGKGLNERECIEELCSKEAREVENDETEFYPAY 58

RESULT 30
Q04284 PRELIMINARY; PRT; 196 AA.
ID Q04284
AC Q04284;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MAP KINASE-LIKE PROTEIN (FRAGMENT).
GN SDN-6R.
OS Selaginella lepidophylla.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

CC CALCIUM, AND PHOSPHOLIPID DURING BLOOD CLOTTING.
CC -1- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: ARG-1-THR AND THEN
CC ARG-1-ILE BONDS IN PROTHROMBIN TO FORM THROMBIN.
CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
CC AND ARE HELD TOGETHER BY 1 OR MORE DISULFIDE BONDS.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR HSSP: P00742; IHG.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001234; trypsin.
DR InterPro: IPR00294; VltK_dep-GLA.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00069; GLA; 1.
DR PROSITE: PS00011; GLU-CARBOXYLATION; FALSE_NEG.
KW Glycoprotein; Hydrolase; Gamma-carboxyglutamic acid; Vitamin K; Venom;
KW Calcium-binding; Blood coagulation.
FT CHAIN 1 40 FACTOR X LIGHT CHAIN (BY SIMILARITY).
FT NON_CONS 40 41 FACTOR X HEAVY CHAIN (BY SIMILARITY).
FT CHAIN 41 98 ACTIVATED FACTOR XA, HEAVY CHAIN
FT CHAIN 41 98 (BY SIMILARITY).
FT DOMAIN 41 98 CATALYTIC (BY SIMILARITY).
FT NON_CONS 78 79 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 7 6 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 14 14 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 16 16 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 19 19 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 20 20 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 25 25 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 26 26 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 29 29 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 32 32 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 35 35 GAMMA-CARBOXYGLUTAMIC ACID.
FT ACT_SITE 91 91 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 17 22 BY SIMILARITY.
FT DISULFID 47 52 BY SIMILARITY.
FT DISULFID 67 7 BY SIMILARITY.
FT NON_TER 98 98
SQ SEQUENCE 98 AA; 11270 MW; 6FD398A3608DCEFF3 CRC64;

Query Match 40.6%; Score 78; DB 13; Length 98;
Best Local Similarity 32.6%; Pred. No. 2.6e-06;
Matches 14; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

OY 1 ANAFLLXLRPGSLRXXKXQCSFFXXARXIFKDXRTKLFWSY 43
DB 1 SNSLFEIRPGNIERECIEKCKSEAREVEFDNEXKTXFTYN 43

RESULT 22
O90YK1 PRELIMINARY; PRT; 433 AA.

AC O90YK1
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE COAGULATION FACTOR VII
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2135085; PubMed=11459993;
RA Sheehan J., Tempier M., Gregory M., Hanumanthalah R., Troyer D.,

RA Phan T., Thankavel B., Jagadeeswaran P.;
RT "Demonstration of the extrinsic coagulation pathway in teleostei;
RT Identification of the zebrafish coagulation factor VII";
RL Proc. Natl. Acad. Sci. U.S.A. 98:8768-8773(2001).
DR EMBL: AY040345; AA:K474192.1;--
SQ SEQUENCE 433 AA; 48680 MW; CD9D1B179601BA4C CRC64;

Query Match 39.1%; Score 75; DB 13; Length 433;
Best Local Similarity 37.8%; Pred. No. 4.3e-05;
Matches 14; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

OY 8 LRPGSLRXXKXQCSFFXXARXIFKDXRTKLFWSY 44
DB 46 LKTNLERECIEKCKSEAREVEFDNEXKTXFTYN 82

RESULT 23
O94EY5 PRELIMINARY; PRT; 431 AA.

AC O94EY5
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PUTATIVE MAP KINASE.
GN F25P22.9.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RP SEQUENCE FROM N.A.
RA Lam B., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF387019; AAK62464.1; --
KW kinase.
SQ SEQUENCE 431 AA; 49425 MW; 471AAFF18FD524C4 CRC64;

Query Match 37.2%; Score 71.5; DB 10; Length 431;
Best Local Similarity 39.1%; Pred. No. 0.00018;
Matches 18; Conservative 4; Mismatches 21; Indels 3; Gaps 2;

OY 1 ANAFLLXLRPGSLRXXKXQCSFFXXARXIFKDXRTKLFWSY 44
DB 210 ANVFHRLDKPKNIILNADCKLKICDGLARVSFNDA-PRATWTDY 254

RESULT 24
O9SMJ7 PRELIMINARY; PRT; 492 AA.

AC O9SMJ7
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MAP KINASE PROTEIN (FRAGMENT).
OS Cicer arietinum (Chickpea) (Garbanzo).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids I; Fabales; Fabaceae; Papilionoideae; Ciceraceae; Cicer.
OX NCBI_TaxID=3827;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. CASTELLANA; TISSUE=ETIOLATED EPICOTYLS;
RA Dopico B., Esteban R., Labrador E.;
RT "A MAP kinase is expressed in chickpea epicotyls";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AB062459; BAB58886.1; JOINED.
DR EMBL: AB062461; BAB58886.1; JOINED.
DR EMBL: AB062463; BAB58886.1; JOINED.
DR EMBL: AB062465; BAB58886.1; JOINED.
DR EMBL: AB062467; BAB58886.1; JOINED.
DR EMBL: AB062469; BAB58886.1; JOINED.
DR EMBL: AB062469; BAB58886.1; JOINED.
SQ SEQUENCE 461 AA; 51695 MW; 8F5A69A525DF65B5 CRC64;

Query Match 43.2%; Score 83; DB 6; Length 461;
Best Local Similarity 44.1%; Pred. No. 1.7e-06;
Matches 15; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

OY 11 GSLRXKXXKCSFXXRXIFKDXRTKLFWISY 44
DB 58 GNLERCEMEKCSFEAREVFENTERTTEFWKQY 91

RESULT 19
Q9BZD6

ID Q9BZD6 PRELIMINARY; PRT; 226 AA.

AC Q9BZD6: 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE TRANSMEBRANE GAMMA-CARBOXYGLUTAMIC ACID PROTEIN 4 TMG4.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21117044; PubMed=11171957;
RA Kulman J.D., Harris J.E., Xie L., Davie E.W.;
RT "Identification of two novel transmembrane gamma-carboxyglutamic acid
RT proteins expressed broadly in fetal and adult tissues.";
RT Proc. Natl. Acad. Sci. U.S.A. 98:1370-1375(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA, CHORIOCARCINOMA;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF326351; AAK0956.1; -;
DR EMBL: BC010052; AAI10052.1; -;
DR HSSP: P00740; ICFH.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR000294; VitK_dep_GLA.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00069; GLA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
SQ SEQUENCE 226 AA; 25403 MW; 45C783E3825797EE CRC64;

Query Match 43.0%; Score 82.5; DB 4; Length 226;
Best Local Similarity 40.9%; Pred. No. 9.7e-07;
Matches 18; Conservative 4; Mismatches 21; Indels 1; Gaps 1;

OY 2 NAF-LXLRPGSLRXKXXKCSFXXRXIFKDXRTKLFWISY 44
DB 53 NRPDLFTFPGNLERCEMEKCSFEAREVFEDXTIAFWQY 96

RESULT 20
Q28994
ID Q28994 PRELIMINARY; PRT; 138 AA.

AC Q28994: 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE MATURP PORCINE FACTOR IX (FRAGMENT).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA MEDLINE=96003866; PubMed=7568220;
RX Brandstetter H., Bauer M., Huber R., Lollar P., Bode W.;
RT "X-ray structure of clotting factor IXa: active site and module
RT structure related to Xase activity and hemophilia B.";
RT Proc. Natl. Acad. Sci. U.S.A. 92:9796-9800(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Lollar P.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U51135; AAA96318.1; -;
DR HSSP: P00740; IEDM.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001438; EGF_IT.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF; 2.
DR Pfam: PF00594; gla; 1.
DR PRINTS: PR00010; EGFBLDOD.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00069; GLA; 1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
FT NON_TER 1
FT NON_TER 138
SQ SEQUENCE 138 AA; 15515 MW; 793BABDEAD5FAFAD CRC64;

Query Match 41.1%; Score 79; DB 6; Length 138;
Best Local Similarity 41.2%; Pred. No. 2.5e-06;
Matches 14; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

OY 11 GSLRXKXXKCSFXXRXIFKDXRTKLFWISY 44
DB 4 GNLERCEMEKCSFEAREVFENTERTTEFWKQY 37

RESULT 21
P82807
ID P82807 PRELIMINARY; PRT; 98 AA.

AC P82807: 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE COAGULATION FACTOR IXA-LIKE PROTEIN (EC 3.4.21.6) (FRAGMENTS).
OS Notochis scutatus scutatus (Mainland tiger snake) (Common tiger
OS snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Acanthophilineae; Notochis.
OX NCBI_TaxID=70142;
RN [1]
RP SEQUENCE, AND CHARACTERIZATION.
RC TISSUE=VENOM;
RX MEDLINE=20347887; PubMed=10779512;
RA Brown M.A., Stenberg L.M., Persson U., Stenflo J.;
RT "Identification and purification of vitamin K-dependent proteins and
RT peptides with monoclonal antibodies specific for gamma-carboxyglutamy
RT (Gla) residues.";
RL J. Biol. Chem. 275:19795-19802(2000).
CC -!- FUNCTION: FACTOR IXA IS A VITAMIN K-DEPENDENT GLYCOPROTEIN THAT
CC CONVERTS PROTHROMBIN TO THROMBIN IN THE PRESENCE OF FACTOR VA,

DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Plasmid;
KW Repeat; Serine protease; Signal.
FT SIGNAL 1 40 POTENTIAL.
FT CHAIN 41 481 COAGULATION FACTOR X.
SQ SEQUENCE 481 AA; 53986 MW; CF702DE5EF9D97AE CRC64;

Query Match 49.0%; Score 94; DB 11; Length 481;
Best Local Similarity 38.6%; Pred. No. 1.8e-08;
Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANAFLXLRPGSLRXKXCCXXCSPFXARXIFDAXRTKLEWISY 44
11:1 : 1:1 11:1 : 1:1 : 1:1 : 1:1 :
Db 41 ANSFEEFKKGNLERECMEICSYEEVREIFEDDEKTKETWTKY 84

RESULT 10
ID 099L32 PRELIMINARY; PRT; 481 AA.
AC 099L32;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE COAGULATION FACTOR X.
GN F10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL: BC003877; AAH03877.1; -.
DR HSSP: P00742; 1XKA.
DR MGD: MGI:103107; F10.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF-Ca.
DR InterPro: IPR001438; EGF_II.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Trypsin.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF; 2.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00181; EGF; 2.
DR SMART: SM00001; EGF_like; 2.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; TYP_SPC; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ SEQUENCE 481 AA; 54004 MW; BD88E96C8A0B7E7F CRC64;

Query Match 49.0%; Score 94; DB 11; Length 481;

Best Local Similarity 38.6%; Pred. No. 1.8e-08;
Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANAFLXLRPGSLRXKXCCXXCSPFXARXIFDAXRTKLEWISY 44
11:1 : 1:1 11:1 : 1:1 : 1:1 : 1:1 :
Db 41 ANSFEEFKKGNLERECMEICSYEEVREIFEDDEKTKETWTKY 84

RESULT 11
ID 09TR0 PRELIMINARY; PRT; 456 AA.
AC 09TR0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE PROTEIN C PRECURSOR.
GN PROC.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxId=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Leeb T., Kopp T., Deppe A., Breen M., Matis U., Brunnberg L.,
RA Brenig B.;
RT "Molecular characterization and chromosomal assignment of the canine
RT protein C gene."
RL Mamm. Genome 10:135-139(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE:9571952; PubMed:10443005;
RA Leeb T., Pfeiffer I., Kopp T., Deppe A., Brenig B.;
RT "Analysis of canine protein C gene polymorphisms."
RL Anim. Genet. 30:237-238(1999).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL: AJ001979; CA05126.1; -.
DR HSSP: P04070; 1PCU.
DR MEROPS: S01.218; -.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF-Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Trypsin.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF; 2.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00181; EGF; 2.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; TYP_SPC; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KW Hydroxylation; Repeat; Serine protease; Signal.
FT SIGNAL 1 42 POTENTIAL.
FT CHAIN 43 192 PROTEIN C LIGHT CHAIN.
FT CHAIN 193 194 PROTEIN C CONNECTING DIPEPTIDE.
FT CHAIN 195 456 PROTEIN C HEAVY CHAIN.
SQ SEQUENCE 456 AA; 50813 MW; 7AD3A8C1C34E59FF CRC64;

Query Match 48.4%; Score 93; DB 6; Length 456;
Best Local Similarity 40.9%; Pred. No. 2.6e-08;


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ID 061109 PRELIMINARY; PRT; 446 AA.
AC 061109;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE COAGULATION FACTOR VII.
GN F7 OR FVII.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=96276538; PubMed=8701412;
RA Idusogie E., Rosen E., Geng J.P., Carmeliet P., Collen D.,
RA Castellino F.J.;
RT "Characterization of a cDNA encoding murine coagulation factor VII."
RL Thromb. Haemost. 75:481-487(1996).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
EMBL: U44795; AAC52570.1; -.
DR HSSP; P08709; 1PAK.
DR MGD; MG1:109325; F7.
DR InterPro: IPR002086; Aldehyde_dehydr.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR001064; Crystallin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF-Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Trypsin.
DR InterPro: IPR000294; Vitk_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla_1.
DR Pfam; PF00089; trypsin_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA_1.
DR SMART; SM00001; EGF_like_1.
DR SMART; SM00069; GLA_1.
DR SMART; SM00020; TYP_Spc_1.
DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01187; EGF_CA_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
KM Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ SEQUENCE 446 AA; 50318 MW; 482FD09BEFDA6870 CRC64;
```

Query Match 66.1%; Score 127; DB 11; Length 446;
Best Local Similarity 59.1%; Pred. No. 1.9e-14;
Matches 26; Conservative 1; Mismatches 17; Indels 0; Gaps 0;

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QY 1 ANAFLLXLRPGSLRKCKXXQCSFXXARXIFKDAKRTKLFWISY 44
   ||| :||||| | | | | | | | | | | | | | | | | |
Db 42 ANSLLELWPGSLERECNEQCSFEARELFKSPERTKQFIWIV 85
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RESULT 3
Q91WN8 PRELIMINARY; PRT; 460 AA.
AC Q91WN8;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE SIMILAR TO PROTEIN C.
```

```
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX Strausberg R.;
RA Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL: BC013896; AAH13896.1; -.
SQ SEQUENCE 460 AA; 51818 MW; 0117F26568FCC274 CRC64;
```

Query Match 56.8%; Score 109; DB 11; Length 460;
Best Local Similarity 47.7%; Pred. No. 3.4e-11;
Matches 21; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

```
QY 1 ANAFLLXLRPGSLRKCKXXQCSFXXARXIFKDAKRTKLFWISY 44
   ||| :||||| | | | | | | | | | | | | | | | | |
Db 42 ANSLLELWPGSLERECNEQCSFEARELFKSPERTKQFIWIV 85
```

```
RESULT 4
Q99PC6 PRELIMINARY; PRT; 460 AA.
AC Q99PC6;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE ANTIACOAGULANT PROTEIN C.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL;
RA Korf I.;
RT "Complete sequence of UC72A01."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
EMBL: AF318182; AAK07918.1; -.
DR HSSP; P04070; 1PCU.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF-Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Trypsin.
DR InterPro: IPR000294; Vitk_dep_GLA.
DR Pfam; PF00089; trypsin_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00001; EGF_2.
DR SMART; SM00069; GLA_1.
DR SMART; SM00020; TYP_Spc_1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
KM Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KW Hydroxylation; Repeat; Serine protease.
SQ SEQUENCE 460 AA; 51784 MW; 0293BC25E9D3ED16 CRC64;
```

Query Match 53.6%; Score 103; DB 11; Length 460;
Best Local Similarity 45.5%; Pred. No. 4.1e-10;

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Tue Sep 3 11:46:30 2002

us-09-302-239-3.rsp

Page 47

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Best Local Similarity    34.5% ; Pred. No. 48;
Matches    10; Conservative    3; Mismatches    9; Indels    7; Gaps    1;
```

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QY      22 CSFXRXRIEKDAX-----RTKLEWIS 43 .
          |   | | | | |         | : : :
Db       1041 CDFGLARDIYKDPDYVRKKGDPRLPLKMAA 1069
```

Search completed: August 30, 2002, 15:45:35
Job time: 855 sec


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FT CARBOHYD 376 376 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 509 509 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 521 521 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 578 578 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 617 617 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 629 629 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 673 673 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 702 702 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 719 719 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD.RES 1057 1057 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CONFLICT 25 25 P -> T (IN REF. 1).
FT CONFLICT 679 679 G -> D (IN REF. 3).
FT CONFLICT 783 784 LV -> VL (IN REF. 1).
FT CONFLICT 917 917 S -> C (IN REF. 1).
FT CONFLICT 1341 1367 QLTSLNGSGSPVAPPPPTGNMERGAA -> RSSPV
SQ SEQUENCE 1367 AA; 152516 MW; EFC99704F1DCA266 CRC64;
      (IN REF. 3).

Query Match 21.6%; Score 41.5; DB 1; Length 1367;
Best Local Similarity 34.5%; Pred. No. 32;
Matches 10; Conservative 3; Mismatches 9; Indels 7; Gaps 1;

QY 22 CSFXRXRXIFKDA-----XRTKLEWIS 43
DB 1043 CDFGLARDIKDPDYVRKKGDARLPKMA 1071

RESULT 46
ID IBMP_SOCMV STANDARD; PRT; 462 AA.
AC P15628;
DT 01-APR-1990 (Rel. 14, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inclusion body matrix protein (Viroplasm).
GN VI.
OS Soybean chlorotic mottle virus.
OC Viruses: Retroviral viruses; Caulimovirus.
OX NCBI_Taxid=10651;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=90098857; Pubmed=2602148;
RA Hasegawa A., Verwer J., Shimada A., Goldbach R.,
RA van Kammen A., Miki K., Kameya-Iwaki M., Hibl T.;
RT "The complete sequence of soybean chlorotic mottle virus DNA and the
RT identification of a novel promoter.";
RL Nucleic Acids Res. 17:9993-10013(1989).
RN
RP REVISIONS.
RA Hibl T.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ENHANCES THE TRANSLATION OF DOWNSTREAM ORF'S ON
CC POLICISTRONIC MRNA'S DERIVED FROM SOYBEAN CHLOROTIC MOTTLE VIRUS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC INCLUSION BODIES.
CC -1- MISCELLANEOUS: THE INCLUSION BODIES ARE THE SITE OF VIRAL DNA
CC SYNTHESIS. VIRION ASSEMBLY AND ACCUMULATION IN THE INFECTED CELL.
CC -1- SIMILARITY: BELONGS TO THE CAULIMOVIRUSES VIROPLASMIN FAMILY.
CC
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CC
CC EMBL; X15828; CAC16946.1; -
CC PIR; J50376; J50376.
CC InterPro: IPR002609; Caulimo_VI.
CC Pfam; PF01693; Caulimo_VI; I.

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KW Trans-acting factor; Translation regulation.
SQ SEQUENCE 462 AA; 53140 MW; 457E9CAFBBECF6CE4 CRC64;

Query Match 21.4%; Score 41; DB 1; Length 462;
Best Local Similarity 36.4%; Pred. No. 13;
Matches 8; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

QY 10 PGSIXRXKXXQCSFXRXRIF 31
DB 265 PKELRRTQOYQLSFAXTRFEV 286

RESULT 47
ID SLT2_YEAST STANDARD; PRT; 484 AA.
AC Q00772;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Mitogen-activated protein kinase SLT2/MPK1 (EC 2.7.1.1-) (MAP kinase
DE MPK1).
GN SLT2 OR MPK1 OR YHR030C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_Taxid=4932;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=AB320;
RX MEDLINE=92140049; Pubmed=1779770;
RA Torres L., Martin H., Garcia-Saez M.I., Arroyo J., Molina M.,
RA Sanchez M., Nombela C.;
RT "A protein kinase gene complements the lytic phenotype of
RT Saccharomyces cerevisiae lyc2 mutants.";
RL Mol. Microbiol. 5:2845-2854(1991).
RN
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=94378003; Pubmed=8091229;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
RA Du Z., Favell A., Fulton L., Gattung S., Geisel C., Kirsten J.,
RA Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
RA Latreille P., Louis E.J., Macri C., Mardis E., Meneses S., Mouser L.,
RA Nhan M., Rifkin L., Riles L., St Peter H., Treviskis E., Vaughan K.,
RA Vignati D., Wilcox L., Wohlman P., Westerton R., Wilson R.,
RA Vaudin M.;
RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
RT VII.1.";
RL Science 265:2077-2082(1994).
RN
RP CHARACTERIZATION.
RX MEDLINE=94103356; Pubmed=8276900;
RA Mazzoni C., Zarzov P., Rambour A., Mann C.;
RT "The SLT2 (MPK1) MAP kinase homolog is involved in polarized cell
RT growth in Saccharomyces cerevisiae.";
RL J. Cell Biol. 123:1821-1833(1993).
CC
CC -1- FUNCTION: SERINE/THREONINE PROTEIN KINASE INVOLVED IN A SIGNAL
CC TRANSDUCTION PATHWAY THAT PLAY A ROLE IN YEAST CELL MORPHOGENESIS
CC AND CELL GROWTH. THIS PATHWAY SEEMS TO STARTS BY SMP3; THEN
CC INVOLVE THE KINASE PKC1 THAT MAY ACT THE BCK1 KINASE THAT THEN
CC PHOSPHORYLATES MKK1 AND MKK2 WHICH THEMSELVES PHOSPHORYLATE THE
CC MPK1 KINASE WHICH ACTS ON A YET UNKNOWN SUBSTRATE.
CC -1- ENZYME REGULATION: ACTIVATED BY TYROSINE AND THREONINE
CC PHOSPHORYLATION BY MKK1 AND MKK2 (PROBABLY).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE SUBFAMILY.
CC
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FT MOD_RES 1059 1059 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CONFLICT 2 2
FT CONFLICT 772 772 Q -> E (IN REF. 2).
FT CONFLICT 787 787 A -> T (IN REF. 3).
FT CONFLICT 835 835 R -> G (IN REF. 3).
FT CONFLICT 848 848 K -> N (IN REF. 3).
FT CONFLICT 1347 1347 V -> E (IN REF. 3).
FT CONFLICT 1347 1347 S -> T (IN REF. 3).
SO SEQUENCE 1356 AA; 151526 MW; 59E/C44B05CFEBB3 CRC64;

Query Match 21.6%; Score 41.5; DB 1; Length 1356;
Best Local Similarity 34.5%; Pred. No. 32;
Matches 10; Conservative 3; Mismatches 9; Indels 7; Gaps 1;

Qy 22 CSFXARXIFKDA-----XRTKLEWIS 43
Db 1045 CDGFIARDIYKDPDYVRKGDARLPKMMMA 1073

RESULT 45
VGR2_MOUSE STANDARD; PRT; 1367 AA.
ID VGR2_MOUSE
AC P35918;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Vascular endothelial growth factor receptor 2 precursor (EC 2.7.1.112)
DE (VEGFR-2) (Protein-tyrosine kinase receptor flk-1) (Fetal liver kinase
DE 1) (kinase NK).
GN KDR OR FLK1 OR FLK-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/C; TISSUE=Embryo;
RX MEDLINE=93205880; PubMed=7681362;
RA Millaer B., Witzmann-Voos S., Schnurch H., Martinez R.,
RA Mueller N.P.H., Rissau W., Ullrich A.;
RT "High affinity VEGF binding and developmental expression suggest
RT Flk-1 as a major regulator of vasculogenesis and angiogenesis.";
RL Cell 72:835-846(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HE; TISSUE=Fetal liver;
RX MEDLINE=92020984; PubMed=1717995;
RA Mathews W., Jordan C.T., Gavin M., Jenkins N.A., Copeland N.G.,
RA Lentschka I.R.;
RT "A receptor tyrosine kinase cDNA isolated from a population of
RT enriched primitive hematopoietic cells and exhibiting close genetic
RT linkage to c-kit.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:9026-9030(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93141255; PubMed=8423988;
RA Oelrichs R.B., Reid H.H., Bernard O., Ziemecki A., Wilks A.F.;
RT "NYK/Flk-1: a putative receptor protein tyrosine kinase isolated from
RT E10 embryonic neuroepithelium is expressed in endothelial cells of
RT the developing embryo.";
RL Oncogene 8:11-18(1993).
RN [4]
RP SEQUENCE OF 1-15 FROM N.A.
RX MEDLINE=96032749; PubMed=7559454;
RA Patterson C., Petrella M.A., Hsieh C.-M., Yoshizumi M., Lee M.-E.,
RA Harber E.;
RT "Cloning and functional analysis of the promoter for KDR/flk-1, a
RT receptor for vascular endothelial growth factor.";
RL J. Biol. Chem. 270:23111-23118(1995).
RN [5]
RP FUNCTION.
RX MEDLINE=93361481; PubMed=8356051;
RA Quinn T.P., Peters K.G., de Vries C., Ferrara N., Williams L.T.;

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RT "Fetal liver kinase 1 is a receptor for vascular endothelial growth
RT factor and is selectively expressed in vascular endothelium.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:7537-7537(1993).
CC -1- FUNCTION: RECEPTOR FOR VEGF OR VEGF-C. HAS A TYROSINE-PROTEIN
CC KINASE ACTIVITY. THE VEGF-KINASE LIGAND/RECEPTOR SIGNALING SYSTEM
CC PLAYS A KEY ROLE IN VASCULAR DEVELOPMENT AND REGULATION OF
CC VASCULAR PERMEABILITY.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine ~ ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN ADULT HEART, LUNG,
CC KIDNEY, BRAIN AND SKELETAL MUSCLE. BUT IS ALSO EXPRESSED AT LOWER
CC LEVELS IN MOST OTHER ADULT TISSUES.
CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
CC -1- SIMILARITY: CONTAINS 7 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -----
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CC -----
DR EMBL; X70842; CAA50192.1; -
DR EMBL; X59397; CAA42040.1; -
DR EMBL; S53103; AAB25043.1; -
DR EMBL; X89777; CAA61917.1; -
DR PIR; A41228; A41228.
DR HSSP; P11362; 1FEK.
DR MGD; MGI:96683; Kdr.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003016; Ig_MHC.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003600; Ig_c2.
DR InterPro: IPR001824; Receptor_Tyr_kin_III.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig; 6.
DR Pfam; PF00069; Pkinase; 2.
DR SMART; SM00410; IG_1like; 4.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00219; TYRC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KM Signal: Transferrin; Tyrosine-protein kinase; Receptor; Transmembrane;
KM Glycoprotein; Phosphorylation; ATP-binding; Immunoglobulin domain;
KM Repeat.
FT SIGNAL 1 19
FT CHAIN 20 1367
FT DOMAIN 20 762
FT TRANSMEM 763 784
FT DOMAIN 785 1367
FT DOMAIN 46 111
FT DOMAIN 143 209
FT DOMAIN 241 306
FT DOMAIN 347 402
FT DOMAIN 440 535
FT DOMAIN 562 647
FT DOMAIN 679 742
FT DOMAIN 832 1160
FT NP_BIND 838 846
FT BINDING 866 866
FT ACT_SITE 1026 1026
FT CARBOHYD 46 46
FT CARBOHYD 98 98
FT CARBOHYD 145 145
FT CARBOHYD 160 160
FT CARBOHYD 247 247
FT CARBOHYD 320 320

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QY 4 FLXXLRGSLXRC---KXXQCSFXXXARKXFKDAXR 36
 DB 262 FFSALHASAMCRCSYKSKCTLANQTIFFSITR 297

RESULT 41
 PFLA_STRMU STANDARD; PRT; 263 AA.

AC 068575;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyruvate formate-lyase activating enzyme (EC 1.97.1.4) (PFL-activating enzyme).
 GN ACT OR PFLC.
 OS Streptococcus mutans.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1309;
 (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=FT11;
 RA Boyd D.A., Hamilton I.R., Cvitkovitch D.G., Bleiweis A.S.;
 RT "Defects in D-alanyl-lipoteichoic acid synthesis in Streptococcus mutans leads to acid sensitivity.";
 RL Submitted (FEB-1998) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GS-5;
 RA Yamamoto Y., Sato Y., Takahashi-Abbe S., Yamada T., Kizaki H.;
 RT "Cloning and characterization of the act gene encoding pyruvate formate-lyase-activating enzyme from Streptococcus mutans.";
 RL Submitted (OCT-1998) to the EMBL/Genbank/DBJ databases.
 RN [1]
 RP FUNCTION: ACTIVATION OF PYRUVATE FORMATE-LYASE UNDER ANAEROBIC CONDITIONS BY GENERATION OF AN ORGANIC FREE RADICAL, USING S-ADENOSYLMETHIONINE AND REDUCED FLAVODOXIN AS COSUBSTRATES TO PRODUCE 5'-DEOXY-ADENOSINE.
 CC -1 CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + DIHYDROFLAVODOXIN + [PYRUVATE FORMATE-LYASE]-GLYCINE = 5'-DEOXYADENOSINE + METHIONINE + FLAVODOXIN + [PYRUVATE FORMATE-LYASE]-GLYCINE RADICAL.
 CC -1 CORPACTOR: BINDS 14FE-4S CLUSTER (BY SIMILARITY).
 CC -1 SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1 SIMILARITY: BELONGS TO THE ORGANIC RADICAL ACTIVATING ENZYMES FAMILY.
 CC -----
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 CC -----
 DR EMBL: AF051356; AAC05773.1; -;
 DR EMBL: AB019417; BAA34998.1; -;
 DR InterPro: IPR001989; Radical_activat.
 DR Pfam: PF002143; Radical_activat; 1.
 DR ProDom: PD004758; Radical_activat; 1.
 DR PROSITE: PS01087; RADICAL_ACTIVATING; 1.
 KW Oxidoreductase; Iron-sulfur; 4Fe-4S.
 FT METAL 37
 FT METAL 41 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
 FT METAL 41 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
 FT METAL 44 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
 FT METAL 44 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
 SQ SEQUENCE 263 AA; 30150 MW; 575405F3E248EFC CRC64;

Query Match 21.9%; Score 42; DB 1; Length 263;
 Best Local Similarity 37.5%; Pred. No. 4.9;
 Matches 9; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 18 KXXQCSFXXXARKXFKDAXR 41
 DB 53 KNDRAITERTAGDVKEALRKFDFW 76

RESULT 42
 NAPA_DESDE STANDARD; PRT; 755 AA.

AC P81186;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Periplasmic nitrate reductase precursor (EC 1.7.99.4).
 GN NAPA OR NAP.
 OS Desulfovibrio desulfuricans.
 OC Bacteria; Proteobacteria; delta subdivision; Desulfovibrio.
 OX NCBI_TaxID=876;
 (1)
 RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RC STRAIN=ATCC 27774;
 RX MEDLINE=99220830; PubMed=10368307;
 RA Dias J.M., Than M.E., Humm A., Huber R., Bourenkov G.P.,
 RA Bartunik H.D., Bursakov S., Calvete J., Caldeira J., Carneiro C.,
 RA Moura J.J.G., Moura I., Romao M.J.;
 RT "Crystal structure of the first dissimilatory nitrate reductase at 1.9 A solved by MAD methods.";
 RL Structure 7:65-79(1999).
 RN [2]
 RP SEQUENCE OF 33-73.
 RC STRAIN=ATCC 27774;
 RX MEDLINE=98042476; PubMed=9367852;
 RA Bursakov S., Liu M.-Y., Payne W.J., Legall J., Moura I., Moura J.J.G.,
 RA Moura I., Moura J.J.G.;
 RT "Enzymatic properties and effect of ionic strength on periplasmic nitrate reductase (NAP) from Desulfovibrio desulfuricans ATCC 27774.";
 RL Biochem. Res. Commun. 239:816-822(1997).
 RN [3]
 RP CHARACTERIZATION.
 RC STRAIN=ATCC 27774;
 RA Bursakov S., Liu M.-Y., Payne W.J., Legall J., Moura I., Moura J.J.G.;
 RT "Isolation and preliminary characterization of a soluble nitrate reductase from the sulfate-reducing bacterium Desulfovibrio desulfuricans 27774.";
 RL Anaerobe 1:55-60(1995).
 CC -1 FUNCTION: LARGE SUBUNIT OF THE PERIPLASMIC NITRATE REDUCTASE (NAP). ONLY EXPRESSED AT HIGH LEVELS DURING AEROBIC GROWTH. NAPA COMPLEX RECEIVES ELECTRONS FROM THE MEMBRANE-ANCHORED TETRAPEMERIC PERIPLASM. ESSENTIAL FUNCTION FOR NITRATE ASSIMILATION AND MAY HAVE A ROLE IN ANAEROBIC METABOLISM.
 CC -1 CATALYTIC ACTIVITY: Nitrite + acceptor = nitrate + reduced acceptor.
 CC -1 CORPACTOR: MOLYBDENUM (MOLYBDOPTERIN); MAY BIND A 4FE-4S CLUSTER.
 CC -1 SUBUNIT: MONOMER.
 CC -1 SUBCELLULAR LOCATION: Periplasmic.
 CC -1 INDUCTION: NITRATE REDUCTASE ACTIVITY IS INDUCED BY POTASSIUM AND SODIUM AND INHIBITED BY MAGNESIUM AND CALCIUM.
 CC -1 SIMILARITY: BELONGS TO THE PROKARYOTIC MOLYBDOPTERIN-CONTAINING OXIDOREDUCTASE FAMILY. NAPA/NAP/NAB SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: Y18045; CAA77019.1; -;
 DR PDB: 2NAP; 19-SEP-99.
 DR InterPro: IPR001467; Molybdopterin.
 DR Pfam: PF00384; molybdopterin; 1.
 DR Pfam: PF01568; Molybdop. binding; 1.
 DR PROSITE: PS00551; MOLYBDOPTERIN_PROK_1; FALSE_NEG.
 DR PROSITE: PS00490; MOLYBDOPTERIN_PROK_2; FALSE_NEG.

DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Vascular endothelial growth factor receptor 3 precursor (EC 2.7.1.112)
DE (VEGFR-3) (Tyrosine-protein kinase receptor FLT4).
GN FLT4 OR FLT-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=93330572; PubMed=8393164;
RA Finerley H., Kelleher K., Morris G.E., Bean K., Merberg D.M.,
RA Kitz R., Morris J.C., Soekhoe H., Turner K.J., Wood C.R.;
RT "Molecular cloning of murine FLT and FLT4.*";
RL Oncogene 8:2293-2298(1993).
CC -1- FUNCTION: RECEPTOR FOR VEGF-C. HAS A TYROSINE-PROTEIN KINASE
CC ACTIVITY.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ADULT LUNG AND LIVER, AND IN
CC FETAL LIVER, BRAIN, INTESTINE AND PLACENTA.
CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
CC -1- SIMILARITY: CONTAINS 7 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -----
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CC -----
DR EMBL: L07296; AAA0077.1; -.
DR HSP; P11362; IFGK.
DR MGD; MGI:95561; Flt4.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR001824; Receptor_Tyr_kin_III.
DR InterPro: IPR001245; Tyr_Pkinase.
DR Pfam: PF00047; Ig_6.
DR Pfam: PF00069; Pkinase; 2.
DR SMART: SM00410; IG_Like; 3.
DR SMART: SM00408; IGC2; 2.
DR SMART: SM00219; TYRK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS00240; RECEPTOR_TYR_KIN_III; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW Transferrase; Tyrosine-protein kinase; Phosphorylation; ATP-binding;
KW Receptor; Transmembrane; Signal; Immunoglobulin domain; Repeat;
KW Glycoprotein.
FT SIGNAL 1 24
FT CHAIN 25 1363
FT TRANSMEM 25 775
FT DOMAIN 776 797
FT DOMAIN 798 1363
FT DOMAIN 44 118
FT DOMAIN 151 213
FT DOMAIN 245 317
FT DOMAIN 351 403
FT DOMAIN 438 541
FT DOMAIN 571 660
FT DOMAIN 692 758
FT DOMAIN 845 1173
FT NP_BIND 851 859
FT BINDING 879 879
FT ACT_SITE 1037 1037
FT
FT VASCULAR ENDOTHELIAL GROWTH FACTOR
FT RECEPTOR 3.
FT EXTRACELLULAR (POTENTIAL).
FT POTENTIAL.
FT CYTOPLASMIC (POTENTIAL).
FT IG-LIKE C2-TYPE DOMAIN 1.
FT IG-LIKE C2-TYPE DOMAIN 2.
FT IG-LIKE C2-TYPE DOMAIN 3.
FT IG-LIKE C2-TYPE DOMAIN 4.
FT IG-LIKE C2-TYPE DOMAIN 5.
FT IG-LIKE C2-TYPE DOMAIN 6.
FT IG-LIKE C2-TYPE DOMAIN 7.
FT PROTEIN KINASE.
FT ATP (BY SIMILARITY).
FT ATP (BY SIMILARITY).
FT BY SIMILARITY.

FT DISULFID 51 111 POTENTIAL.
FT DISULFID 158 206 POTENTIAL.
FT DISULFID 252 310 POTENTIAL.
FT DISULFID 445 534 POTENTIAL.
FT DISULFID 578 653 POTENTIAL.
FT DISULFID 699 751 POTENTIAL.
FT MOD_RES 1068 1068 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 33 33 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 104 104 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 251 251 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 411 411 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 515 515 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 527 527 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 582 582 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 594 594 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 683 683 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 690 690 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 758 758 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 1363 AA; 153015 MW; F1BF8A2BDEF99BE9 CRC64;

Query Match 22.7%; Score 43.5; DB 1; Length 1363;
Best Local Similarity 34.5%; Pred. No. 14;
Matches 10; Conservative 4; Mismatches 8; Indels 7; Gaps 1;

OY 22 CSFXXRXIFPD-----AXRTKLEWIS 43
DB 1054 CDFGLARDIYDPDYVRKGSARLPKMA 1082

RESULT 40
YOL3_CABEL
ID YOL3_CABEL STANDARD: PRT; 322 AA.
AC 009292;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Hypothetical 35.9 kDa protein C56G7.3 in chromosome III.
GN C56G7.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Percy C.;
RL Submitted (NOV-1994) to the EMBL/Genbank/DBJ databases.
RN [2]
RP REVISIONS.
RA Jones S.J.M.;
RL Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.
CC -----
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CC -----
DR EMBL: Z46793; CAAB6771.1; -.
DR WormPeP: C56G7.3; CE1/608.
KW Hypothetical protein.
SQ SEQUENCE 322 AA; 35890 MW; 4B0ADB6F5D27AFc4 CRC64;

Query Match 22.1%; Score 42.5; DB 1; Length 322;
Best Local Similarity 25.0%; Pred. No. 4.9;
Matches 9; Conservative 6; Mismatches 18; Indels 3; Gaps 1;

DT 01-MAR-2002 (rel. 41, Last annotation update)
 DE Vascular endothelial growth factor receptor 3 precursor (EC 2.7.1.112)
 GN (VEGFR-3) (Tyrosine-protein kinase receptor FLT4).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 .OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 .NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA MEDLINE=93241723; PubMed=836825;
 RA Galland F., Karamyshva A., Pebusque M.-J., Borg J.-P., Rottapel R.,
 RA Dubreuil P., Rosnet O., Birbaum D.;
 RT "The FLT4 gene encodes a transmembrane tyrosine kinase related to the
 RT vascular endothelial growth factor receptor.";
 RN Oncogene 8:1231-1240(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93007958; PubMed=1337515;
 RA Pajusola K., Aprelikova O., Korhonen J., Kaipainen A., Pertovaara L.,
 RA Allitalo R., Allitalo K.;
 RT "FLT4 receptor tyrosine kinase contains seven immunoglobulin-like
 RT loops and is expressed in multiple human tissues and cell lines.";
 RL Cancer Res. 52:5738-5743(1992).
 RN [3]
 RP ERRATUM.
 RA Pajusola K., Aprelikova O., Korhonen J., Kaipainen A., Pertovaara L.,
 RA Allitalo R., Allitalo K.;
 RL Cancer Res. 53:3845-3845(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Lee J., Gray A., Yuan J., Luoh S.M., Avraham H., Wood W.I.;
 RL Submitted (Jan-1996) to the EMBL/Genbank/DBD databases.
 RN [5]
 RP SEQUENCE OF 761-1190 FROM N.A.
 RX MEDLINE=92119639; PubMed=1310071;
 RA Aprelikova O., Pajusola K., Partanen J., Armstrong E., Allitalo R.,
 RA Bailey S.K., McMahon J., Wasmuth J., Huebner K., Allitalo K.;
 RT "FLT4, a novel class III receptor tyrosine kinase in chromosome 5q33-
 RT qter.";
 RL Cancer Res. 52:746-748(1992).
 CC -1- FUNCTION: RECEPTOR FOR VEGF-C. HAS A TYROSINE-PROTEIN KINASE
 CC ACTIVITY.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: PLACENTA, LUNG, HEART, AND KIDNEY, DOES NOT
 CC SEEM TO BE EXPRESSED IN PANCREAS AND BRAIN.
 CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES.
 CC -1- SIMILARITY: CONTAINS 7 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
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 CC -----
 DR EMBL: X69878; CAA49505.1; -
 DR EMBL: X68203; CAA48290.1; ALT_INIT.
 DR EMBL: U43143; AAB85215.1; -
 DR PIR: S36130; S36130.
 DR HSSP: P11362; IFBK.
 DR MIM: 136352; -
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003598; Ig_C2.
 DR InterPro: IPR003600; Ig_Like.
 DR InterPro: IPR001824; Receptor_tyr_kin_III.
 DR InterPro: IPR001245; Tyr_pkinase.

DR Pfam: PF00047; Ig_6.
 DR Pfam: PF00069; pkinase; 2.
 DR SMART: SM00410; Ig_Like; 2.
 DR SMART: SM00408; ICG2; 2.
 DR SMART: SM00219; Tyrc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00240; RECEPTOR_TYR_KIN_III; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW Transferase; Tyrosine-protein kinase; Phosphorylation; ATP-binding;
 KW Receptor; Transmembrane; Signal; Immunoglobulin domain; Repeat;
 KW Glycoprotein.
 FT SIGNAL 1 23
 FT CHAIN 24 1298
 FT
 FT DOMAIN 24 775
 FT TRANSMEM 776 797
 FT DOMAIN 798 1298
 FT DOMAIN 44 118
 FT DOMAIN 151 213
 FT DOMAIN 245 317
 FT DOMAIN 351 403
 FT DOMAIN 438 541
 FT DOMAIN 571 660
 FT DOMAIN 692 758
 FT DOMAIN 845 1173
 FT NP_BIND 851 859
 FT BINDING 879 879
 FT ACT_SITE 1037 1037
 FT DISULFID 51 111
 FT DISULFID 158 206
 FT DISULFID 252 310
 FT DISULFID 445 534
 FT DISULFID 578 653
 FT DISULFID 699 751
 FT CARBOHYD 33 33
 FT CARBOHYD 104 104
 FT CARBOHYD 166 166
 FT CARBOHYD 251 251
 FT CARBOHYD 299 299
 FT CARBOHYD 411 411
 FT CARBOHYD 515 515
 FT CARBOHYD 527 527
 FT CARBOHYD 594 594
 FT CARBOHYD 683 683
 FT CARBOHYD 680 680
 FT CARBOHYD 758 758
 FT MOD_RES 1068 1068
 FT CONFLICT 24 24
 FT CONFLICT 745 745
 FT CONFLICT 752 753
 FT CONFLICT 890 890
 FT CONFLICT 1128 1128
 FT CONFLICT 1146 1146
 FT CONFLICT 1164 1164
 SQ SEQUENCE 1298 AA; 145598 MW; 3DC469ED3C8BB3B1 CRC64;

 Query Match 22.7%; Score 43.5; DB 1; Length 1298;
 Best Local Similarity 34.5%; Pred. No. 13;
 Matches 10; Conservative 4; Mismatches 8; Indels 7; Gaps 1;

 QY 22 CSFXXARXIFKDK-----AXRTKLWIS 43
 DB 1054 CDFGLARDYKDPDYVRKGSARLPLKMA 1082

 RESULT 39
 VGR3 MOUSE STANDARD: PRT; 1363 AA.
 ID VGR3 MOUSE
 AC P35917;
 DT 01-JUN-1994 (rel. 29, Created)
 DT 01-JUN-1994 (rel. 29, Last sequence update)

AC P42837;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Hypothetical 101.7 kDa protein in EGT2-KRE1 Intergenic region.
GN YNL325C OR N0330.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Saccharomycetes; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycos.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=5288C / FY1676;
RA MEDLINE=95373280; PubMed=7645347;
RX Medfahl M., Nicoud J.-M., Levesque H., Galliardin C.;
RT "Sequencing analysis of a 15.4 kb fragment of yeast chromosome XIV
RT identifies the RPD3, PAS8 and KRE1 loci, five new open reading
RT frames.";
RL Yeast 11:567-572(1995).
CC -1- SIMILARITY: TO YEAST RSD1/SAC1, AND TO HUMAN KIAA0274.
CC -1- SIMILARITY: CONTAINS 1 SAC DOMAIN.
CC -----
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CC -----
CC
CC EMBL; Z46259; CAAB6373.1; -;
CC EMBL; Z71601; CAAB6256.1; -;
CC SGD; S0005269; YNL325C.
CC InterPro: IPR002013; SYJa-N.
CC Pfam: PF02383; SYJa-N: 1.
CC PROSITE: PS50275; SAC: 1.
CC DR Hypothetical protein; Transmembrane.
CC KW TRANSMEM 101 122 POTENTIAL.
CC FT DOMAIN 166 528 SAC.
CC FT SEQUENCE 879 AA; 101745 MW; 872B3231104185FA CRC64;
SQ

Query Match 23.4%; Score 45; DB 1; Length 879;
Best Local Similarity 60.0%; Pred. No. 4.8;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 30 IFKXDRFKLFWISY 44
Db 165 IFKDLDTKTFYSY 179

RESULT 37
SPML_SCHPO STANDARD; PRT: 422 AA.
ID SPML_SCHPO
AC Q92396;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Mitogen-activated protein kinase spml (Ec 2.7.1.1-) (MAP kinase spml)
DE (MAP kinase pmk1).
GN SPML OR PMK1 OR SPC119.08.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycos.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97098653; PubMed=8943330;
RX Toda T., Dhut S., Superti-Furga G., Gotoh G., Nishida E., Sugitara R.,
RA Kuno T.;
RT "The fission yeast pmk1+ gene encodes a novel mitogen-activated
RT protein kinase homolog which regulates cell integrity and functions

RT coordinately with the protein kinase C pathway.";
RL Mol. Cell. Biol. 16:6752-6764(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97280820; PubMed=9135147;
RA Zaitsevskaia-Carter T., Cooper J.A.;
RT "Spml, a stress-activated MAP kinase that regulates morphogenesis in
RN S.pombe.";
RN EMBO J. 16:1318-1331(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Wood V., Rajandream M.A., Barrell B.G., Skelton J., Churcher C.M.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: REGULATES CELL INTEGRITY AND FUNCTIONS COORDINATELY WITH
CC THE PROTEIN KINASE C PATHWAY (PKC1 AND PKC2). INVOLVED THE
CC REGULATION OF WALL ARCHITECTURE, CELL SHAPE, CYTOKINESIS IN
CC EXPONENTIAL AND STATIONARY PHASE, AND METABOLISM OF IONS.
CC -1- ENZYME REGULATION: ACTIVATED BY TYROSINE AND THREONINE
CC PHOSPHORYLATION BY SKH1/PEK1.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE SUBFAMILY.
CC -----
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CC -----
CC
CC EMBL; X98243; CAAB6899.1; -;
CC EMBL; U65405; AAC49707.1; -;
CC EMBL; AL022117; CAA17923.1; -;
CC HSSP; Q16539; IMFC
CC InterPro: IPR000719; Euk-Pkinase.
CC InterPro: IPR003527; Map_Kin.
CC InterPro: IPR002290; Ser_thr_pkinase.
CC Pfam: PF00069; Pkinase; 1.
CC SMART: SM00220; S_TKc; 1.
CC DR PROSITE: PS01351; MAPK: 1.
CC DR PROSITE: PS00107; PROTEIN_KINASE_ATP: 1.
CC DR PROSITE: PS50011; PROTEIN_KINASE_DOM: 1.
CC DR PROSITE: PS00108; PROTEIN_KINASE_ST: 1.
CC KW Transferrase; Serine/threonine-protein kinase; ATP-binding;
CC Cell cycle; Phosphorylation.
CC FT DOMAIN 21 314 PROTEIN KINASE.
CC FT NP_BIND 27 35 ATP (BY SIMILARITY).
CC FT BINDING 52 52 ATP (BY SIMILARITY).
CC FT ACT_SITE 149 149 BY SIMILARITY.
CC FT MOD_RES 186 186 PHOSPHORYLATION (ACTIVATES THE KINASE)
CC FT MOD_RES 188 188 (BY SIMILARITY).
CC FT MOD_RES 188 188 PHOSPHORYLATION (ACTIVATES THE KINASE)
CC FT DOMAIN 389 394 (BY SIMILARITY).
CC FT SEQUENCE 422 AA; 48261 MW; FD02521E64EBB82 CRC64;
SQ

Query Match 22.9%; Score 44; DB 1; Length 422;
Best Local Similarity 28.3%; Pred. No. 3.4;
Matches 13; Conservative 5; Mismatches 26; Indels 2; Gaps 1;

OY 1 ANAFLLXLRPGSL-XRXCXXXCSFFXARXIFPDAXTKLFWISY 44
Db 143 ANVHRDLKPGNLVYNADCEIKICDFGLRCSENPENPGFWTEY 188

RESULT 38
VGR3_HUMAN STANDARD; PRT: 1298 AA.
ID VGR3_HUMAN
AC P35916;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)

Query Match 30.2%; Score 58; DB 1; Length 400;
 Best Local Similarity 32.5%; Pred. No. 0.0098;
 Matches 13; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

5 LXXLRGSLRXCKXKXCSFXXRXIFKDXRTKLFWISY 44
 46 LELFPGNLEKCEYECIEYEEAREVEFNVTDFWRRY 85

RESULT 35
 PRTS_MOUSE
 ID PRTS_MOUSE STANDARD; PRT; 675 AA.
 AC 008761: P43483;
 DT 01-NOV-1995 (rel. 32, Created)
 DT 01-NOV-1995 (rel. 32, Last sequence update)
 DT 01-MAR-2002 (rel. 41, Last annotation update)
 DE Vitamin K-dependent protein S precursor.
 GN PROS1 OR PROS.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94198297; PubMed=8148380;
 RA Chu M.D., Sun J., Bird P.I.;
 RT "Cloning and sequencing of a cDNA encoding the murine vitamin K-
 RT dependent protein S.";
 RL Biochim. Biophys. Acta 1217:325-328(1994).
 RN [2]
 RP SEQUENCE OF 33-675 FROM N.A.
 RX MEDLINE=94302659; PubMed=8029814;
 RA Lu D., Schmidt D.K., Long G.L.;
 RT "Structure of mouse protein S as determined by PCR amplification and
 RT DNA sequencing of cDNA.";
 RL Thromb. Res. Suppl. 74:135-142(1994).
 CC -1- FUNCTION: ANTICOAGULANT PLASMA PROTEIN; IT IS A COFACTOR TO
 CC ACTIVATED PROTEIN C IN THE DEGRADATION OF COAGULATION FACTORS VA
 CC AND VIIIA. IT HELP TO PREVENT COAGULATION AND STIMULATING
 CC FIBRINOLYSIS.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- SIMILARITY: CONTAINS 2 LAMININ G-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 4 EGF-LIKE DOMAINS.
 CC
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 CC
 CC EMBL: Z25469; CAAB0961.1; -
 CC EMBL: L27439; AAA40006.1; -
 CC HSSP: P00740; 1CRH.
 CC MGD: MGI:1095733; Prosl.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001791; Laminin_G.
 DR InterPro: IPR000294; Vitk_dep_GLA.
 DR Pfam: PF00008; EGF_4.
 DR Pfam: PF00594; gla; 1.
 DR Pfam: PF00054; laminin_G; 1.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00179; EGF_CA; 3.
 DR SMART: SM00001; EGF_like; 1.
 DR SMART: SM00069; GLA; 1.
 DR SMART: SM00282; LamG; 2.

DR PROSITE: PS00010; ASX_HYDROXYL; 4.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 3.
 DR PROSITE: PS01187; EGF_CA; 3.
 DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE: PS50025; LAM_G_DOMAIN; 2.
 KW Plasma; Gamma-carboxyglutamic acid; Calcium; Vitamin K; Zymogen;
 KW Blood coagulation; Hydroxylation; Glycoprotein; Signal; Repeat;
 KW EGF-like domain.
 FT SIGNAL 1 24
 FT PROPEP 25 41 BY SIMILARITY.
 FT CHAIN 42 675 VITAMIN K-DEPENDENT PROTEIN S.
 FT DOMAIN 42 86 GLA.
 FT DOMAIN 87 116 THROMBIN-SENSITIVE.
 FT DOMAIN 117 155 EGF-LIKE 1.
 FT DOMAIN 157 200 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 201 242 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 243 283 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 299 475 LAMININ G-LIKE 1.
 FT DOMAIN 484 665 LAMININ G-LIKE 2.
 FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID
 FT MOD_RES 48 48 (BY SIMILARITY).
 FT MOD_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID
 FT MOD_RES 55 55 (BY SIMILARITY).
 FT MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID
 FT MOD_RES 57 57 (BY SIMILARITY).
 FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID
 FT MOD_RES 61 61 (BY SIMILARITY).
 FT MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID
 FT MOD_RES 66 66 (BY SIMILARITY).
 FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID
 FT MOD_RES 67 67 (BY SIMILARITY).
 FT MOD_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID
 FT MOD_RES 70 70 (BY SIMILARITY).
 FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID
 FT MOD_RES 73 73 (BY SIMILARITY).
 FT MOD_RES 73 73 GAMMA-CARBOXYGLUTAMIC ACID
 FT MOD_RES 77 77 (BY SIMILARITY).
 FT MOD_RES 77 77 GAMMA-CARBOXYGLUTAMIC ACID
 FT MOD_RES 136 136 (BY SIMILARITY).
 FT DISULFID 121 134 HYDROXYLATION (BY SIMILARITY).
 FT DISULFID 126 143 BY SIMILARITY.
 FT DISULFID 145 154 BY SIMILARITY.
 FT DISULFID 161 175 BY SIMILARITY.
 FT DISULFID 171 184 BY SIMILARITY.
 FT DISULFID 186 199 BY SIMILARITY.
 FT DISULFID 205 217 BY SIMILARITY.
 FT DISULFID 212 226 BY SIMILARITY.
 FT DISULFID 228 241 BY SIMILARITY.
 FT DISULFID 247 256 BY SIMILARITY.
 FT DISULFID 252 265 BY SIMILARITY.
 FT DISULFID 267 282 BY SIMILARITY.
 FT CARBOHYD 499 499 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 509 509 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CONFLICT 493 493 F -> L (IN REF. 2).
 SQ SEQUENCE 675 AA; 74934 MW; 79D51203E85AF31F CRC64;

Query Match 29.2%; Score 56; DB 1; Length 675;
 Best Local Similarity 29.5%; Pred. No. 0.036;
 Matches 13; Conservative 29; Mismatches 25; Indels 0; Gaps 0;

1 ANAFLXLRGSLRXCKXKXCSFXXRXIFKDXRTKLFWISY 44
 42 ANLFEETMKGNLRECIELCKEAREVEFNPTDVFYPRY 85

RESULT 36
 YN65_YEAST
 ID YN65_YEAST STANDARD; PRT; 879 AA.


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FT DOMAIN 109 187 KRINGLE 1.
FT DOMAIN 214 292 KRINGLE 2.
FT DOMAIN 367 625 SERINE PROTEASE.
FT SITE 199 200 CLEAVAGE (BY THROMBIN).
FT SITE 317 318 CLEAVAGE (BY FACTOR XA).
FT SITE 366 367 CLEAVAGE (BY FACTOR XI).
FT ACT_SITE 409 409 CHARGE RELAY SYSTEM.
FT ACT_SITE 465 465 CHARGE RELAY SYSTEM.
FT MOD_RES 571 571 CHARGE RELAY SYSTEM.
FT MOD_RES 50 50 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 51 51 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 58 58 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 63 63 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 64 64 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 73 73 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 76 76 GAMMA-CARBOXYGLUTAMIC ACID.
FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .).

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Query Match 32.8%; Score 63; DB 1; Length 625;
Best Local Similarity 34.18; Pred. No. 0.0019;
Matches 14; Conservative 3; Mismatches 24; Indels 0; Gaps 0;

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QY 4 FLXLRPGSLRXCKKXCSFXXARXIFKDXRTKFLWISY 44
DB 48 FLEEVKRNKNERCLEPCREAFALBSLSTDAFWAKY 88

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RESULT 33

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PRTS_RAT ID PRTS_RAT STANDARD; PRT; 675 AA.
AC P53813;

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DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)

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DE Vitamin K-dependent protein S precursor.
GN PROSI OR PROS.
OS Rattus norvegicus (Rat).

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OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

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ON NCBI_Taxid=10116;

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RP SEQUENCE FROM N.A.

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RC TISSUE=Liver;

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RX MEDLINE=95332263; PubMed=7608128;

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RA Yasuda F., Hayashi T., Tanitame K., Nishiohara J., Suzuki K.;
RA "Molecular cloning and functional characterization of rat plasma
RA protein S."

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RL J. Biochem. 117:374-383(1995).

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CC -1- FUNCTION: ANTICOAGULANT PLASMA PROTEIN; IT IS A COFACTOR TO
CC ACTIVATED PROTEIN C IN THE DEGRADATION OF COAGULATION FACTORS VA
CC AND VIIIA. IT HELPS TO PREVENT COAGULATION AND STIMULATING
CC FIBRINOLYSIS.

```

```

CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: PLASMA.

```

```

CC -1- SIMILARITY: CONTAINS 2 LAMININ G-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 4 EGF-LIKE DOMAINS.

```

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DR EMBL: S78744; AAC60704.1; -

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DR HSP: P00740; 1CFH.

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DR InterPro: IPR000152; Asx_hydroxyl.

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DR InterPro: IPR000561; EGF-like.

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DR InterPro: IPR001881; EGF_Ca.

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DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001791; Laminin_G.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF; 4.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00054; laminin_G; 1.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 3.
DR SMART: SM00001; EGF_like; 1.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00282; LamG; 2.
DR PROSITE: PS00010; ASX_HYDROXYL; 4.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 3.
DR PROSITE: PS01187; EGF_CA; 3.
DR PROSITE: PS00011; GLI_CARBOXYLATION; 1.
DR PROSITE: PS50025; LAM_G_DOMAIN; 1.
KW Plasma; Gamma-carboxyglutamic acid; Calcium; Vitamin K; Zymogen;
KW Blood coagulation; Hydroxylation; Glycoprotein; Signal; Repeat;
KW EGF-like domain.
FT SIGNAL 1 24 BY SIMILARITY.
FT PROPEP 25 41 BY SIMILARITY.
FT CHAIN 42 675 VITAMIN K-DEPENDENT PROTEIN S.
FT DOMAIN 42 86 GLA.
FT DOMAIN 87 116 THROMBIN-SENSITIVE.
FT DOMAIN 117 155 EGF-LIKE 1.
FT DOMAIN 157 200 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 201 242 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 243 283 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 299 475 LAMININ G-LIKE 1.
FT DOMAIN 484 665 LAMININ G-LIKE 2.
FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT MOD_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT MOD_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT MOD_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT MOD_RES 73 73 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT MOD_RES 77 77 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT MOD_RES 136 136 HYDROXYLATION (BY SIMILARITY).
FT DISULFID 121 134 BY SIMILARITY.
FT DISULFID 126 143 BY SIMILARITY.
FT DISULFID 145 154 BY SIMILARITY.
FT DISULFID 161 175 BY SIMILARITY.
FT DISULFID 171 184 BY SIMILARITY.
FT DISULFID 186 199 BY SIMILARITY.
FT DISULFID 205 217 BY SIMILARITY.
FT DISULFID 212 226 BY SIMILARITY.
FT DISULFID 228 241 BY SIMILARITY.
FT DISULFID 247 256 BY SIMILARITY.
FT DISULFID 252 265 BY SIMILARITY.
FT DISULFID 267 282 BY SIMILARITY.
FT CARBOHYD 499 499 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 509 509 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 675 AA; 74626 MW; B4338F56B86075 CRC64;

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Query Match 32.8%; Score 63; DB 1; Length 675;
Best Local Similarity 31.8%; Pred. No. 0.0021;

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RA Park C.H., Tullinsky A.;
 RT "Three-dimensional structure of the kringle sequence: structure of
 RL prothrombin fragment 1.";
 RN Biochemistry 25:3977-3982(1986).
 [5]
 RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF ACTIVATION PEPTIDE 1.
 RA MEDLINE=91311686; PubMed=1856869;
 RT Seshadri T.-P., Tullinsky A., Skrzypczak-Jankun E., Park C.H.;
 RL "Structure of bovine prothrombin fragment 1 refined at 2.25-A
 resolution.";
 RN J. Mol. Biol. 220:481-494(1991).
 [6]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF ACTIVATION PEPTIDE 1.
 RA MEDLINE=92190185; PubMed=1547238;
 RT Soriano-Garcia M., Padmanabhan K., de Vos A.M., Tullinsky A.;
 RL "The Ca2+ ion and membrane binding structure of the Gla domain of Ca-
 prothrombin fragment 1.";
 RN Biochemistry 31:2554-2566(1992).
 [7]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RA MEDLINE=92218459; PubMed=1560020;
 RT Martin P.D., Robertson W., Turk D., Huber R., Bode W., Edwards B.F.P.;
 RL "The structure of residues 7-16 of the A alpha-chain of human
 fibrinogen bound to bovine thrombin at 2.3-A resolution.";
 RN J. Biol. Chem. 267:7911-7920(1992).
 [8]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RA MEDLINE=92389319; PubMed=1518046;
 RT Brandstetter H., Turk D., Hoeffken H.W., Grosse D., Stuezebecher J.,
 Martin P.D., Edwards B.F.P., Bode W.;
 RL "Refined 2.3 A x-ray crystal structure of bovine thrombin complexes
 formed with the benzamidine and arginine-based thrombin inhibitors
 NAPAP, 4-TAPAP and MQPA. A starting point for improving
 antithrombotics.";
 RN J. Mol. Biol. 226:1085-1089(1992).
 [9]
 RP X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF COMPLEX WITH ORNITHODORIN.
 RA MEDLINE=97102783; PubMed=8947023;
 RT van de Loch A., Stubbs M.T., Bode W., Friedrich T., Bollschweiler C.,
 Hoeffken W., Huber R.;
 RL "The ornithodorin-thrombin crystal structure, a key to the TAP
 enigma?";
 RN EMBO J. 15:6011-6017(1996).
 [10]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF COMPLEX WITH TRIABIN.
 RA MEDLINE=98004486; PubMed=9342325;
 RT Fuentes-Prior P., Noeske-Jungblut C., Donner P., Schleuning W.D.,
 Huber R., Bode W.;
 RL "Structure of the thrombin complex with triabin, a lipocalin-like
 exosite-binding inhibitor derived from a triatomine bug.";
 RN Proc. Natl. Acad. Sci. U.S.A. 94:11845-11850(1997).
 [11]
 RP GENE STRUCTURE.
 RA MEDLINE=86077733; PubMed=3000440;
 RT Irwin D.M., Ahern K.G., Pearson G.D., McGillivray R.T.A.;
 RL "Characterization of the bovine prothrombin gene.";
 RN Biochemistry 24:6854-6861(1985).
 CC -1- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS
 CC FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,
 CC AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: SYNTHESIZED IN THE LIVER; FOUND IN PLASMA.
 CC -1- PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
 CC RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL
 CC ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES
 CC ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY
 CC CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
 CC OF PROTHROMBIN TO THROMBIN.
 CC -1- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A
 CC PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &
 CC FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES
 CC THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &
 CC HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR

CC V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
 CC THROMBIN.
 CC -1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL
 CC FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
 CC BY FACTOR XA.
 CC -1- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 CC -1- DATABASE: NAME=Prozyme technical fact sheet;
 CC WWW="http://www.prozyme.com/technical/thrombdata.html".
 CC -----
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 CC -----
 CC EMBL: V00135; CAA23451.1; -;
 CC EMBL: J00041; AAA0781.1; -;
 CC PIR: A00915; TBRO.
 CC PIR: S02537; S02537.
 CC PDB: 1B8R; 31-JAN-94.
 CC PDB: 1ETR; 31-JAN-94.
 CC PDB: 1ETS; 31-JAN-94.
 CC PDB: 1ETT; 31-JAN-94.
 CC PDB: 1HRT; 31-JAN-94.
 CC PDB: 2PFI; 31-JAN-94.
 CC PDB: 2PFI; 31-JAN-94.
 CC PDB: 2SPT; 31-MAY-94.
 CC PDB: 1MKW; 07-JUL-97.
 CC PDB: 1MKX; 07-JUL-97.
 CC PDB: 1TBR; 14-OCT-96.
 CC PDB: 1TBR; 14-OCT-96.
 CC PDB: 1TOC; 23-JUL-97.
 CC PDB: 1VIT; 21-APR-97.
 CC PDB: 1YCP; 06-MAY-98.
 CC PDB: 1A0H; 17-JUN-98.
 CC PDB: 1AVG; 16-FEB-99.
 CC MEROPS: S01.217; -;
 CC InterPro: IPR001314; Chymotrypsin.
 CC InterPro: IPR002383; GLA_blood.
 CC InterPro: IPR000001; Kringle.
 CC InterPro: IPR003966; Prothrombin.
 CC InterPro: IPR001254; Trypsin.
 CC InterPro: IPR000294; Vitk_dep_GLA.
 CC Pfam: PF00594; gla; 1.
 CC Pfam: PF00051; kringle; 2.
 CC Pfam: PF00089; trypsin; 1.
 CC PRINTS: PR00722; CHYMOTRYPSIN.
 CC PRINTS: PR00001; GLABLOOD.
 CC PRINTS: PR00018; KRINGLE.
 CC PRINTS: PR01505; PROTHROMBIN.
 CC SMART: SM00069; GLA; 1.
 CC SMART: SM00130; KR; 2.
 CC SMART: SM00020; Tryp_Spc; 1.
 CC PROSITE: PS00011; GLU_CARBOXYLATION; 1.
 CC PROSITE: PS00021; KRINGLE_1; 2.
 CC PROSITE: PS50070; KRINGLE_2; 2.
 CC PROSITE: PS50240; TRYPSIN_DOM; 1.
 CC PROSITE: PS00134; TRYPSIN_HIS; 1.
 CC PROSITE: PS00135; TRYPSIN_SER; 1.
 CC Blood coagulation; Plasma; Calcium-binding; Glycoprotein; Repeat;
 CC Vitamin K; zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver;
 CC Hydrolyse; Serine protease; Signal; 3D-structure.
 CC SIGNAL
 CC PROPEP 1 24
 CC CHAIN 25 43
 CC CHAIN 44 625
 CC PEPTIDE 44 199
 CC PEPTIDE 200 317
 CC CHAIN 318 366
 CC CHAIN 367 625
 CC PROTHROMBIN.
 CC ACTIVATION PEPTIDE (FRAGMENT 1).
 CC ACTIVATION PEPTIDE (FRAGMENT 2).
 CC THROMBIN LIGHT CHAIN (A).
 CC THROMBIN HEAVY CHAIN (B).

ID PRT2-BOVIN STANDARD: PRT: 396 AA.
AC P00744;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Vitamin K-dependent protein Z.
GN PROZ.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
ON NCBI_TaxId=9913;
RX MEDLINE=914709; PubMed=2129367;
RT "A new trisaccharide sugar chain linked to a serine residue in the first EGF-like domain of clotting factors VII and IX and protein Z.";
RT Adv. Exp. Med. Biol. 281:121-131(1990).
CC -1- FUNCTION: APPEARS TO ASSIST HEMOSTASIS BY BINDING THROMBIN AND PROMOTING ITS ASSOCIATION WITH PHOSPHOLIPID VESICLES.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- SIMILARITY: ALTHOUGH HOMOLOGOUS WITH THE VITAMIN K-DEPENDENT CLOTTING FACTORS, IT HAS LOST TWO OF THE ESSENTIAL CATALYTIC RESIDUES AND HAS NO ENZYMIC ACTIVITY.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
DR PIR: A2171; KXBOZ.
DR HSSP: P00740; 1CFM.
DR MEROPS: S01.979; -.
DR GlycoSuiteDB: P00744; -.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF-2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Trypsin.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; gla_1.
DR Pfam: PF00089; trypsin_1.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00181; EGF_2.
DR SMART: SM00069; GLA_1.
DR SMART: SM00020; TRYP_SPE_1.
DR PROSITE: PS00010; ASX_HYDROXYL_1.
DR PROSITE: PS01186; EGF_1_1.
DR PROSITE: PS01186; EGF_2_1.
DR PROSITE: PS00011; GLU_CARBOXYLATION_1.
DR PROSITE: PS00240; TRYPsin_DOM_1.
KW Plasma; Glycoprotein; Gamma-carboxyglutamic acid; Hydroxylation;
KW Calcium; Serine protease homolog; Vitamin K; EGF-like domain.
FT DOMAIN 47 83 EGF-LIKE 1.
FT DOMAIN 85 126 EGF-LIKE 2.
FT DOMAIN 135 357 SERINE PROTEASE.
FT MOD_RES 7 7 GAMMA-CARBOXYGLUTAMIC ACID.

FT MOD_RES 8 8 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 11 11 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 15 15 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 17 17 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 20 20 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 21 21 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 26 26 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 27 27 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 30 30 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 33 33 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 36 36 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 40 40 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 64 64 GAMMA-CARBOXYGLUTAMIC ACID.
FT DISULFID 51 62 HYDROXYLATION.
FT DISULFID 56 71 BY SIMILARITY.
FT DISULFID 73 82 BY SIMILARITY.
FT DISULFID 89 101 BY SIMILARITY.
FT DISULFID 97 110 BY SIMILARITY.
FT DISULFID 112 125 BY SIMILARITY.
FT CARBOHYD 53 53 O-LINKED (GLC. . .).
FT CARBOHYD 59 59 /FTID-CAR_000032.
FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .).
FT CARBOHYD 388 388 O-LINKED.
SQ SEQUENCE 396 AA; 43112 MW; 04C5D7A35849B116 CRC64;

Query Match 32.8%; Score 63; DB 1; Length 396;
Best Local Similarity 35.0%; Pred. No. 0.0012;
Matches 14; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 5 LXXLRGCSLXKCKXXKXXCSFXKXRXIFKDXKPKLWISY 44
Db 6 LEELEFGEHLKEKCEWEICVYEAAREVFEDDETDERMRY 45

RESULT 32

ID THR3-BOVIN STANDARD: PRT: 625 AA.
AC P00735;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Prothrombin precursor (EC 3.4.21.5).
GN F2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
ON NCBI_TaxId=9913;
RX MEDLINE=88245190; PubMed=3379642;
RX Irwin D.M., Robertson K.A., Macgillivray R.F.A.;
RT "Structure and evolution of the bovine prothrombin gene.";
RL J. Mol. Biol. 200:31-45(1988).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=84203525; PubMed=6326805;
RA McGillivray R.F.A., Davie E.W.;
RT "Characterization of bovine prothrombin mRNA and its translation product.";
RL Biochemistry 23:1626-1634(1984).
RN (3)
RP SEQUENCE OF 44-625, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RA Magnusson S., Sottrup-Jensen L., Petersen T.E., Claess H.;
RL (In) Henker H.C., Veltkamp J.J. (eds.);
RL Boerhaave symposium on prothrombin and related coagulation factors,
pp.25-46, Leiden University Press, Leiden (1975).
RN (4)
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF ACTIVATION PEPTIDE 1.
RX MEDLINE=86296631; PubMed=3741841;

[9]
RP VARIANT TOKUSHIMA.
RX MEDLINE-94129009; PubMed-8298131;
RA Hayashi T., Nishioka J., Shigekiyo T., Saito S., Suzuki K.;
RT "Protein S Tokushima: abnormal molecule with a substitution of Glu
for Lys-155 in the second epidermal growth factor-like domain of
protein S.";
RL Blood 83:683-690(1994).
CC -1- FUNCTION: ANTICOAGULANT PLASMA PROTEIN. IT IS A COFACTOR TO
CC ACTIVATED PROTEIN C IN THE DEGRADATION OF COAGULATION FACTORS VA
CC AND VIIIA. IT HELPS TO PREVENT COAGULATION AND STIMULATING
CC FIBRINOLYSIS.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- DISEASE: DEFECTS IN PROS1 ARE ASSOCIATED WITH AN INCREASED RISK TO
CC DEVELOP THROMBOTIC DISEASE (THROMBOPHILIA).
CC -1- SIMILARITY: CONTAINS 2 LAMININ G-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 4 EGF-LIKE DOMAINS.

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DR EMBL; M57853; AAA60357.1; -;
DR EMBL; M57840; AAA60357.1; JOINED.
DR EMBL; M57841; AAA60357.1; JOINED.
DR EMBL; M57842; AAA60357.1; JOINED.
DR EMBL; M57844; AAA60357.1; JOINED.
DR EMBL; M57845; AAA60357.1; JOINED.
DR EMBL; M57846; AAA60357.1; JOINED.
DR EMBL; M57847; AAA60357.1; JOINED.
DR EMBL; M57848; AAA60357.1; JOINED.
DR EMBL; M57849; AAA60357.1; JOINED.
DR EMBL; M57850; AAA60357.1; JOINED.
DR EMBL; M57851; AAA60357.1; JOINED.
DR EMBL; M57852; AAA60357.1; JOINED.
DR EMBL; M57854; AAA60180.1; -;
DR EMBL; M36551; AAA60180.1; JOINED.
DR EMBL; M36552; AAA60180.1; JOINED.
DR EMBL; M36553; AAA60180.1; JOINED.
DR EMBL; M36554; AAA60180.1; JOINED.
DR EMBL; M36555; AAA60180.1; JOINED.
DR EMBL; M36556; AAA60180.1; JOINED.
DR EMBL; M36557; AAA60180.1; JOINED.
DR EMBL; M36558; AAA60180.1; JOINED.
DR EMBL; M36559; AAA60180.1; JOINED.
DR EMBL; M36560; AAA60180.1; JOINED.
DR EMBL; M36561; AAA60180.1; JOINED.
DR EMBL; M36563; AAA60180.1; JOINED.
DR EMBL; Y00692; CAA68687.1; -;
DR EMBL; Y00692; CAA68687.1; -;
DR EMBL; M15036; AAA36479.1; -;
DR EMBL; M15036; AAA36479.1; -;
DR EMBL; M15036; AAA36479.1; -;
DR PIR; A35610; A35610.
DR PIR; A26157; A26157.
DR PIR; A25891; A25891.
DR PIR; S02424; S02424.
DR PIR; S09519; S09519.
DR HSSP; P07204; 1EGT.
DR MIM; 176880; -;
DR InterPro; IPR001052; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_Blood.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF; 4.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00054; laminin_G; 1.
DR PRINTS; PR00001; GLABLOOD.

DR SMART; SM00179; EGF_CA; 3.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00282; LamG; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 4.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS01187; EGF_CA; 3.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50025; LAM_G_DOMAIN; 2.
KW Plasma: gamma-carboxyglutamic acid; Calcium; Vitamin K; Zymogen;
KW Blood coagulation; Hydroxylation; Glycoprotein; Signal; Repeat;
KW EGF-like domain; Polymorphism; Disease mutation; Thrombophilia.
KW SIGNAL
FT PROPE 1 24
FT CHAIN 25 41
FT CHAIN 42 676
FT DOMAIN 42 86
FT DOMAIN 87 116
FT DOMAIN 117 155
FT DOMAIN 157 200
FT DOMAIN 201 242
FT DOMAIN 243 283
FT DOMAIN 299 475
FT DOMAIN 484 666
FT MOD_RES 47 47
FT MOD_RES 48 48
FT MOD_RES 55 55
FT MOD_RES 57 57
FT MOD_RES 60 60
FT MOD_RES 61 61
FT MOD_RES 66 66
FT MOD_RES 67 67
FT MOD_RES 70 70
FT MOD_RES 73 73
FT MOD_RES 77 77
FT MOD_RES 136 136
FT DISULFID 121 134
FT DISULFID 126 143
FT DISULFID 145 154
FT DISULFID 161 175
FT DISULFID 171 184
FT DISULFID 186 199
FT DISULFID 205 217
FT DISULFID 212 226
FT DISULFID 228 241
FT DISULFID 247 265
FT DISULFID 252 265
FT DISULFID 267 282
FT CARBOHYD 499 499
FT CARBOHYD 509 509
FT CARBOHYD 530 530
FT VARIANT 196 196
FT VARIANT 258 258
FT VARIANT 501 501
FT VARIANT 501 501
FT CONFLICT 11 11
FT CONFLICT 26 26
FT SEQUENCE 676 AA: 75122 MW: 2888A04F85403F23 CRC64;

Query Match 33.3%; Score 64; DB 1; Length 676;
Best local similarity 31.8%; Pred. No. 0.0014; Matches 22; Indels 0; Gaps 0;
Matches 14; Conservative 8; Mismatches 22; Indels 0; Gaps 0;
QY 1 ANAFLXLRPGSLRXKXQCSPFYXARXIFDAXRFLFWISY 44
DB 42 ANSLLEETKQGNLEKEICIELCNKEAREVFEENDETDFYFPKY 85
RESULT 31
PRT2_BOVIN

DR InterPro: IPR001791; Laminin_G.
 DR InterPro: IPR000294; Vitk_dep_GLA.
 DR Pfam: PF00008; EGF_4.
 DR Pfam: PF00594; gla; 1.
 DR Pfam: PF00054; laminin_G; 1.
 DR SMART: SM00179; EGF_CA; 3.
 DR SMART: SM00069; GLA; 1.
 DR SMART: SM00282; LamG; 2.
 DR PROSITE: PS00010; ASX_HYDROXYL; 4.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 3.
 DR PROSITE: PS01187; EGF_CA; 3.
 DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE: PS50025; LAM_G_DOMAIN; 2.
 DR Plasma; Gamma-carboxyglutamic acid; Calcium; Vitamin K; zymogen;
 KW Blood coagulation; Hydroxylation; Glycoprotein; Repeat;
 KW EGF-like domain.
 FT NON_TER 1 1
 FT PROPEP <1 14
 FT CHAIN 15 649
 FT DOMAIN 15 59
 FT DOMAIN 60 89
 FT DOMAIN 90 128
 FT DOMAIN 130 173
 FT DOMAIN 173 215
 FT DOMAIN 215 256
 FT DOMAIN 272 448
 FT DOMAIN 457 639
 FT MOD_RES 20 20
 FT MOD_RES 21 21
 FT MOD_RES 28 28
 FT MOD_RES 30 30
 FT MOD_RES 33 33
 FT MOD_RES 34 34
 FT MOD_RES 39 39
 FT MOD_RES 40 40
 FT MOD_RES 43 43
 FT MOD_RES 46 46
 FT MOD_RES 50 50
 FT MOD_RES 109 109
 FT DISULFID 94 107
 FT DISULFID 99 116
 FT DISULFID 118 127
 FT DISULFID 134 148
 FT DISULFID 144 157
 FT DISULFID 159 172
 FT DISULFID 178 190
 FT DISULFID 185 199
 FT DISULFID 201 214
 FT DISULFID 220 229
 FT DISULFID 225 238
 FT DISULFID 240 255
 FT CARBOHYD 472 482
 FT CARBOHYD 482 482
 FT CARBOHYD 503 503
 SQ SEQUENCE 649 AA: 72402 MW: 57C13D31CD7EB6B CRC64;

Query Match 33.3%; Score 64; DB 1; Length 649;
 Best Local Similarity 31.8%; Pred. No. 0.0013;
 Matches 14; Conservative 8; Mismatches 22; Indels 0; Gaps 0;

OY 1 ANAFLLXLRPGSLXRXCKXXCSEFXAXRIEFDANKTKLFMTSY 44
 DB 15 ANSMLEETKQGNLECEICELCNKEAREVFEFNDETDYFYPKY 58
 RESULT 30
 PRIS_HUMAN STANDARD; PRT; 676 AA.
 AC P07225; Q15518;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Vitamin K-dependent protein S precursor.
 GN PROS1 OR PROS.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9108444; PubMed=2148110;
 RA Schmidt D.K., Tatro A.V., Phelps L.G., Tomczak J.A., Long G.L.;
 RT "Organization of the human protein S genes."
 RL Biochemistry 29:7845-7852(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Ploos van Amstel H.K.;
 RL Submitted (Aug-1987) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 27-676 FROM N.A.
 RX MEDLINE=91084445; PubMed=2148111;
 RA Ploos van Amstel H.K., Reitsma P.H., der Logt C.P., Bertina R.M.;
 RT "Intron-exon organization of the active human protein S gene PS alpha
 and its pseudogene PS beta: duplication and silencing during primate
 evolution."
 RL Biochemistry 29:7853-7861(1990).
 RN [4]
 RP SEQUENCE OF 1-42 FROM N.A.
 RX MEDLINE=88005138; PubMed=2820795;
 RA Ploos van Amstel H.K., van der Zanden A.L., Reitsma P.H.,
 RA Bertina R.M.;
 RT "Human protein S cDNA encodes Phe-16 and Tyr 222 in consensus
 sequences for the post-translational processing."
 RL FEBS Lett. 222:186-190(1987).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87092407; PubMed=3467362;
 RA Hoskins J., Norman D.K., Beckmann R.J., Long G.L.;
 RT "Cloning and characterization of human liver cDNA encoding a protein
 S precursor."
 RL Proc. Natl. Acad. Sci. U.S.A. 84:349-353(1987).
 RN [6]
 RP SEQUENCE OF 27-676 FROM N.A.
 RX MEDLINE=86313649; PubMed=2944113;
 RA Lundwall A., Dackowski W., Cohen E., Shaffer M., Mahr A., Dahlback B.,
 RA Stenflo J., Wydro R.;
 RT "Isolation and sequence of the cDNA for human protein S, a regulator
 of blood coagulation."
 RL Proc. Natl. Acad. Sci. U.S.A. 83:6716-6720(1986).
 RN [7]
 RP VARIANT HEERLEN.
 RX MEDLINE=90335440; PubMed=2143091;
 RA Bertina R.M., Ploos van Amstel H.K., van Wijngaarden A.,
 RA Coenen J., Leemhuis M.P., Deutz-Terlouw P.P., van der Linden I.K.,
 RA Reitsma P.H.;
 RT "Heerlen polymorphism of protein S, an immunologic polymorphism due
 to dimorphism of residue 460."
 RL Blood 76:538-548(1990).
 RN [8]
 RP VARIANT SER-258.
 RA Cooper D.N.;
 RL Unpublished observations (SEP-1993).


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RESULT 27
PRTS_BOVIN STANDARD: PRT: 675 AA.
ID PRTS_BOVIN STANDARD: PRT: 675 AA.
AC P07224;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Vitamin K-dependent protein S precursor.
GN PROS1 OR PROS.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-86233400; PubMed-2940598;
RA Dahlback B., Lundwall A., Stenflo J.;
RT "Primary structure of bovine vitamin K-dependent protein S.";
RN [2]
RP Proc. Natl. Acad. Sci. U.S.A. 83:4199-4203(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-86168236; PubMed-2937785;
RA Dahlback B., Lundwall A., Stenflo J.;
RT "Localization of thrombin cleavage sites in the amino-terminal region
of bovine protein S.";
RN [4]
RP J. Biol. Chem. 261:5111-5115(1986).
RN [5]
RP FUNCTION: ANTICOAGULANT PLASMA PROTEIN; IT IS A COFACTOR TO
ACTIVATED PROTEIN C IN THE DEGRADATION OF COAGULATION FACTORS VA
AND VIIIA. IT HELP TO PREVENT COAGULATION AND STIMULATING
FIBRINOLYSIS.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- SIMILARITY: CONTAINS 2 LAMININ G-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 4 EGF-LIKE DOMAINS.
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M13044; AAA30757.1; -
DR EMBL; X12891; CAA31382.1; -
DR PIR; A24759; A24759.
DR HSP; P00740; ICFH.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF-like.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001791; Laminin_G.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 4.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00054; laminin_G; 1.
DR PRINTS; PR00001; laminin_G; 1.
DR SMART; SM00179; EGF_CA; 3.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 4.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS01187; EGF_CA; 3.
DR PROSITE; PS00011; GLT_CARBOXYLATION; 1.

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DR PROSITE; PS00025; LAM_G_DOMAIN; 2.
KW Plasma; Gamma-carboxyglutamic acid; Calcium; Vitamin K; Zymogen;
KW Blood coagulation; Hydroxylation; Glycoprotein; Signal; Repeat;
KW EGF-like domain.
FT SIGNAL 1 24
FT PROPEP 25 41
FT CHAIN 42 675
FT DOMAIN 42 86
FT DOMAIN 87 116
FT DOMAIN 117 155
FT DOMAIN 157 200
FT DOMAIN 201 242
FT DOMAIN 243 283
FT DOMAIN 299 475
FT DOMAIN 484 665
FT MOD_RES 47 47
FT MOD_RES 48 48
FT MOD_RES 55 55
FT MOD_RES 57 57
FT MOD_RES 60 60
FT MOD_RES 61 61
FT MOD_RES 66 66
FT MOD_RES 67 67
FT MOD_RES 70 70
FT MOD_RES 73 73
FT MOD_RES 77 77
FT MOD_RES 136 136
FT DISULFID 121 134
FT DISULFID 126 143
FT DISULFID 145 154
FT DISULFID 161 175
FT DISULFID 171 184
FT DISULFID 186 199
FT DISULFID 205 217
FT DISULFID 212 226
FT DISULFID 228 241
FT DISULFID 247 256
FT DISULFID 252 265
FT DISULFID 267 282
FT CARBOHYD 499 499
FT CARBOHYD 509 509
SQ SEQUENCE 675 AA; 75132 MW; CF7EC5HC1C318DEE CRC64;

Query Match 34.4%; Score 66; DB 1; Length 675;
Best Local Similarity 34.1%; Pred. No. 0.0006;
Matches 15; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

OY 1 ANAFXXLRGSLRXCKXXCFSXXRXIFKAXRKLFWISY 44
DB 42 ANTLLEETKKNLRECEIEELCKKEPARELFENNPEYFYRY 85

RESULT 28
PRTS_RABIT STANDARD: PRT: 646 AA.
ID PRTS_RABIT STANDARD: PRT: 646 AA.
AC P98118;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Vitamin K-dependent protein S precursor (Fragment).
GN PROS1 OR PROS.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-94039141; PubMed-8223642;
RA He X., Dahlback B.;
RT "Molecular cloning, expression and functional characterization of
rabbit anticoagulant vitamin-K-dependent protein S.";
RT Eur. J. Biochem. 217:857-865(1993).

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FA9_CANFA STANDARD: PRT: 452 AA.

AC P19540;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Coagulation factor IX precursor (EC 3.4.21.22) (Christmas factor).

GN F9.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=90311364; PubMed=2367529;

RA Axelrod J.H., Read M.S., Brinkhous K.M., Verma I.M.;

RT "Phenotypic correction of factor IX deficiency in skin fibroblasts of hemophilic dogs.";

RL Proc. Natl. Acad. Sci. U.S.A. 87:5173-5177(1990).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=89323338; PubMed=2752110;

RA Evans J.P., Matzke H.H., Ware J.L., Stafford D.W., High K.A.;

RT "Molecular cloning of a cDNA encoding canine factor IX.";

RL Blood 74:207-212(1989).

RN [3]

RP VARIANT HEMOPHILIA B GLU-418.

RX MEDLINE=9009303; PubMed=2481310;

RA Evans J.P., Brinkhous K.M., Brayer G.D., Reisner H.M., High K.A.;

RT "Canine hemophilia B resulting from a point mutation with unusual consequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 86:10095-10099(1989).

CC -1- FUNCTION: FACTOR IX IS A VITAMIN K-DEPENDENT PLASMA PROTEIN THAT PARTICIPATES IN THE INTRINSIC PATHWAY OF BLOOD COAGULATION BY CONVERTING FACTOR X TO ITS ACTIVE FORM IN THE PRESENCE OF CA++ IONS, PHOSPHOLIPIDS, AND FACTOR VIIIa.

CC -1- CATALYTIC ACTIVITY: Hydrolyses one Arg-|-Ile bond in factor X to form factor Xa.

CC -1- SUBUNIT: FACTOR IX IS ACTIVATED BY FACTOR XIa, WHICH EXCISES THE ACTIVATION PEPTIDE AND THUS PRODUCES A MOLECULE CONSISTING OF 2 CHAINS HELD TOGETHER BY ONE OR MORE DISULFIDE BONDS.

CC -1- DISEASE: HEMOPHILIA B IS DUE TO DEFECTS IN FACTOR IX.

CC -1- MISCELLANEOUS: CALCIUM BINDS TO THE GAMMA-CARBOXYGLUTAMIC ACID (GLA) RESIDUES AND, WITH STRONGER AFFINITY, TO ANOTHER SITE, BEYOND THE GLA DOMAIN.

CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.

CC -----

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CC -----

DR EMBL: M21757; AAA5006.1; -

DR EMBL: M33826; AAA30844.1; -

DR PIR: A30351; A30351.

DR HSP: P00740; 1CFH.

DR MEROPS: S01.214; -

DR InterPro: IPR000152; Asx_hydroxyl.

DR InterPro: IPR001314; Chymotrypsin.

DR InterPro: IPR000561; EGF-like.

DR InterPro: IPR000742; EGF_2.

DR InterPro: IPR001881; EGF_Ca.

DR InterPro: IPR002383; GLA_blood.

DR InterPro: IPR001254; Trypsin.

DR InterPro: IPR000294; Vitk_dep_GLA.

DR Pfam: PF00008; EGF_2.

DR Pfam: PF00594; gla; 1.

DR Pfam: PF00089; trypsin; 1.

DR PRINTS: PR00722; CHYMOTRYPSIN.

DR PRINTS: PR00001; GLABLOOD.

DR SMART: SM00179; EGF_CA; 1.

DR SMART: SM00069; GLA; 1.

DR SMART: SM00020; TRYP_SPC; 1.

DR PROSITE: PS00010; ASX_HYDROXYL; 1.

DR PROSITE: PS00022; EGF_1; 1.

DR PROSITE: PS01186; EGF_2; 2.

DR PROSITE: PS01187; EGF_CA; 1.

DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.

DR PROSITE: PS00240; TRYPSIN_DOM; 1.

DR PROSITE: PS00134; TRYPSIN_HIS; 1.

DR PROSITE: PS00135; TRYPSIN_SER; 1.

KW Blood coagulation; plasma; serine protease; calcium-binding;

KW Hydrolyase; glycoprotein; vitamin K; gamma-carboxyglutamic acid;

KW Hemophilia; hydroxylation; zymogen; signal; EGF-like domain;

KW Repeat; disease mutation.

FT SIGNAL 1 21

FT PROPER 22 39

FT CHAIN 40 183

FT PROPEP 184 217

FT CHAIN 218 452

FT DOMAIN 86 122

FT DOMAIN 123 164

FT DOMAIN 218 452

FT SITE 183 184

FT SITE 217 218

FT MOD_RES 46 46

FT MOD_RES 47 47

FT MOD_RES 54 54

FT MOD_RES 56 56

FT MOD_RES 59 59

FT MOD_RES 60 60

FT MOD_RES 65 65

FT MOD_RES 66 66

FT MOD_RES 69 69

FT MOD_RES 72 72

FT MOD_RES 75 75

FT MOD_RES 79 79

FT MOD_RES 103 103

FT DISULFID 57 62

FT DISULFID 90 101

FT DISULFID 95 110

FT DISULFID 112 121

FT DISULFID 127 138

FT DISULFID 134 148

FT DISULFID 150 163

FT CARBOHYD 197 197

FT CARBOHYD 207 207

FT CARBOHYD 297 297

FT ACT_SITE 258 258

FT ACT_SITE 306 306

FT ACT_SITE 402 402

FT VARIANT 418 418

SO SEQUENCE 452 AA; 50827 MW; 1F6537C46A960ED CRC64;

Query Match

Best Local Similarity

40.6%; Score 78; DB 1; Length 452;

41.2%; Pred. No. 2.7e-06;

ID	THRM_MOUSE	STANDARD:	PRT:	618 AA.
AC	P19221.			
DT	01-NOV-1990 (Rel. 16, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Prothrombin precursor (EC 3.4.21.5).			
GN	F2 OR CF2.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6; TISSUE=Liver;			
RC	MEDLINE=91025551; PubMed=2228210;			
RA	Fritzenr Degen S.J., Schaffer L.A., Jamison C.S., Grant S.G.,			
RA	Fitzgibbon J.J., Pal J.-A., Chapman V.M., Elliott R.W.;			
RT	"Characterization of the cDNA coding for mouse prothrombin and			
RL	localization of the gene on mouse chromosome 2.";			
RN	DNA Cell Biol. 9:487-498(1990).			
RP	[2]			
RC	SEQUENCE OF 384-618 FROM N.A.			
RC	TISSUE=Liver;			
RC	MEDLINE=92212913; PubMed=1557383;			
RA	Banfield D.K., Macgillivray R.T.;			
RT	"Partial characterization of vertebrate prothrombin cDNAs:			
RT	amplification and sequence analysis of the B chain of thrombin from			
RT	nine different species.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).			
CC	-1- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS			
CC	FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,			
CC	AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.			
CC	-1- P1M: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,			
CC	RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOAL			
CC	ENZYME. THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES			
CC	ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY			
CC	CHARGED PROSTHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION			
CC	OF PROTHROMBIN TO THROMBIN.			
CC	-1- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A			
CC	PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &			
CC	FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS: FACTOR XA REMOVES			
CC	THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &			
CC	HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR			
CC	V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF			
CC	THROMBIN.			
CC	-1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL			
CC	FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION			
CC	BY FACTOR XA.			
CC	-1- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.			
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE			
CC	TRYPSIN FAMILY.			
CC	-----			
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CC	or send an email to license@isb-slb.ch).			
CC	-----			
DR	EMBL; X52308; CAA36548.1; -			
DR	EMBL; M81394; AAA40435.1; -			
DR	PIR; A35827; A35827.			
DR	HSSP; P00734; 1B7X.			
DR	MEROFS; S01.217; -			
DR	MGD; MGI:88380; F2.			
DR	InterPro; IPR001314; Chymotrypsin.			
DR	InterPro; IPR002383; GLA_blood.			
DR	InterPro; IPR000001; Kringle.			
DR	InterPro; IPR003966; Prothrombin.			
DR	InterPro; IPR001254; Trypsin.			
DR	InterPro; IPR000294; vitk_dep_GLA.			
DR	Pfam; PF00594; gla; 1.			

DR	Pfam; PF00051; kringler; 2.	
DR	Pfam; PF00089; trypsin; 1.	
DR	PRINTS; PR00722; CHYMOTRYPSIN.	
DR	PRINTS; PR00001; GLABLOOD.	
DR	PRINTS; PR00018; KRINGLE.	
DR	PRINTS; PR01505; PROTHROMBIN.	
DR	SMART; SM00059; GLA; 1.	
DR	SMART; SM00020; tryp_spec; 1.	
DR	SMART; SM00130; KR; 2.	
DR	PROSITE; PS00011; GLU CARBOXYLATION; 1.	
DR	PROSITE; PS00021; KRINGLE_2; 2.	
DR	PROSITE; PS50070; KRINGLE_2; 2.	
DR	PROSITE; PS50240; TRYPsin_DOM; 1.	
DR	PROSITE; PS00134; TRYPsin_HIS; 1.	
DR	PROSITE; PS00135; TRYPsin_SER; 1.	
KW	Blood coagulation; Plasma; Calcium-binding; Glycoprotein; Repeat;	
KW	Vitamin K; zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver;	
KW	Hydrolase; Serine protease; Kringle; Signal.	
FT	SIGNAL	1
FT	PROPEL	24
FT	CHAIN	25
FT	PEPTIDE	44
FT	PEPTIDE	44
FT	PEPTIDE	201
FT	CHAIN	325
FT	CHAIN	361
FT	DOMAIN	109
FT	DOMAIN	215
FT	DOMAIN	361
FT	SITE	200
FT	SITE	324
FT	SITE	324
FT	SITE	360
FT	ACT_SITE	403
FT	ACT_SITE	459
FT	ACT_SITE	565
FT	MOD_RES	50
FT	MOD_RES	51
FT	MOD_RES	58
FT	MOD_RES	60
FT	MOD_RES	63
FT	MOD_RES	64
FT	MOD_RES	69
FT	MOD_RES	70
FT	MOD_RES	73
FT	MOD_RES	76
FT	DISULFID	61
FT	DISULFID	104
FT	DISULFID	91
FT	DISULFID	109
FT	DISULFID	130
FT	DISULFID	158
FT	DISULFID	215
FT	DISULFID	236
FT	DISULFID	264
FT	DISULFID	333
FT	DISULFID	388
FT	DISULFID	533
FT	DISULFID	547
FT	CARBOHYD	122
FT	CARBOHYD	144
FT	CARBOHYD	413
FT	CARBOHYD	553
SO	SEQUENCE	618 AA; 70268 MW; B89F719A9FDD01ED C8C64;

RESULT 25

A:Molecule type: protein
 A:Residues: 41-179 <MCM>
 R:Inoue, K.; Morita, T.
 Eur. J. Biochem. 218, 153-163, 1993
 A:Title: Identification of O-linked oligosaccharide chains in the activation peptides of
 A:Reference number: S39414; MUID:94062825
 A:Accession: S39415
 A:Molecule type: protein
 A:Residues: 183-234 <INO>
 A:Note: glycosylation sites
 A:Note: Identification and characterization of beta-hydroxyaspartic acid
 R:Jagadeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hamsabhusanam, K.; Lyman, G.
 Gene 84, 517-519, 1989
 A:Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human
 A:Reference number: I54051; MUID:90128299
 A:Accession: I54051
 A:Status: translation not shown; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-23 <RES>
 A:Cross-references: GB:M33297; NID:g183860; PIDN:AAA52636.1; PID:g553330
 R:Padmanabhan, K.; Padmanabhan, K.P.; Tulinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Bie
 J. Mol. Biol. 232, 947-966, 1993
 A:Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.
 A:Reference number: A49458; MUID:93360277
 A:Contents: annotation; X-ray crystallography, 2.2 angstroms
 C:Comment: The two chains held together by one disulfide bond are formed from a single-c
 C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or
 C:Genetics:
 A:Gene: GDB:F10
 A:Cross-references: GDB:119890; OMIM:227600
 A:Map position: 13q34-13q34
 A:Insertions: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1
 A:Note: deficiency of this factor causes Stuart disease
 C:Function:
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
 A:Pathway: blood coagulation
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutan
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-40/Domain: propeptide #status predicted <PRO>
 F:25-84/Domain: Gla domain homology <GLA>
 F:41-179/Product: coagulation factor X light chain #status experimental <LCH>
 F:90-121/Domain: EGF homology <EG1>
 F:129-164/Domain: EGF homology <EG2>
 F:183-488/Product: coagulation factor X heavy chain #status experimental <HCH>
 F:183-234/Domain: activation peptide #status experimental <AP>
 F:235-488/Product: coagulation factor Xa heavy chain #status experimental <ACT>
 F:235-462/Domain: trypsin homology <TRY>
 F:46/47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #stat
 F:57-62/Disulfide bonds: #status predicted
 F:90-101,95-110,112-121,129-140,136-149,151-164,172-342,241-246,261-277,390-404,415-443/
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:129,211/Binding site: carboxylate (Thr) (covalent) #status experimental
 F:231,231/Binding site: carboxylate (Asn) (covalent) #status experimental
 F:234-235/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #stat
 F:276,322,419/Active site: His, Asp, Ser #status experimental

Query Match 48.5%; Score 94; DB 1; Length 488;
 Best Local Similarity 36.4%; Pred. No. 2.2e-08;
 Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Oy 1 ANGFLXKLRPGSLKRCXKXLCFSFXAHXIRNXXRTQFVSVY 44
 DB 41 ANSFLERKKGHLRECEKERTCSYEAREVEDSDKTNEFWNKY 84

RESULT 9
 KXHU
 protein C (activated) (EC 3.4.21.69) precursor - human
 N:Alternate names: autoproteolthrombin IIA; plasma protein C
 C:Species: Homo sapiens (hmn)
 C>Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999

C:Accession: A22331; A25426; A21781; A23789; A00922
 R:Foster, D.C.; Yoshitake, S.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985
 A:Title: The nucleotide sequence of the gene for human protein C.
 A:Reference number: A22331; MUID:85270390
 A:Accession: A22331
 A:Molecule type: DNA
 A:Residues: 1-461 <FOS1>
 A:Cross-references: GB:M11228; NID:g190333; PIDN:AAA60166.1; PID:g190334
 R:Plutsky, J.; Hoskins, J.A.; Long, G.L.; Crabtree, G.R.
 Proc. Natl. Acad. Sci. U.S.A. 83, 546-550, 1986
 A:Title: Evolution and organization of the human protein C gene.
 A:Reference number: A25426; MUID:86120978
 A:Accession: A25426
 A:Molecule type: DNA
 A:Residues: 1-445; 'L', 446-461 <PLD>
 A:Cross-references: GB:M12712; NID:g190330; PIDN:AAA60165.1; PID:g190332
 R:Foster, D.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 81, 4766-4770, 1984
 A:Title: Characterization of a cDNA coding for human protein C.
 A:Reference number: A21781; MUID:84272714
 A:Accession: A21781
 A:Molecule type: mRNA
 A:Residues: 'C', 107-461 <FOS2>
 A:Cross-references: GB:X02059; NID:g190322; PIDN:AAA60164.1; PID:g190323
 R:Beckmann, R.U.; Schmidt, R.U.; Sauter, R.F.; Plutsky, J.; Crabtree, G.R.; Long, G
 Nucleic Acids Res. 13, 5233-5247, 1985
 A:Title: The structure and evolution of a 461 amino acid human protein C precursor an
 A:Reference number: A23789; MUID:85269639
 A:Accession: A23789
 A:Molecule type: mRNA
 A:Residues: 1-461 <BEC>
 A:Cross-references: GB:X02750; NID:g35689; PIDN:CAA26528.1; PID:g763120
 R:Mieliach, J.P.; Broze Jr., G.J.
 J. Biol. Chem. 265, 11397-11404, 1990
 A:Title: Beta protein C is not glycosylated at asparagine 329. The rate of translatio
 A:Reference number: A44605; MUID:90293094
 A:Contents: annotation; carbohydrate binding sites; activation peptide
 A:Note: The alpha form of protein C is glycosylated at Asn-329, and the beta form is
 R:Harris, R.J.; Ling, V.T.; Spellman, M.W.
 J. Biol. Chem. 267, 5102-5107, 1992
 A:Title: O-linked fucose is present in the first epidermal growth factor domain of fa
 A:Reference number: A44606; MUID:9184750
 A:Contents: annotation; beta-hydroxyaspartic acid
 C:Comment: protein C is the zymogen of the vitamin K-dependent serine proteinase that
 C:Comment: protein C is strongly enhanced by complexing with protein S. Protein C als
 C:Comment: protein C is synthesized in the liver as a single chain precursor, which i
 bin, which cleaves a dodecapeptide from the amino end of the heavy chain; this reacti
 C:Genetics:
 A:Gene: GDB:PROC
 A:Cross-references: GDB:120317; OMIM:176860
 A:Map position: 2q13-2q21
 A:Insertions: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol
 C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium bind
 F:1-32/Domain: signal sequence #status predicted <SIG>
 F:27-86/Domain: Gla domain homology <GLA>
 F:33-42/Domain: propeptide #status predicted <PRO>
 F:43-197/Product: protein C light chain #status predicted <LCH>
 F:92-131/Domain: EGF homology <EG1>
 F:140-175/Domain: EGF homology <EG2>
 F:200-461/Product: protein C heavy chain #status predicted <HCH>
 F:200-211/Domain: activation peptide #status experimental <AP>
 F:212-445/Domain: trypsin homology <TRY>
 F:48,49,56,58,61,62,67,68,71/Modified site: gamma-carboxyglutamic acid (Glu) #status
 F:59-64,92-105,101-120,122-131,140-151,147-160,162-175,183-319,238-254,373-387,398-42
 F:106-111/Disulfide bonds: #status predicted
 F:110/Binding site: carboxylate (Thr) (covalent) #status absent
 F:113/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:139,290,355/Binding site: carboxylate (Asn) (covalent) #status experimental
 F:211-212/Cleavage site: Arg-Leu (thrombin) #status experimental
 F:253,299,402/Active site: His, Asp, Ser #status predicted
 F:371/Binding site: carboxylate (Asn) (covalent) (partial) #status atypical

```

Query Match      45.9%; Score 89; DB 1; Length 461;
Best Local Similarity 46.3%; Pred. No. 1.6e-07;
Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLXLRPGSLXRCRXXLCSEFXAHXIFRXXXTROFWSY 41
   |||||:::|||||:::|||||:::|||||:::|||||
Db 43 ANSFLEELRHRSLERCIEICDFEAKELIFQVDDTLAFW 83

RESULT 10
EXBO
coagulation factor Xa (EC 3.4.21.6) precursor - bovine
N:Alternate names: Stuart factor
C:Species: Bos primigenius taurus (cattle)
C>Date: 24-Apr-1984 #sequence, revision 17-Mar-1987 #extl, change 16-Jul-1999
C:Accession: A22867; A14997; A12030; A34412; S39414; A00925
R:Fung, M.R.; Campbell, R.M.; Macgillivray, T.A.
Nucleic Acids Res. 12, 4481-4492, 1984
A:Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a
A:Reference number: A22867; MUID:84247315
A:Accession: A22867
A:Molecule type: mRNA
A:Residues: 1-487 <FUN>
A:Cross-references: GB:X00673; NID:9192; PIDN:CA25286.1; PID:9193
R:Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K.
Biochemistry 19, 659-667, 1980
A:Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).
A:Reference number: A14997; MUID:80130563
A:Accession: A14997
A:Molecule type: protein
A:Residues: 41-102, 'N', 104-180 <ENF>
R:McMullen, B.A.; Fujikawa, K.; Kistiel, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co
A:Reference number: A20274; MUID:83308813
R:Titani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.
Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975
A:Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.
A:Reference number: A12030; MUID:76053069
A:Accession: A12030
A:Molecule type: protein
A:Residues: 183-292, 294-295, 'GDE', 299-334, 336-348, 'AE', 351-354, 356-441, 'GKFG', 446-492 <T
A:Note: carboxylate binding sites and disulfide bonds were determined
R:Petersen, E.; Selander, M.; Linse, S.; Drakenberg, T.; Oehlin, A.K.; Stenflo, J.
J. Biol. Chem. 264, 16897-16904, 1989
A:Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal
A:Reference number: A34412; MUID:89380326
A:Accession: A34412
A:Molecule type: protein
A:Residues: 85-126 <PER>
A:Note: beta-hydroxyaspartic acid site
R:Inoue, K.; Morita, T.
Eur. J. Biochem. 218, 153-163, 1993
A:Title: Identification of O-linked oligosaccharide chains in the activation peptides of
A:Reference number: S39414; MUID:94062825
A:Accession: S39414
A:Molecule type: protein
A:Residues: 183-196, 199-209, 216-233 <INO>
A:Note: carbohydrate binding sites
R:Titani, K.; Hermodson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.; D
Biochemistry 11, 4899-4903, 1972
A:Title: Bovine factor X-1a (activated Stuart factor). Evidence of homology with mammal
A:Reference number: A12453; MUID:73053314
A:Accession: A12453
A:Contents: annotation; active site
R:Fujikawa, K.; Titani, K.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975
A:Title: Activation of bovine factor X (Stuart factor): conversion of factor Xa1pha to
A:Reference number: A13504; MUID:76053121
A:Contents: annotation; activation
R:Sugo, T.; Bjork, I.; Holmgren, A.; Stenflo, J.

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J. Biol. Chem. 259, 5705-5710, 1984
A:Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxylate
A:Reference number: A38024; MUID:84185716
A:Contents: annotation; calcium binding
R:Morita, T.; Jackson, C.M.
J. Biol. Chem. 261, 4008-4014, 1986
A:Reference number: A38025; MUID:86140210
A:Contents: annotation; sulfate binding
C:Comment: Factor Xa converts prothrombin to thrombin during blood clotting.
C:Comment: The two chains are formed from a single-chain precursor by the excision of
C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway)
activation.
C:Comment: Calcium binds to the gamma-carboxylutamic acid (Glu) residues and, with s
C:Comment: The gamma-carboxylutamic acid residues arise by a posttranslational, vita
A:Gene: F10
A:Map position: 13q34
C:Function:
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the
A:Pathway: blood coagulation
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylu
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-40/Domain: propeptide #status predicted <PRO>
F:25-84/Domain: Gla domain homology <GLA>
F:41-180/Product: coagulation factor X light chain #status experimental <LCH>
F:90-121/Domain: EGF homology <EG1>
F:129-164/Domain: EGF homology <EG2>
F:183-492/Product: coagulation factor X heavy chain #status experimental <HCH>
F:183-233/Domain: activation peptide #status experimental <AP>
F:234-492/Product: coagulation factor Xa heavy chain #status experimental <AHC>
F:234-461/Domain: trypsin homology <TR>
F:46-47, 54, 56, 59, 60, 65, 66, 69, 72, 75, 79/Modified site: gamma-carboxylutamic acid (Glu)
F:57-62, 90-101, 95-110, 112-121, 129-140, 136-149, 151-164, 172-241/Disulfide bonds: #statu
F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F:208-485/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental
F:218/Binding site: carboxylate (Thr) (covalent) #status experimental
F:233-234/Cleavage site: Arg-11e (coagulation factor IXa, coagulation factor VIIa) #s
F:240-245, 260-276, 389-403, 414-442/Disulfide bonds: #status experimental
F:275, 321, 418/Active site: His, Asp, Ser #status predicted

Query Match      45.9%; Score 89; DB 1; Length 492;
Best Local Similarity 36.4%; Pred. No. 1.7e-07;
Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

QY 1 ANGFLXLRPGSLXRCRXXLCSEFXAHXIFRXXXTROFWSY 44
   |||||:::|||||:::|||||:::|||||:::|||||
Db 41 ANSFLEELVKGNLRECLERACSLERAREVEEDADOTDERWSY 84

RESULT 11
KRFU
coagulation factor IXa (EC 3.4.21.22) precursor [validated] - human
N:Alternate names: antithemophilic factor B; Christmas factor
C:Species: Homo sapiens (man)
C>Date: 17-Dec-1982 #sequence, revision 30-Jun-1987 #extl, change 15-Sep-2000
C:Accession: A00922; A37570; A30511; A32989; A22673; A21337; A37546; A30623; A60486;
R:Yoshitake, S.; Schach, B.G.; Foster, D.C.; Davie, E.W.; Kurechi, K.
Biochemistry 24, 3736-3750, 1985
A:Title: Nucleotide sequence of the gene for human factor IX (antithemophilic factor B
A:Reference number: A00922; MUID:86000558
A:Accession: A00922
A:Molecule type: DNA
A:Residues: 1-461 <YOS>
A:Cross-references: GB:K02402; NID:9182612; PIDN:AAB59620.1; PID:9182613
R:Anson, D.S.; Choo, K.H.; Rees, D.J.G.; Giannelli, F.; Gould, K.; Huddleston, J.A.;
EMBO J. 3, 1053-1060, 1984
A:Title: The gene structure of human anti-haemophilic factor IX.
A:Reference number: A37570; MUID:84236100
A:Accession: A37570
A:Molecule type: DNA

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A:Residues: 1-461 <ANS>
A:Cross-references: GB:K02048
R:Reitma, P.H.; Bertina, R.M.; Ploos van Amstel, J.K.; Riemens, A.; Briet, E.
Blood 72, 1074-1076, 1988
A:Title: The putative factor IX gene promoter in hemophilia B Leyden.
A:Reference number: A30511; MUID:88327116
A:Accession: A30511
A:Molecule type: DNA
A:Residues: 8-24 <RE>
R:Cross-references: EMBL:X55008; NID:g311288; PIDN:CAB38245.2; PID:g4469253
R:Koebel, D.D.; Bottema, C.D.K.; Buestedde, J.M.; Sommer, S.S.
Am. J. Hum. Genet. 45, 448-457, 1989
A:Title: Functionally important regions of the factor IX gene have a low rate of polymor
A:Reference number: A32989; MUID:89371752
A:Accession: A32989
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 30-92 <ROE>
R:McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Lundblad, R.L.; Roberts, H.R.; Graham, J.B.; S
Proc. Natl. Acad. Sci. U.S.A. 82, 2847-2851, 1985
A:Title: Evidence for a prevalent dimorphism in the activation peptide of human coagulat
A:Reference number: A2673; MUID:85190593
A:Accession: A2673
A:Molecule type: mRNA
A:Residues: 1-193, 'T', 195-461 <MC>
A:Cross-references: GB:M1309; NID:g180552; PIDN:AA52023.1; PID:g180553
A:Note: the authors translated the codon ACA for residue 29 as Tyr
R:Jaye, M.; de la Salle, H.; Schamber, F.; Balland, A.; Kohl, V.; Findell, A.; Tolstosh
Nucleic Acids Res. 11, 2325-2335, 1983
A:Title: Isolation of a human anti-haemophilic factor IX cDNA clone using a unique 52-ba
A:Reference number: A21337; MUID:83220788
A:Accession: A21337
A:Molecule type: mRNA
A:Residues: 1-193, 'T', 195-461 <JAG>
A:Cross-references: GB:J00137; NID:g182610; PIDN:AA52763.1; PID:g182611
R:Jagadeeswaran, P.; Lavelle, D.E.; Kaul, R.; Mohandas, T.; Warren, S.T.
Somat. Cell Mol. Genet. 10, 465-473, 1984
A:Title: Isolation and characterization of a human factor IX cDNA: identification of Tag I
A:Reference number: A37546; MUID:84300526
A:Accession: A37546
A:Molecule type: mRNA
A:Residues: 38-193, 'T', 195-326 <JAG>
A:Cross-references: GB:M35672
R:Kurachi, K.; Davis, E.W.
Proc. Natl. Acad. Sci. U.S.A. 79, 6461-6464, 1982
A:Title: Isolation and characterization of a cDNA coding for human factor IX.
A:Reference number: A30623; MUID:83065193
A:Accession: A30623
A:Molecule type: mRNA
A:Residues: 1-12, 'S', 14-73, 'P', 75-82, 'K', 84-203, 'P', 205-216, 'G', 218-298, 'A', 299-356, 'A',
A:Cross-references: GB:J00136; NID:g182608; PIDN:AA598726.1; PID:g182609
R:Tharakan, J.; Strickland, D.; Burgess, W.; Drohan, W.N.; Clark, D.B.
Vox Sang. 58, 21-29, 1990
A:Title: Development of an immunoaffinity process for factor IX purification.
A:Reference number: A60486; MUID:90194857
A:Accession: A60486
A:Molecule type: protein
A:Residues: 47-52, 'XX', 55-60, 'X', 62, 'XX', 65 <THA>
R:McMullen, B.A.; Fujikawa, K.; Kistiel, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co
A:Reference number: A20274; MUID:83308813
A:Accession: A20274
A:Molecule type: protein
A:Residues: 105-109, 'X', 111-115 <MC>
R:Balland, A.; Faure, T.; Carvallo, D.; Cordier, P.; Ulrich, P.; Fournet, B.; de la Sall
Eur. J. Biochem. 172, 565-572, 1988
A:Title: Characterisation of two differently processed forms of human recombinant factor
A:Reference number: S02527; MUID:86166735
A:Accession: S02527
A:Molecule type: protein
A:Residues: 29-63 <BAL>

A:Note: processed forms expressed in recombinant system
R:Jallat, S.; Perraud, F.; Dalemans, W.; Balland, A.; Dieterle, A.; Faure, T.; Meulle
EMBO J. 9, 3295-3301, 1990
A:Title: Characterization of recombinant human Factor IX expressed in transgenic mice
A:Reference number: S12058; MUID:91006024
A:Accession: S12058
A:Molecule type: protein
A:Residues: 1-68 <JAL>
A:Note: processed forms expressed in recombinant system
R:Handford, P.A.; Baron, M.; Mayhew, M.; Willis, A.; Beesley, T.; Brownlee, G.G.; Cam
EMBO J. 9, 475-480, 1990
A:Title: The first EGF-like domain from human factor IX contains a high-affinity calc
A:Reference number: S12377; MUID:90151623
A:Accession: S12377
A:Molecule type: protein
A:Residues: 92-130 <HAN>
A:Note: NMR detection of calcium binding by domain expressed in recombinant system
R:de la Salle, C.; Charanier, J.L.; Baas, M.J.; Schwartz, A.; Wiesel, M.L.; Grunbe
Thromb. Haemost. 70, 370-371, 1993
A:Title: A deletion located in the 3' non translated part of the factor IX gene respo
A:Reference number: S19612; MUID:94054330
A:Accession: S19612
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 444-461 <RES>
A:Cross-references: GB:S66752; NID:g439773; PIDN:AA28588.1; PID:g439774
R:Stoffel, E.S.; Koebel, D.D.; Sarkar, G.; Sommer, S.S.
Science 239, 491-494, 1988
A:Title: Genomic amplification with transcript sequencing.
A:Reference number: S19529; MUID:88127096
A:Accession: S19529
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 290-359 <RE>
A:Cross-references: GB:M19063; NID:g182622; PIDN:AA52456.1; PID:g182623
R:Adavala, K.L.; Kawabata, S.; Takao, T.; Murata, H.; Shimomatsu, Y.; Nishimura, H.;
Biochemistry 33, 5167-5171, 1994
A:Title: Activation peptide of human factor IX has oligosaccharides O-glycosidically
A:Reference number: A54255; MUID:94227047
A:Accession: A54255
A:Molecule type: protein
A:Residues: 'D', 204, 'X', 206-211, 212, 'D', 214, 'X', 216-221, 'D' <AGA>
A:Note: the residues designated 'X' were determined to be threonine bound to carboxy
R:Di Scipio, R.G.; Kurachi, K.; Davis, E.W.
J. Clin. Invest. 61, 1528-1538, 1978
A:Title: Activation of human factor IX (Christmas factor).
A:Reference number: A18483; MUID:78194509
A:Accession: A18483
A:Contents: annotation; activation; active site; carbohydrate binding
R:McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Graham, J.B.; Roberts, H.R.; Stafford, D.W.
Ann. Soc. Hematol. Abstr. 64(Suppl.1), 262a, 1984
A:Reference number: A37569
A:Accession: A37569
A:Contents: annotation
R:Morita, T.; Isaacs, B.S.; Esmon, C.T.; Johnson, A.E.
A:Note: 194-Thr was also found
J. Biol. Chem. 259, 5698-5704, 1984
A:Title: Derivatives of blood coagulation factor IX contain a high affinity Ca2+-bind
A:Reference number: A37543; MUID:84185715
A:Accession: A37543
A:Contents: annotation; calcium binding
R:Morita, T.; Isaacs, B.S.; Esmon, C.T.; Johnson, A.E.
J. Biol. Chem. 260, 2583, 1985
A:Reference number: A37544
A:Accession: A37544
A:Contents: annotation; calcium binding, correction
R:Bentley, A.K.; Rees, D.J.G.; Rizza, C.; Brownlee, G.G.
Cell 45, 343-348, 1986
A:Title: Defective propeptide processing of blood clotting factor IX caused by mutat
A:Reference number: A37545; MUID:86189947
A:Accession: A37545
A:Contents: annotation; signal sequence cleavage site
R:Suehiro, K.; Kawabata, S.T.; Miyata, T.; Takeya, H.; Takamatsu, J.; Ogata, K.; Kami
J. Biol. Chem. 264, 21257-21265, 1989
A:Title: Blood clotting factor IX B(M) Nagoya: substitution of arginine 180 by trypt
A:Reference number: A30622; MUID:90078229
A:Accession: A30622
A:Contents: annotation; sequence of mutant B(M) Nagoya
A:Note: carboxylation, glycosylation, and cleavage sites

R.Barton, M.; Norman, D.G.; Harvey, T.S.; Hanford, P.A.; Mayhew, M.; Tse, A.G.D.; Brownle submitted to the Brookhaven Protein Data Bank, November 1991
A:Reference number: A51252; PDB:1IXA
A:Contents: annotation; conformation by (1)H-NMR, residues 92-130
A:Note: recombinant form expressed in yeast
C:Comment: Factor IX is activated by factor X_{IIa}, which excises the activation peptide pr
C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K
C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stro
C:Genetics:
A:Gene: GDB:F9
A:Cross-references: GDB:119900; OMIM:306900
A:Map position: Xq27.1-Xq27.2
A:Intons: 30/1, 84/2, 93/1, 131/1, 174/1, 241/3, 280/1
C:Function:
A:Description: catalyzes the proteolytic activation of coagulation factor X in the prese
A:Pathway: blood coagulation intrinsic pathway
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglu
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-46/Domain: propeptide #status experimental <PPT>
F:31-91/Domain: Gla domain homology <GLA>
F:47-191/Product: coagulation factor IXa light chain #status experimental <ALC>
F:97-128/Domain: EGF homology <EG1>
F:134-170/Domain: EGF homology <EG2>
F:192-226/Domain: activation peptide #status experimental <ACT>
F:227-461/Product: coagulation factor IXa heavy chain #status experimental <AHC>
F:227-454/Domain: trypsin homology <TRY>
F:53-54, 61-63, 66-67, 72-73, 76-79, 82-86/Modified site: gamma-carboxyglutamic acid (Glu) #
F:64-69, 97-108, 102-117, 119-128, 134-145, 141-155, 157-170, 178-335, 252-266, 382-396, 407-435/Mod
F:99/Binding site: carboxylate (Ser) (covalent) #status experimental
F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F:191-192/Cleavage site: Arg-Ala (coagulation factor X_{IIa}) #status experimental
F:203, 213/Binding site: carboxylate (Asn) (covalent) #status experimental
F:205, 215/Binding site: carboxylate (Thr) (covalent) #status experimental
F:226-227/Cleavage site: Arg-Val (coagulation factor X_{IIa}) #status experimental

Query Match 44.8%; Score 87; DB 1; Length 461;
Best local Similarity 39.5%; Pred. No. 3.5e-07;
Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

Qy 2 NGFLXXLRPGSLXRCRXXLCSPFXAHXIFRNXXRTRQFVWSY 44
Db 49 SGRLEEFVGNLERECMEKCSFEAREVFNERTTEFEKQY 91

RESULT 12

coagulation factor IXa (EC 3.4.21.22) precursor - bovine
N:Alternate names: Christmas factor
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Nov-1980 #sequence_revision 03-Aug-1984 #text_change 16-Jul-1999
C:Accession: A14757; B20274; I45891; A00923
R:Katayama, K.; Erlanson, L.H.; Enfield, D.L.; Walsh, K.A.; Neurath, H.; Davle, E.W.; T
Proc. Natl. Acad. Sci. U.S.A. 76, 4990-4994, 1979
A:Title: Comparison of amino acid sequence of bovine coagulation factor IX (Christmas fa
A:Reference number: A14757; M01D:80056619
A:Accession: A14757
A:Molecule type: protein
A:Residues: 1-63, 'T', 65-416 <KAT>
R:McMullen, B.A.; Fujikawa, K.; Kistiel, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co
A:Reference number: A20274; M01D:83308813
A:Accession: B20274
A:Molecule type: protein
A:Residues: 59-63, 'X', 65-69 <KCM>
R:Choo, K.H.; Gould, K.G.; Rees, D.J.G.; Brownlee, G.G.
Nature 299, 178-180, 1982
A:Title: Molecular cloning of the gene for human anti-haemophilic factor IX.
A:Reference number: I45891; M01D:8222386
A:Accession: I45891
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA

A:Residues: 52-139 <CHO>
A:Cross-references: GB:J00007; M01D:9163053; P1DN:AAA30520.1; P1D:9163054
R:Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanag
J. Biochem. 104, 867-868, 1988
A:Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood c
A:Reference number: A44556; M01D:89213999
A:Contents: annotation
A:Note: structure and location of a carboxylate covalently bound to Ser
C:Comment: Factor IX is activated by factor X_{IIa}, which excises the activation peptide
C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitam
C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with s
C:Function:
A:Description: catalyzes the proteolytic activation of coagulation factor X in the pr
A:Pathway: blood coagulation intrinsic pathway
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglu
F:1-16/Product: coagulation factor IXa light chain #status experimental <ALC>
F:1-45/Domain: Gla domain homology (fragment) <GLA>
F:51-82/Domain: EGF homology <EG1>
F:88-124/Domain: EGF homology <EG2>
F:147-181/Domain: activation peptide #status experimental <APT>
F:182-416/Product: coagulation factor IXa heavy chain #status experimental <AHC>
F:182-409/Domain: trypsin homology <TRY>
F:7.8, 15, 17, 20, 21, 26, 27, 30, 33, 36, 40/Modified site: gamma-carboxyglutamic acid (Glu) #
F:18-23, 51-62, 56-71, 73-82, 88-99, 95-109, 111-124, 132-230, 207-223, 337-351, 362-390/Disulf
F:53/Binding site: carboxylate (Ser) (covalent) #status experimental
F:54/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F:158, 168, 173, 261/Binding site: carboxylate (Asn) (covalent) #status experimental
F:222, 270, 366/Active site: His, Asp, Ser #status predicted

Query Match 44.3%; Score 86; DB 1; Length 416;
Best local Similarity 37.2%; Pred. No. 4.8e-07;
Matches 16; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

Qy 2 NGFLXXLRPGSLXRCRXXLCSPFXAHXIFRNXXRTRQFVWSY 44
Db 3 SGRLEEFVGNLERECMEKCSFEAREVFNERTTEFEKQY 45

RESULT 13

coagulation factor IXa (EC 3.4.21.22) precursor - dog
A30351
C:Species: Canis lupus familiaris (dog)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A30351; I46201
R:Evans, J.P.; Matzke, H.H.; Ware, J.L.; Stafford, D.W.; Hlgh, K.A.
Blood 74, 207-212, 1989
A:Title: Molecular cloning of a cDNA encoding canine factor IX.
A:Reference number: A30351; M01D:89323338
A:Accession: A30351
A:Molecule type: mRNA
A:Residues: 1-452 <EVA>
A:Cross-references: GB:M21757; M01D:9972719; P1DN:AAA75006.1; P1D:9163948
R:Axelrod, J.H.; Reed, M.S.; Brinkhous, K.M.; Verma, I.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 5173-5177, 1990
A:Title: Phenotypic correction of factor IX deficiency in skin fibroblasts of hemophi
A:Reference number: I46201; M01D:90311364
A:Accession: I46201
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-452 <XME>
A:Cross-references: GB:M33826; M01D:9163949; P1DN:AAA30844.1; P1D:9163950
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglu
F:1-21/Domain: signal sequence #status predicted <PPT>
F:22-40/Domain: propeptide #status predicted <PRO>
F:24-84/Domain: Gla domain homology <GLA>
F:41-452/Product: coagulation factor IX #status predicted <MAT>
F:90-121/Domain: EGF homology <EG2>
F:127-163/Domain: EGF homology <EG3>
F:218-445/Domain: trypsin homology <TRY>

R.Walt, D.A.: Hewett-Emmett, D.; Seegers, W.H.
 Proc. Natl. Acad. Sci. U.S.A. 74, 1969-1972, 1977
 A:Reference number: A37549; MUID:77193964
 A:Accession: A37549
 A:Molecule type: protein
 A:Residues: 44-118, 'N', 120, 'S', 122-163, 'I', 165-175, 'A', 177-182, 'T', 184-193, 'W', 196-308,
 J. Biol. Chem. 252, 4942-4957, 1977
 R. Butkowski, R.J.; Ellison, J.; Downing, M.R.; Mann, K.G.
 A:Title: Primary structure of human prothrombin 2 and alpha-thrombin.
 A:Reference number: A37550; MUID:77207112
 A:Accession: A37550
 A:Molecule type: protein
 A:Residues: 315-334, 'N', 336-348, 'N', 350-368, 'N', 370-397, 'N', 399-413, 'N', 415-484, 'N', 486-
 J. Biol. Chem. 261, 13210-13215, 1986
 R. Rabiet, M.J.; Blashill, A.; Furtle, B.; Furtle, B.C.
 A:Reference number: A37551; MUID:87008532
 A:Contents: annotation: activation cleavages
 A:MacGillivray, R.T.; Irwin, D.M.; Guinto, E.R.; Stone, J.C.
 Ann. N. Y. Acad. Sci. 485, 73-79, 1986
 A:Title: Recombinant genetic approaches to functional mapping of thrombin.
 A:Reference number: I51952; MUID:87182874
 A:Accession: I51952
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-2, 'R', 5-100 <RES>
 A:Cross-references: GB:M33031; NID:9190723; PIDN:AAA60220.1; PID:9190724
 C:Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibrin
 C:Comment: Prothrombin is activated on the surface of a phospholipid membrane that binds
 C:Comment: can be removed either by factor Xa or thrombin: the cleavage into light and heavy chain
 C:Comment: ter 314-Arg, are released in natural blood clotting.
 C:Comment: The cleavage after Arg-198, observed in vitro, does not occur in plasma.
 C:Comment: The gamma-carboxyglutamyl residues bind calcium ions, result from the carboxy
 C:Comment: ent interaction with the negatively charged phospholipid membrane surface.
 C:Comment: The prothrombin precursor is synthesized in the liver.
 C:Genetics:
 A:Gene: GDB:F2
 A:Cross-references: GDB:119894; OMIM:176930
 A:Map position: 11P11-11Q12
 A:Intons: 27/1; 80/3; 89/1; 106/1; 141/2; 187/1; 292/1; 335/1; 377/2; 433/2; 491/2; 552
 C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
 C:Keywords: acute phase; blood coagulation; calcium binding; carboxyglutamic acid; dupl
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-43/Domain: propeptide #status predicted <PRO>
 F:28-87/Domain: Gla domain homology <GLA>
 F:44-622/Domain: prothrombin #status experimental <MAT>
 F:44-327/Domain: activation peptide #status experimental <APT>
 F:108-186/Domain: kringle homology <KR1>
 F:213-291/Domain: kringle homology <KR2>
 F:328-363/Product: thrombin light chain #status experimental <LCH>
 F:364-622/Product: thrombin heavy chain #status experimental <HCH>
 F:364-613/Domain: trypsin homology <TRY>
 F:49-50, 57, 59, 62, 63, 68, 69, 72, 75/Modified site: gamma-carboxyglutamic acid (Glu) #status
 F:60-65, 90-103, 108-186, 129-169, 157-181, 213-291, 234-274, 262-286/Disulfide bonds: #status
 F:121, 143/Binding site: carboxylate (Asn) #status predicted
 F:336-482, 536-550, 564-594/Disulfide bonds: #status predicted
 F:391-407/Disulfide bonds: #status experimental
 F:406, 462/Active site: His, Asp #status predicted
 F:416/Binding site: carboxylate (Asn) (covalent) #status experimental
 F:568/Active site: Ser #status experimental

Query Match 40.2%; Score 78; DB 1; Length 622;
 Best Local Similarity 36.4%; Pred. No. 1.7e-05;
 Matches 16; Conservative 4; Mismatches 24; Indels 0; Gaps 0;

QY 1 ANGFLLXLRPGSLXRCRXXLCSPFXAHXIFRNXXRRPFWSY 44
 DB 44 ANFLLEVRKGNLERCEVETGSTEERFALESSTADVFMAKY 87

RESULT 17
 S10511
 thrombin (EC 3.4.21.5) B chain precursor - rat

C:Species: Rattus norvegicus (Norway rat)
 C:Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 22-Jun-1999
 C:Accession: S10511; A60576; B42696
 R:DiHanch, M.; Monard, D.
 Nucleic Acids Res. 18, 4251, 1990
 A:Title: cDNA sequence of rat prothrombin.
 A:Reference number: S10511; MUID:90332426
 A:Accession: S10511
 A:Molecule type: mRNA
 A:Residues: 1-617 <DIR>
 A:Cross-references: EMBL:X52835; NID:956969; PIDN:CAA37017.1; PID:956970
 R:Kentkson, K.P.; Jazin, E.E.; Greenwood, J.A.; Dickerman, H.W.
 Endocrinology 126, 167-175, 1990
 A:Title: Prothrombin levels are increased in the estrogen-treated immature rat uterus
 A:Reference number: A60576; MUID:90091942
 A:Accession: A60576
 A:Molecule type: protein
 A:Residues: 44-58 <HEN>
 A:Note: the authors purified the proenzyme from the estrogen-stimulated maturing rat
 R:Banfield, D.K.; MacGillivray, R.T.A.
 Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
 A:Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and
 A:Reference number: A42696; MUID:92212913
 A:Accession: B42696
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 383-617, 'E' <BAN>
 A:Cross-references: GB:M81397
 C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
 C:Keywords: blood coagulation; calcium binding; carboxyglutamic acid; glycoprotein; h
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-43/Domain: propeptide #status predicted <PRO>
 F:28-88/Domain: Gla domain homology <GLA>
 F:44-617/Product: prothrombin #status experimental <PMAT>
 F:109-187/Domain: kringle homology <KR1>
 F:215-292/Domain: kringle homology <KR2>
 F:360-609/Domain: trypsin homology <TRY>
 F:50, 51, 58, 60, 63, 64, 69, 70, 73, 76/Modified site: gamma-carboxyglutamic acid (Glu) #stat
 F:61-66, 91-104, 109-187, 130-170, 158-182, 215-292, 236-276, 264-287, 332-478, 387-403, 532-54
 F:402, 458, 564/Active site: His, Asp, Ser #status predicted

Query Match 38.7%; Score 75; DB 2; Length 617;
 Best Local Similarity 37.2%; Pred. No. 5.7e-05;
 Matches 16; Conservative 4; Mismatches 23; Indels 0; Gaps 0;

QY 2 NGFLXLRPGSLXRCRXXLCSPFXAHXIFRNXXRRPFWSY 44
 DB 46 SGFLLEVRKGNLERCEVETGSTEERFALESSTADVFMAKY 88

RESULT 18
 A35827
 thrombin (EC 3.4.21.5) B chain precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 22-Jun-1999
 C:Accession: A35827; A42696; S12081
 R:Begeer, S.J.F.; Schaefer, L.A.; Jamison, C.S.; Grant, S.G.; Fitzgibbon, J.J.; Pal, J
 DNA Cell Biol. 9, 487-498, 1990
 A:Title: Characterization of the cDNA coding for mouse prothrombin and localization o
 A:Reference number: A35827; MUID:91025551
 A:Accession: A35827
 A:Molecule type: mRNA
 A:Residues: 1-618 <DEG>
 A:Cross-references: GB:X52308; NID:953813; PIDN:CAA35548.1; PID:953814
 A:Experimental source: strain C57BL/6
 A:Note: the data were obtained from females resulting from the cross of M. domesticus
 R:Banfield, D.K.; MacGillivray, R.T.A.
 Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
 A:Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and
 A:Reference number: A42696; MUID:92212913
 A:Accession: A42696

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 384-618, 'E' <BANT>
A:Cross-references: GB:M81394
C:Superfamily: Thrombin; Gla domain homology; trypsin homology
C:Keywords: blood coagulation; calcium binding; carboxyglutamic acid; glycoprotein; hyd
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-43/Domain: propeptide #status predicted <PRO>
F:28-88/Domain: Gla domain homology <GLA>
F:44-618/Product: prothrombin B #status predicted <MAT>
F:109-187/Domain: kringle homology <KR1>
F:215-293/Domain: kringle homology <KR2>
F:361-610/Domain: trypsin homology <TRY>
F:50-51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #status
F:61-66,91-104,109-187,130-170,158-182,215-293,236-276,264-288,333-479,388-404,533-547,5
F:403,459,565/Active site: His, Asp, Ser #status predicted

Query Match 38.7%; Score 75; DB 2; Length 618;
Best Local Similarity 37.2%; Pred. No. 5,7e-05;
Matches 16; Conservative 4; Mismatches 23; Indels 0; Gaps 0;

Oy 2 NGFLXLRPGSLKRXCRXXLCSPXXAHIFRNXXRTQFWVS 44
Db 46 SGFLELRKGNLERECVEEQCYEEAFEALESPODTDFVMAKY 88

RESULT 19
553433
Plasma protein S precursor, vitamin K dependent - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 01-Aug-1995 #sequence-revision 18-Jul-1997 #text-change 16-Jul-1999
C:Accession: S53433
R:Greenberg, J.S.; Fernandez, J.A.; Radtke, K.P.; Griffin, J.H.
Biochem. J. 305, 397-403, 1995
A:Title: Identification of candidate residues for interaction of protein S with C4b bind
A:Reference number: S53433; MUID:95134217
A:Accession: S53433
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-642 <GRE>
A:Cross-references: EMBL:L31379
A:Experimental source: tissue type liver
C:Genetics:
A:Gene: PROS
C:Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom
F:1-51/Domain: Gla domain homology (fragment) <GLA>
F:1-7/Domain: signal sequence (fragment) #status predicted <SIG>
F:8-642/Product: plasma protein S #status predicted <MAT>
F:87-120/Domain: EGF homology <EG1>
F:127-165/Domain: EGF homology <EG2>
F:171-207/Domain: EGF homology <EG3>
F:213-248/Domain: EGF homology <EG4>
F:281-633/Domain: sex hormone-binding globulin homology <SHB>
F:291-444/Domain: laminin G repeat homology <LGR>

Query Match 38.1%; Score 74; DB 2; Length 642;
Best Local Similarity 36.4%; Pred. No. 8.9e-05;
Matches 16; Conservative 5; Mismatches 23; Indels 0; Gaps 0;

Oy 1 ANGFLXLRPGSLKRXCRXXLCSPXXAHIFRNXXRTQFWVS 44
Db 8 ANSMLEERKGNLERECIEELCKSEAREVEFNDETEYFPAY 51

RESULT 20
KXBOS
Plasma protein S precursor - bovine
N:Alternate names: vitamin K-dependent protein S
C:Species: Bos primigenius taurus (cattle)
C:Date: 08-Aug-1987 #sequence-revision 26-Jan-1996 #text-change 16-Jul-1999
C:Accession: A24759; A23888

R:Dahlback, B.; Lundvall, A.; Stenflo, J.
Proc. Natl. Acad. Sci. U.S.A. 83, 4199-4203, 1986
A:Title: Primary structure of bovine vitamin K-dependent protein S.
A:Reference number: A24759; MUID:86233400
A:Accession: A24759
A:Molecule type: mRNA
A:Residues: 1-675 <DNH>

A:Cross-references: GB:M13044; NID:g163697; PID:AAA30757.1; PID:g163698
A>Note: parts of this sequence, including the amino end of the mature protein, were d
R:Dahlback, B.; Lundvall, A.; Stenflo, J.
J. Biol. Chem. 261, 5111-5115, 1986

A:Title: Localization of thrombin cleavage sites in the amino-terminal region of bovi
A:Reference number: A23888; MUID:66168236
A:Accession: A23888

A:Molecule type: protein
A:Residues: 42-141 <DA2>
C:Complex: in plasma forms a complex with C4b binding protein
C:Function:

A:Description: a cofactor for activated protein C (EC 3.4.21.69); thrombin cleavage d
C:Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat
C:Keywords: beta-hydroxyaspartagine; beta-hydroxyaspartic acid; blood coagulation; car
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-41/Domain: propeptide #status predicted <PRO>
F:26-85/Domain: Gla domain homology <GLA>
F:42-675/Product: plasma protein S #status experimental <MAT>

F:121-154/Domain: EGF homology <EG1>
F:161-199/Domain: EGF homology <EG2>
F:205-241/Domain: EGF homology <EG3>
F:247-282/Domain: EGF homology <EG4>
F:315-666/Domain: sex hormone-binding globulin homology <SHB>
F:325-418/Domain: laminin G repeat homology <LGR>
F:47-48,55-57,60,61,66,67,70,73,77/Modified site: gamma-carboxyglutamic acid (Glu) #
F:58-63,88-113,121-134,126-143,145-154,161-175,171-184,186-199,205-217,212-226,228-24
F:93-94/Cleavage site: Arg-Ala (thrombin) #status experimental
F:111-112/Cleavage site: Arg-Ser (thrombin) #status experimental
F:116/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F:117,219,258/Modified site: erythro-beta-hydroxyaspartagine (Asn) #status experimenta
F:288-567,449-475,638-665/Disulfide bonds: #status experimental
F:499/Binding site: carboxylate (Asn) (covalent) #status predicted
F:509/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 36.1%; Score 70; DB 1; Length 675;
Best Local Similarity 36.4%; Pred. No. 0.00046;
Matches 16; Conservative 4; Mismatches 24; Indels 0; Gaps 0;

Oy 1 ANGFLXLRPGSLKRXCRXXLCSPXXAHIFRNXXRTQFWVS 44
Db 42 ANTLLEERTKGNLERECIEELCKNKEAREIFENNPETETFPKY 85

RESULT 21
TBBO
Thrombin (EC 3.4.21.5) precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 24-Apr-1984 #sequence-revision 14-Jul-1994 #text-change 18-Jun-1999
C:Accession: S02537; A00915; A57552; 146045; S67518
R:Irwin, D.M.; Robertson, K.A.; MacGillivray, R.T.A.
J. Mol. Biol. 200, 31-45, 1988
A:Title: Structure and evolution of the bovine prothrombin gene.
A:Reference number: S02537; MUID:88245190
A:Accession: S02537
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-625 <IRW>
R:MacGillivray, R.T.A.; Davie, E.W.
Biochemistry 23, 1626-1634, 1984
A:Title: Characterization of bovine prothrombin mRNA and its translation product.
A:Reference number: A00915; MUID:84203525
A:Accession: A00915
A:Molecule type: mRNA
A:Residues: 1-230, 'H', 223-625 <MAC>
A>Note: 600-Asn was also found

R.Magnusson, S.: Sottrup-Jensen, L.; Petersen, T.E.; Cleys, H.
In Boerhaave Symposium on Prothrombin and Related Coagulation Factors, Hemker, H.C., and
A:Reference number: A37552
A:Accession: A37552
A:Molecule type: protein
A:Residues: 44-287, 'N', 289-352, 'E', 354, 'Q', 356-548, 'ND', 551-599, 'N', 601-625 <MA2>
A:Note: the evidence for 231-Ser is strong
A:Note: disulfide bonds and carbohydrate binding sites were determined
R:Park, C.H.; Tullinsky, A.
Biochemistry 25, 3977-3982, 1986
A:Title: Three-dimensional structure of the kringle sequence: structure of prothrombin
A:Reference number: A37553; PMID:86296631
A:Contents: annotation; residues 44-317, X-ray crystallography, 2.8 angstroms
R:Irwin, D.M.; Ahern, K.G.; Pearson, G.D.; Macgillivray, R.T.A.
Biochemistry 24, 6854-6861, 1985
A:Title: Characterization of the bovine prothrombin gene.
A:Reference number: A37554; PMID:86077733
A:Contents: annotation; gene structure
R:Macgillivray, R.T.; Degen, S.J.; Chandra, T.; Woo, S.L.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 77, 5153-5157, 1980
A:Title: Cloning and analysis of a cDNA coding for bovine prothrombin.
A:Reference number: I46045; PMID:81054926
A:Accession: I46045
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 466-599, 'N', 601-625 <MA2>
A:Cross-References: EMBL:V00135; NID:q772; PIDN:CAA23451.1; PID:g808945
R:Pejler, G.; Karlstrom, A.R.; Berg, L.
Eur. J. Biochem. 227, 102-107, 1995
A:Title: Identification of the proteolytic thrombin fragments formed after cleavage with
A:Reference number: S67518; PMID:95154277
A:Accession: S67518
A:Status: preliminary
A:Molecule type: protein
A:Residues: 318-325, 333-338, 'X', 340, 367-374, 481-484, 'X', 486-488, 515-522 <PE3>
A:Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibrin
C:Comment: Prothrombin is activated on the surface of a phospholipid membrane that binds
Ligation peptide and cleaves the remaining part into light and heavy chains. The activat
C:Comment: Thrombin can cleave the amino-terminal activation peptide 1 from prothrombin,
C:Comment: The gamma-carboxylutamic acid residues bind calcium ions, result from the carboxy
ent interaction with the negatively charged phospholipid membrane surface.
C:Comment: The prothrombin precursor is synthesized in the liver.
C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C:Keywords: blood coagulation; calcium binding; carboxylutamic acid; duplication; glyco
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-43/Domain: propeptide #status predicted <PRO>
F:28-88/Domain: Gla domain homology <GLA>
F:44-625/Product: prothrombin #status experimental <MP>
F:44-199/Domain: activation peptide 1 #status experimental <FR1>
F:109-187/Domain: kringle homology <KR1>
F:200-317/Domain: activation peptide 2 #status experimental <FR2>
F:214-292/Domain: kringle homology <KR2>
F:318-366/Product: thrombin light chain #status experimental <CH>
F:367-625/Product: thrombin heavy chain #status experimental <CH>
F:367-616/Domain: trypsin homology <TRY>
F:501, 51, 58, 60, 63, 64, 69, 70, 73, 76/Modified site: gamma-carboxylutamic acid (Glu) #status
F:61-66, 91-104, 109-187, 130-158, 182, 214-292, 235-275, 263-287, 339-485, 394-410, 539-553, 5
F:120, 144, 419/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:409, 465, 571/Active site: His, Asp, Ser #status experimental

plasma protein S precursor, vitamin K dependent - rhesus macaque (fragment)
C:Species: Macaca mulatta (rhesus macaque)
C:Date: 19-Mar-1997 #sequence_Revision 18-Jul-1997 #text_change 16-Jul-1999
C:Accession: S53434
R:Greenard, J.S.; Fernandez, J.A.; Radtke, K.P.; Griffin, J.H.
Biochem. J. 305, 397-403, 1995
A:Title: Identification of candidate residues for interaction of protein S with C4b b
A:Reference number: S53433; PMID:95134217
A:Accession: S53434
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-642 <GRE>
A:Cross-References: EMBL:L31380
A:Experimental source: tissue type liver
A:Note: the source is designated as rhesus monkey
C:Genetics:
A:Gene: PROS
C:Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat
F:1-51/Domain: Gla domain homology (fragment) <GLA>
F:1-7/Domain: signal sequence (fragment) #status predicted <SIG>
F:8-642/Product: plasma protein S #status predicted <MAT>
F:87-120/Domain: EGF homology <EG1>
F:127-165/Domain: EGF homology <EG2>
F:171-207/Domain: EGF homology <EG3>
F:213-248/Domain: EGF homology <EG4>
F:281-633/Domain: sex hormone-binding globulin homology <SHB>
F:291-444/Domain: laminin G repeat homology <LGR>

Query Match 35.6%; Score 69; DB 2; Length 642;
Best Local Similarity 34.1%; Pred. No. 0.00066;
Matches 15; Conservative 5; Mismatches 24; Indels 0; Gaps 0;
OY 1 ANGLXLRPGSLKRCXKXLCSPFXAHXIFRNXXRTROFWYX 44
DB 8 ANSMLEETKOGNLEFCEICELCKKEAREVENDPETDYFPRY 51

RESULT 23
S38819
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 18-Feb-1994 #sequence_Revision 21-Jul-1995 #text_change 16-Jul-1999
C:Accession: S38819; S37238
R:He, X.; Dahlback, B.
Eur. J. Biochem. 217, 857-865, 1993
A:Title: Molecular cloning, expression and functional characterization of rabbit anti
A:Reference number: S38819; PMID:94039141
A:Accession: S38819
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-646 <HEX>
A:Cross-References: EMBL:226485
R:He, X.; Dahlback, B.
Submitted to the EMBL Data Library, September 1993
A:Description: Molecular Cloning and Expression of Rabbit Anticoagulant Vitamin K-dep
A:Reference number: S37238
A:Accession: S37238
A:Molecule type: mRNA
A:Residues: 1-502, 'L', 504-646 <HE2>
A:Cross-References: EMBL:226485; NID:q403306; PIDN:CAA81259.1; PID:q403307
C:Superfamily: Plasma protein S; EGF homology; Gla domain homology; laminin G repeat
F:1-56/Domain: Gla domain homology (fragment) <GLA>
F:92-125/Domain: EGF homology <EG1>
F:132-170/Domain: EGF homology <EG2>
F:176-212/Domain: EGF homology <EG3>
F:218-253/Domain: EGF homology <EG4>
F:286-637/Domain: sex hormone-binding globulin homology <SHB>
F:296-449/Domain: laminin G repeat homology <LGR>

Query Match 35.6%; Score 69; DB 1; Length 625;
Best Local Similarity 35.7%; Pred. No. 0.00065;
Matches 15; Conservative 3; Mismatches 24; Indels 0; Gaps 0;
OY 3 GFLXLRPGSLKRCXKXLCSPFXAHXIFRNXXRTROFWYX 44
DB 47 GFLEEVKRGKLEECLEPCSPREAFEALESLSATDAFWAKY 88

RESULT 22
S53434

Query Match 28.4%; Score 55; DB 2; Length 674;
Best Local Similarity 33.3%; Pred. No. 0.19;
Matches 12; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

QY 9 RRGSLXKCRXXLCSEFXAHXIFRNXXRTQRFVSY 44
DB 54 KQGLERECVEEVCSEKREAREVFENDPETDYFPRY 89

RESULT 33

probable MAP kinase [Imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: D84859
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
Neus, D.; Mierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: D84859
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-594 <STO>
A:Cross-references: GB:AE002093; NID:g4512667; PIDN:AAD21721.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g42880
A:Map position: 2

Query Match 28.1%; Score 54.5; DB 2; Length 594;
Best Local Similarity 30.4%; Pred. No. 0.21;
Matches 14; Conservative 6; Mismatches 23; Indels 3; Gaps 2;

QY 1 ANGFLXXLRPGL--XRXCXXLCSEFXAHXIFRNXXRTQRFVSY 44
DB 133 ANYHHDLPKRNILANANCKLKICDFGLARVAF-NDPTTFVFTDY 177

RESULT 34

probable MAP kinase ATPMK9, 98271-101224 [Imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: C96575
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hultzer, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Martelli,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: C96575
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-603 <STO>
A:Cross-references: GB:AE005173; NID:g10645353; PIDN:AAG21473.1; GSPDB:GN00141
C:Genetics:
A:Gene: F22G10.12
A:Map position: 1

Query Match 28.1%; Score 54.5; DB 2; Length 603;
Best Local Similarity 30.4%; Pred. No. 0.22;
Matches 14; Conservative 6; Mismatches 23; Indels 3; Gaps 2;

QY 1 ANGFLXXLRPGL--XRXCXXLCSEFXAHXIFRNXXRTQRFVSY 44
DB 133 ANYHHDLPKRNILANANCKLKICDFGLARVAF-NDPTTFVFTDY 177

RESULT 35

WIMLB
E1 protein - bovine papillomavirus type 1
C:Species: bovine papillomavirus type 1
C:Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 28-Jul-2000
C:Accession: A03663
R:Chen, E.Y.; Howley, P.M.; Levinson, A.D.; Seeburg, P.H.
Nature 299, 529-534, 1982
A:Title: The primary structure and genetic organization of the bovine papillomavirus
A:Reference number: A93289; MUID:83012974
A:Accession: A03663
A:Molecule type: DNA
A:Residues: 1-605 <CHE>
A:Cross-references: GB:X02346; GB:J02044; GB:M24622; GB:X00473; NID:g60965; PIDN:CAB4
C:Superfamily: papillomavirus E1 protein
C:Keywords: early protein

Query Match 26.8%; Score 52; DB 1; Length 605;
Best Local Similarity 45.5%; Pred. No. 0.59;
Matches 10; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 21 LCSEFXAHXIFRNXXRTQRFV 42
DB 172 LCSEFHDTRFLFKNDKTTNQOV 193

RESULT 36

WIMLB2
E1 protein - bovine papillomavirus type 2
C:Species: bovine papillomavirus type 2
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 12-Jun-1998
C:Accession: C31169
R:Groff, D.E.; Mitera, R.; Lancaster, W.D.
submitted to Genbank, May 1988
A:Reference number: A94519
A:Accession: C31169
A:Molecule type: DNA
A:Residues: 1-620 <GRO>
A:Cross-references: GB:M20219; GB:M19551; NID:g333996
C:Superfamily: papillomavirus E1 protein
C:Keywords: early protein; glycoprotein
P/2,109,173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 26.8%; Score 52; DB 1; Length 620;
Best Local Similarity 45.5%; Pred. No. 0.61;
Matches 10; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 21 LCSEFXAHXIFRNXXRTQRFV 42
DB 187 LCSEFHDTRFLFKNDKTTNQOV 208

RESULT 37

VHVNII
nucleoprotein - infectious hematopoietic necrosis virus
N:Alternate names: nucleocapsid protein
C:Species: infectious hematopoietic necrosis virus
C:Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 16-Jul-1999
C:Accession: A31834
R:Gilmore Jr., R.D.; Leong, J.C.
Virology 167, 644-648, 1988
A:Title: The nucleocapsid gene of infectious hematopoietic necrosis virus, a fish rhabdovirus
A:Reference number: A31834; MUID:89073771
A:Accession: A31834
A:Molecule type: mRNA
A:Residues: 1-413 <GIL>

A:Cross-references: GB:J04321; NID:9331304; PIDN:AAA6240.1; PID:9331305
C:Superfamily: Infectious hematopoietic necrosis virus nucleoprotein
C:Keywords: nucleocapsid, nucleoprotein

Query Match 26.3%; Score 51; DB 1; Length 413;
Best Local Similarity 32.3%; Pred. No. 0.63;
Matches 10; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

Oy 11 GSLRXCXRLCSFXAHXIFRNXXRTROFW 41
Db 57 GEGTRRALGLCAFYIAETVHGEARSPNFW 87

RESULT 38

S43737 protein kinase SLR2 (EC 2.7.1.1) - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein H8179.16; protein YHR030C

C:Species: Saccharomyces cerevisiae

C>Date: 30-Sep-1993 #sequence_revision 27-Jan-1995 #text_change 23-Mar-2001

C:Accession: S43737; S46743; S19051

R:Nombela, C.
submitted to the EMBL Data Library, January 1994

A:Reference number: S43737

A:Accession: S43737

A:Molecule type: DNA

A:Residues: 1-484 <NOM>

A:Cross-references: EMBL:X59262; NID:9455518; PIDN:CAA1954.1; PID:9455519

A>Note: this is a revision to the sequence from reference S19051

R:Du, Z.

submitted to the EMBL Data Library, May 1994

A:Description: The sequence of S. cerevisiae cosmid 8179.

A:Reference number: S46732

A:Accession: S46732

A:Molecule type: DNA

A:Residues: 1-484 <DUZ>

A:Cross-references: EMBL:U00062; NID:9488162; PIDN:AAB68912.1; PID:9488177; MIPS:YHR030C

R:Torres, L.; Martin, H.; Garcia-Siez, M.L.; Arroyo, J.; Molina, M.; Sanchez, M.; Nombela

MOL. Microbiol. 5, 2845-2854, 1991

A:Title: A protein kinase gene complements the lytic phenotype of Saccharomyces cerevisiae

A:Reference number: S19051; MUID:92140049

A:Accession: S19051

A:Molecule type: DNA

A:Residues: 1-55, 'L', 57-466, 'S', 468-484 <TOR>

A:Cross-references: EMBL:X59262

A>Note: this sequence has been revised in reference S43737

C:Genetics:

A:Gene: SGD:SLR2

A:Cross-references: SGD:S0001072; MIPS:YHR030C

A:Map position: 8R

C:Function: phosphotransferase; serine/threonine-specific protein kinase

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog

C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

F:21-287/Domain: protein kinase homology <KIN>

F:29-37/Region: protein kinase ATP-binding motif

F:153/Active site: Asp #status predicted

Query Match 26.3%; Score 51; DB 2; Length 484;
Best Local Similarity 30.8%; Pred. No. 0.73;
Matches 12; Conservative 4; Mismatches 21; Indels 2; Gaps 1;

Oy 8 LRPGSL--XRKCRXLCSEFXAHXIFRNXXRTROFW 44
Db 154 LKPGNLVNAQCQIKICDFGLARGYSENPVENSQFLTEY 192

RESULT 39

T51517 telomerase reverse transcriptase - Arabidopsis thaliana

N:Alternate names: protein F5E19_190

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C:Accession: T51517

R:Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.;

submitted to the Protein Sequence Database, August 2000

A:Reference number: 225394

A:Accession: T51517

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1123 <SAT>

A:Cross-references: EMBL:AL391147

A:Experimental source: cultivar Columbia; BAC clone F5E19

C:Genetics:

A:Map position: 5

A:Introns: 100/3; 125/3; 147/3; 185/1; 300/3; 325/1; 369/2; 414/3; 765/3; 942/2; 1033

A>Note: F5E19_190

Query Match 24.5%; Score 47.5; DB 2; Length 1123;

Best Local Similarity 25.0%; Pred. No. 6.3;

Matches 12; Conservative 6; Mismatches 25; Indels 5; Gaps 1;

Oy 2 NGFLXXLRPGSLXRCRXLCSEFXAHXIFRNXXRTRO----FWVS 44
Db 498 NQFLHKVKSPPFPARKELCCMVNGHEDSISIRSTQMLCTKWISW 545

RESULT 40

C72226 hypothetical protein TM1677 - Thermotoga maritima (strain MSB8)

C:Species: Thermotoga maritima

C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000

C:Accession: C72226

R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hlic

Gartelt, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,

C.M.

Nature 399, 323-329, 1999

A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome

A:Reference number: A72200; MUID:99287316

A:Accession: C72226

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-402 <ARN>

A:Cross-references: GB:AE001808; GB:AE000512; NID:94982233; PIDN:AA036744.1; PID:9498

A:Experimental source: strain MSB8

C:Genetics:

A:Gene: TM1677

C:Superfamily: hypothetical protein b1432

Query Match 23.7%; Score 46; DB 2; Length 402;
Best Local Similarity 28.2%; Pred. No. 4.6;
Matches 11; Conservative 5; Mismatches 19; Indels 4; Gaps 1;

Oy 10 PGSLRXC---RXXLCSEFXAHXIFRNXXRTROFW 44
Db 14 PGHLSQTCBLNRRTAARIYKMTWISYVRKTKRKGWLSW 52

RESULT 41

T39306 mitogen-activated protein kinase - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000

C:Accession: T39306; T45129; T48694

R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.

submitted to the EMBL Data Library, March 1998

A:Reference number: 221843

A:Accession: T39306

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-422 <MOO>

A:Cross-references: EMBL:AL022117; PIDN:CAA17923.1; GSPDB:GN00067; SPDB:SPC119.08

A:Experimental source: strain 972h-, cosmid c119

R: Toda, T.; Dhut, S.; Superfili-Funga, G.; Gotoh, Y.; Nishida, E.; Sugiyura, R.; Kuno, T.
Mol. Cell. Biol. 16, 6752-6764, 1996
A: Title: The fission yeast pmk1+ gene encodes a novel mitogen-activated protein kinase
A: Reference number: Z07420; MUID: 97098653
A: Accession: T45129
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: DNA
A: Residues: 1-422 <TOD>
A: Cross-references: EMBL: X98243; NID: g1666670; PIDN: CAA66899.1; PID: g1666671
R: Zaitsevskaya-Carter, T.; Cooper, J.A.
EMBO J. 16, 1318-1331, 1997
A: Title: Spml, a stress-activated MAP kinase that regulates morphogenesis in *S. pombe*.
A: Reference number: Z24537; MUID: 97280820
A: Accession: T48694
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: DNA
A: Residues: 1-422 <ZAI>
A: Cross-references: EMBL: U65405; NID: g1513145; PIDN: AAC49707.1; PID: g1513146
C: Genetics:
A: Gene: spml; SPBC119.08; pmk1
A: Map position: 2
A: Introns: 22/3; 82/3; 106/3
C: Function:
A: Description: pmk1 probably lies on a novel MAPK pathway, which does not overlap function stress-sensing pathway
C: Superfamily: kinase-related transforming protein; protein kinase homology
C: Keywords: phosphoprotein; protein kinase; signal transduction

Query Match 23.2%; Score 45; DB 2; Length 422;
Best Local Similarity 28.3%; Pred. No. 7.2;
Matches 13; Conservative 3; Mismatches 28; Indels 2; Gaps 1;

Qy 1 ANGFLXLRPGSL-
DB 143 ANYIHDLKRGNLVNADELKICDFGLARGCEENPENGFMTEY 188

RESULT 42
T08528
probable DNA topoisomerase (EC 5.99.1.2) III - Enterobacter aerogenes plasmid R751
C: Species: Enterobacter aerogenes
C: Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C: Accession: T08528
R: Thorsted, P.B.; Shah, D.S.; Macartney, D.; Kostelidou, K.; Thomas, C.M.
Plasmid 36, 95-111, 1996
A: Title: Conservation of the genetic switch between replication and transfer genes of *IncA*.
A: Reference number: Z16434; MUID: 97118926
A: Accession: T08528
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: DNA
A: Residues: 1-687 <THO>
A: Cross-references: EMBL: U67194; NID: g1572520; PIDN: AAC64472.1; PID: g1572577
C: Genetics:
A: Gene: traE
A: Genome: plasmid R751
C: Superfamily: DNA topoisomerase I topA
C: Keywords: DNA binding; isomerase

Query Match 23.2%; Score 45; DB 2; Length 687;
Best Local Similarity 61.5%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 31 FRNXRTROFWS
DB 125 FRNSKVRFRWS 137

RESULT 43
T18556
O-antigen biosynthesis protein homolog rfbC - Myxococcus xanthus
C: Species: Myxococcus xanthus

C: Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C: Accession: T18556
R: Guo, D.; Bowden, M.G.; Pershad, R.; Kaplan, H.B.
J. Bacteriol. 178, 1631-1639, 1996
A: Title: The *Myxococcus xanthus* rfbABC operon encodes an ATP-binding cassette transpo
A: Reference number: Z18970; MUID: 96198166
A: Accession: T18556
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: DNA
A: Residues: 1-1275 <GUO>
A: Cross-references: EMBL: U36795; NID: g1235659; PID: g1235662; PIDN: AAB05019.1
C: Genetics:
A: Note: rfbC

Query Match 23.2%; Score 45; DB 2; Length 1275;
Best Local Similarity 38.5%; Pred. No. 19;
Matches 10; Conservative 1; Mismatches 15; Indels 0; Gaps 0;

Qy 3 GFLXXLRPGSLRXRCXXLCSPFXAH
DB 1144 GMLPAERTGALRECDVGLCFMFTRH 1169

RESULT 44
T15137
hypothetical protein T28F2.3 - *Caenorhabditis elegans*
C: Species: *Caenorhabditis elegans*
C: Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C: Accession: T15137
R: Madsen, C.; Fromick, B.
submitted to the EMBL Data Library, April 1997
A: Description: The sequence of *C. elegans* cosmid T28F2.
A: Reference number: Z18300
A: Accession: T15137
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: DNA
A: Residues: 1-319 <MAD>
A: Cross-references: EMBL: AF000198; NID: g2047345; PID: g2047348; PIDN: AAB53054.1; GSPDB
A: Experimental source: strain Bristol N2; clone T28F2
C: Genetics:
A: Gene: CSP-128F2.3
A: Map position: 1
A: Introns: 90/2; 189/3; 266/3; 295/3

Query Match 22.9%; Score 44.5; DB 2; Length 319;
Best Local Similarity 28.9%; Pred. No. 6.9;
Matches 11; Conservative 6; Mismatches 20; Indels 1; Gaps 1;

Qy 5 LXXLRPGSLRXRCXXLCSPFXAHXIFRNXXRTROFVW 42
DB 201 LNLPLQVVIYKGECKKCSFD-
QTFEPVAEKKEKFEWM 237

RESULT 45
G84993
glutathione synthase (EC 6.3.2.3) [Imported] - *Buchnera* sp. (strain APS)
C: Species: *Buchnera* sp.
C: Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C: Accession: G84993
R: Shigenobu, S.; Matanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-84, 2000
A: Title: Genome sequence of the endocellular bacterial symbiont of aphids *Buchnera* sp.
A: Reference number: A84930; MUID: 20445173
A: Accession: G84993
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-320 <STO>
A: Cross-references: GB: AP000398; GSPDB: GN00144
A: Experimental source: strain APS
C: Genetics:
A: Gene: gshB; BU547

Query Match	22.28;	Score 43;	DB 2;	Length 555;
Best Local Similarity	33.38;	Pred. NO. 21;		
Matches 13;	Conservative 5;	Mismatches 15;	Indels 6;	Gaps 2;

QY 9 RPSGL----XRCCRXLCSFAXAHXIFRKKXRTQFWVS 433
 |||| : || : || : ||
 Db 61 RPSGLVLGGLKACRDYNC--RSKYFFFRDPRTKEVTLIS 977

RESULT 50
 681710
 Hypothetical protein TC0352 [imported] - Chlamydia muridarum (strain Nigg)
 C:Species: Chlamydia muridarum; Chlamydia trachomatis MOPn
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 16-Feb-2001
 C:Accession: 681710
 R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
 C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolony, J.; McClarty, G.; Salzberg,
 Nucleic Acids Res. 28, 1397-1406, 2000
 A:Title: Genome sequences of Chlamydia trachomatis MOPn and Chlamydia pneumoniae AR39.
 A:Reference number: AB1500; MUID:20150255
 A:Accession: 681710
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-133 <FFT>
 A:Cross-references: GB:AE002303; GB:AE002160; NID:g7190392; PIDN:AAF39213.1; PID:g7190339
 C:Experimental source: strain Nigg (MOPn)
 C:Genetics
 A:Gene: TC0352
 A:Superfamily: Chlamydia muridarum hypothetical protein TC0352

Query Match	21.6%;	Score 42;	DB 2;	Length 133;
Best Local Similarity	33.3%;	Pred. NO. 8.7;		
Matches 12;	Conservative 1;	Mismatches 17;	Indels 6;	Gaps 1;

```

QY      4 FLXLLRPGSLRXRCRXLLCS-----FXAHXJFRN 33
          ||| : |||
Db      50 FLRLSSFLKICAHRCSLSLWQVFSCFHAFELN 85

```

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Search completed: August 30, 2002, 15:32:48
Job time: 5843 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 30, 2002, 15:45:35 ; Search time 77.99 Seconds
(Without alignments)
21.845 Million cell updates/sec

Title: US-09-302-239-4

Perfect score: 194
Sequence: 1 ANGFLXLRPGSLRXRCRX.....XXAHXIFRXRXTRQFWYSY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	165	85.1	407	FA7_BOVIN	P22457 bos taurus
2	139	71.6	444	FA7_RABIT	P81139 oryctolagus
3	131	67.5	466	FA7_HUMAN	P08709 homo sapien
4	115	59.3	461	PRTC_MOUSE	P33587 mus musculu
5	114	58.8	446	FA7_MOUSE	P70375 mus musculu
6	110	56.7	459	PRTC_PIG	Q991p2 sus scrofa
7	107	55.2	218	TMG1_HUMAN	Q14668 homo sapien
8	106	54.6	461	PRTC_RAT	P13394 rattus norv
9	105	54.1	456	PRTC_BOVIN	P00745 bos taurus
10	99	51.0	231	TMG3_HUMAN	Q9bzd7 homo sapien
11	94	48.5	488	FA10_HUMAN	P00742 homo sapien
12	92	47.4	458	PRTC_RABIT	Q28661 oryctolagus
13	92	47.4	490	FA10_RABIT	Q19045 oryctolagus
14	89	45.9	461	PRTC_HUMAN	P04070 homo sapien
15	89	45.9	492	FA10_BOVIN	P00743 bos taurus
16	87	44.8	461	FA9_HUMAN	P00740 homo sapien
17	86	44.3	416	FA9_BOVIN	P00741 bos taurus
18	81	41.8	452	FA9_CANFA	P19540 canis famill
19	81	41.8	459	FA9_MOUSE	P16294 mus musculu
20	81	41.8	475	FA10_CHICK	P25155 gallus galli
21	79	40.7	202	TMG2_HUMAN	Q14669 homo sapien
22	78	40.2	226	TMG4_HUMAN	Q9bzd6 homo sapien
23	78	40.2	622	THRB_HUMAN	P00734 homo sapien
24	77	39.7	376	FA10_TROCA	P81138 tropidichis
25	75	38.7	617	THRB_RAT	P18292 rattus norv
26	75	38.7	618	THRB_MOUSE	P18291 mus musculu
27	70	36.1	625	PRTC_BOVIN	P00723 bos taurus
28	69	35.6	625	THRB_BOVIN	P00735 bos taurus
29	69	35.6	646	PRTC_RABIT	P81136 oryctolagus
30	69	35.6	649	PRTC_MACMU	Q28520 macaca mula
31	69	35.6	676	PRTC_HUMAN	P07225 homo sapien
32	67	34.5	675	PRTC_RAT	P53813 rattus norv
33	66	34.0	400	PRTC_HUMAN	P22891 homo sapien

ALIGNMENTS

RESULT 1	FA7_BOVIN	STANDARD:	PRT:	407 AA.
AC	P22457:			
DT	01-AUG-1991 (Rel. 19, Created)			
DT	01-AUG-1991 (Rel. 19, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Coagulation factor VII (EC 3.4.21.21) (Serum prothrombin conversion accelerator).			
GN	F7.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=89008362; PubMed=3049594;			
RA	Takeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T.,			
RA	Iwanaga S.;			
RT	"Bovine factor VII. Its purification and complete amino acid			
RT	sequence.";			
RL	J. Biol. Chem. 263:14868-14877(1988).			
RN	[2]			
RP	STRUCTURE OF CARBOHYDRATE ON SER-52.			
RX	MEDLINE=89213999; PubMed=3149637;			
RA	Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T.,			
RA	Miyata T., Iwanaga S., Takao T., Shimonishi Y., Ikenaka T.;			
RT	"A new trisaccharide sugar chain linked to a serine residue in bovine			
RT	blood coagulation factors VII and IX.";			
RL	J. Biochem. 104:867-868(1988).			
RN	[3]			
RP	STRUCTURE OF CARBOHYDRATE ON SER-52.			
RX	MEDLINE=91344709; PubMed=21293677.			
RA	Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;			
RT	"A new trisaccharide sugar chain linked to a serine residue in the			
RT	first EGF-like domain of clotting factors VII and IX and protein Z.";			
RL	Adv. Exp. Med. Biol. 281:121-131(1990).			
CC	-I- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS			
CC	CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR			
CC	THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR			
CC	AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR Xa			
CC	BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO			
CC	FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.			
CC	-I- CATALYTIC ACTIVITY: Hydrolyses one Arg-I-Ile bond in factor X to			
CC	form factor Xa.			
CC	-I- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED			
CC	BY A DISULFIDE BOND.			
CC	-I- TISSUE SPECIFICITY: PLASMA.			
CC	-I- PM: THE VITAMIN K-DEPENDENT. ENZYMIC CARBOXYLATION OF SOME			
CC	GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND			

34	62	32.0	396	1	PRTC_BOVIN	P00744 bos taurus
35	60	30.9	675	1	PRTC_MOUSE	P08761 mus musculu
36	52	26.8	604	1	VE1_BPv2	P11298 bovine papil
37	52	26.8	605	1	VE1_BPv1	P03116 bovine papil
38	51	26.3	413	1	NCAP_IHNV	P19691 infectious
39	51	26.3	484	1	SLT2_YEAST	Q00772 saccharomyc
40	45	23.2	422	1	SPML_SCHPO	Q92398 schizosacch
41	45	23.2	501	1	MKCL_CANAL	P43068 candida alb
42	45	23.2	1275	1	RPBC_MYXXA	Q50864 myxococcus
43	44	22.7	320	1	GSHB_BUCAI	P57612 buchnera ap
44	43	22.2	551	1	FX10_HUMAN	Q9uk96 homo sapien
45	42	21.6	345	1	VG59_HSV11	Q00138 ictaluriid h
46	42	21.6	368	1	MPK7_ARATH	Q39027 arabidopsis
47	42	21.6	755	1	NAPA_DESDE	P81186 desulfotribir
48	41.5	21.4	184	1	ADML_MOUSE	P97297 mus musculu
49	41	21.1	3859	1	RPOA_LELY	Q04561 lelystad vi
50	40.5	20.9	270	1	TSNR_STRU1U	P52393 streptomyces

CC CALCIUM.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 DR PIR: A31979; A31979.
 DR HERSP: P08709; 1BF9.
 DR MERSP: S01.215; -.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000742; EGF-2.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR001438; EGF_II.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Trypsin.
 DR InterPro: IPR000294; Vitk_dep_GLA.
 DR Pfam: PF00008; EGF_2.
 DR Pfam: PF00594; gla; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00010; EGFBL00D.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00179; EGF_CA; 1.
 DR SMART: SM00001; EGF_Like; 1.
 DR SMART: SM00069; GLA; 1.
 DR SMART: SM00020; tryp_Spec; 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; 1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF_CA; 1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Hydrolyase: Serine protease: Blood coagulation: Glycoprotein;
 KW Liver: Plasma: Vitamin K: Calcium-binding; Gamma-carboxyglutamic acid;
 KW EGF-like domain; Repeat.
 FT CHAIN 1 152
 FT CHAIN 153 407
 FT DOMAIN 6 35
 FT DOMAIN 46 82
 FT DOMAIN 87 128
 FT DOMAIN 153 407
 FT SITE 152 153
 FT ACT_SITE 153 193
 FT ACT_SITE 242 344
 FT BINDING 338 338
 FT DISULFID 17 22
 FT DISULFID 50 61
 FT DISULFID 55 70
 FT DISULFID 72 81
 FT DISULFID 91 102
 FT DISULFID 98 112
 FT DISULFID 114 127
 FT DISULFID 135 262
 FT DISULFID 159 164
 FT DISULFID 178 194
 FT DISULFID 310 329
 FT DISULFID 340 368
 FT MOD_RES 6 6
 FT MOD_RES 7 7
 FT MOD_RES 14 14
 FT MOD_RES 16 16
 FT MOD_RES 19 19
 FT MOD_RES 20 20
 FT MOD_RES 25 25
 FT MOD_RES 26 26
 FT MOD_RES 29 29
 FT MOD_RES 35 35
 FT MOD_RES 52 52
 FT CARBOHYD 145 145

FT CARBOHYD 203 203 N-LINKED (GLCNAC...)
 SQ SEQUENCE 407 AA; 44431 MW; 703E1FE0636F7E10 CRC64;
 Query Match 85.1%; Score 165; DB 1; Length 407;
 Best Local Similarity 72.7%; Pred. No. 5.8e-22;
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 Qy 1 ANGFELXLRPGSLRXRCXXLCSEFXAHXIFRNXXTRQFWWSY 44
 Db 1 ANGFELXLRPGSLRXRCXXLCSEFXAHXIFRNXXTRQFWWSY 44
 RESULT 2
 FA7_RABIT STANDARD; PRT; 444 AA.
 ID FA7_RABIT P979224;
 AC P98139; 15-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 40, Last annotation update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
 DE conversion accelerator).
 GN F7.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA MEDLINE=93190306; Pubmed=8383365;
 RX Brothers A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;
 RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation
 RT factor VII.";
 RL Thromb. Res. suppl. 69:231-238(1993).
 RN [2]
 RP REVISION TO 395.
 RC TISSUE=Liver;
 RA Ruiz S.R., Blajchman M.A., Clarke B.J.;
 RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
 CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR
 CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
 CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
 CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
 CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
 CC SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Hydrolyses one Arg-1-Ile bond in factor X to
 CC form factor Xa.
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
 CC BY A DISULFIDE BOND (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC EMBL: U77477; AAB37326.1; -.
 DR HSSP: P08709; 1BF9.
 DR MERSP: S01.215; -.
 DR InterPro: IPR002086; Aldehyde-dehydr.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.

DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000742; EGF_2.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR002383; GLA_Dlood.
 DR InterPro: IPR001254; trypsin.
 DR InterPro: IPR000294; YlTK_dep-GLA.
 DR Pfam: PF00008; EGF_1.
 DR Pfam: PF00594; gla; 2.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRPSIN.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00179; EGF_CA; 1.
 DR SMART: SM00001; EGF_Like; 1.
 DR SMART: SM00069; GLA; 1.
 DR SMART: SM00020; TRYP_SPC; 1.
 DR PROSITE: PS00010; ASK_HYDROXYL; 1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS01187; EGF_CA; 1.
 DR PROSITE: PS00011; GLU CARBOXYLATION; 1.
 DR PROSITE: PSS0240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 DR Hydrolyase: Serine protease; Blood coagulation; Zymogen; Glycoprotein;
 KM Liver: Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
 KW EGF-like domain; Repeat; Signal; Hydroxylation.
 FT SIGNAL 1 21
 FT PROPEP 22 39
 FT CHAIN 40 191
 FT CHAIN 192 444
 FT DOMAIN 45 74
 FT DOMAIN 126 167
 FT DOMAIN 192 444
 FT SITE 191 192
 FT ACT_SITE 232 232
 FT ACT_SITE 281 281
 FT BINDING 383 383
 FT BINDING 377 377
 FT DISULFID 56 61
 FT DISULFID 89 100
 FT DISULFID 94 109
 FT DISULFID 111 120
 FT DISULFID 130 141
 FT DISULFID 137 151
 FT DISULFID 153 166
 FT DISULFID 174 301
 FT DISULFID 198 203
 FT DISULFID 217 233
 FT DISULFID 349 368
 FT DISULFID 379 407
 FT MOD_RES 45 45
 FT MOD_RES 46 46
 FT MOD_RES 53 53
 FT MOD_RES 55 55
 FT MOD_RES 58 58
 FT MOD_RES 59 59
 FT MOD_RES 64 64
 FT MOD_RES 65 65
 FT MOD_RES 68 68
 FT MOD_RES 74 74
 FT MOD_RES 102 102
 FT CARBOHYD 211 211
 FT CARBOHYD 242 242
 FT CARBOHYD 306 306
 FT SEQUENCE 444 AA; 49011 MW; 0481ABC4FE542788 CMC64;

Query Match 71.6%; Score 139; DB 1; Length 444;
 Best Local Similarity 54.5%; Pred. No. 2.9e-17;
 Matches 24; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

Oy 1 ANGFLXLRPGSLXKRCXKXLCSPFXAHXIFRNXXRTQFWWSY 44
 |||||
 Db 40 ANSFLELRPGSLERCKEELCSPEAREVFOSTERTKQFWITY 83
 RESULT 3
 FA7_HUMAN STANDARD; PRT; 466 AA.
 ID FA7_HUMAN
 AC P08709; Q14339;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
 DE conversion accelerator) (Eptacog alfa).
 GN F7.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=86205965; PubMed=3486420;
 RA Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C.,
 RA Woodbury R.G., Hart C.E., Insley M.Y., Kistiel W., Kurachi K.,
 RA Davie E.W.;
 RA "Characterization of a cDNA coding for human factor VII.";
 RA Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).
 RL [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87260948; PubMed=3037537;
 RA O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y.,
 RA Hagen F.S., Murray M.J.;
 RA "Nucleotide sequence of the gene coding for human factor VII, a
 RA vitamin K-dependent protein participating in blood coagulation.";
 RA Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).
 RL [3]
 RP SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.
 RX MEDLINE=89088153; PubMed=3264725;
 RA Thim L., Bjørn S., Christensen M., Nicolaisen E.M., Lund-Hansen T.,
 RA Pedersen A.H., Hedner U.;
 RA "Amino acid sequence and posttranslational modifications of human
 RA factor VIIa from plasma and transfected baby hamster kidney cells.";
 RA Biochemistry 27:7785-7793(1988).
 RL [4]
 RP CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.
 RX MEDLINE=91250411; PubMed=1904059;
 RA Bjørn S., Foster D.C., Thim L., Wiberg F.C., Christensen M.,
 RA Komiyama Y., Pedersen A.H., Kistiel W.;
 RA "Human plasma and recombinant factor VII. Characterization of O-
 RA glycosylations at serine residues 52 and 60 and effects of site-
 RA directed mutagenesis of serine 52 to alanine.";
 RA J. Biol. Chem. 266:11051-11057(1991).
 RL [5]
 RP STRUCTURE OF CARBOHYDRATE ON SER-112.
 RX MEDLINE=90062160; PubMed=2511201;
 RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T., Takao T.,
 RA Shimomishi Y., Iwanaga S.;
 RA "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
 RA (Xyl2-Glc) O-glycosidically linked to a serine residue in the first
 RA epidermal growth factor-like domain of human factors VII and IX and
 RA protein 2 and bovine protein 2.";
 RA J. Biol. Chem. 264:20320-20325(1989).
 RL [6]
 RP STRUCTURE OF CARBOHYDRATE ON SER-112.
 RX MEDLINE=91344709; PubMed=2129367;
 RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;
 RA "A new trisaccharide sugar chain linked to a serine residue in the
 RA first EGF-like domain of clotting factors VII and IX and protein 2.";
 RA Adv. Exp. Med. Biol. 281:121-131(1990).
 RL [7]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE=96175641; PubMed=8598903;

RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,
RA Kohnsberg W.H., Nemerson Y., Kirchhofer D.,
RT "The crystal structure of the complex of blood coagulation factor
RT VIIa with soluble tissue factor.";
RL Nature 380:41-46(1996).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
RX MEDLINE=99126538; PubMed=9925787;
RA Zhang E., St Charles R., Tullinsky A.;
RT "Structure of extracellular tissue factor complexed with factor VIIa
RT inhibited with a BPTI mutant.";
RL J. Mol. Biol. 285:2089-2104(1999).
RN [9]
RP STRUCTURE BY NMR OF 105-145.
RX MEDLINE=96367502; PubMed=9692950;
RA Muranyi A., Finn B.E., Gippert G.P., Forsen S., Steinflo J.,
RA Drakenberg T.,
RT "Solution structure of the N-terminal EGF-like domain from human
RT factor VII.";
RL Biochemistry 37:10605-10615(1998).
RN [10]
RP VARIANT GLN-364.
RX MEDLINE=91300046; PubMed=2070047;
RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,
RA Weede T.W., Tuddenham E.G.D.;
RT "Purification and characterization of factor VII 304-Gln: a variant
RT molecule with reduced activity isolated from a clinically unaffected
RT male.";
RL Blood 78:132-140(1991).
RN [11]
RP VARIANTS GLN-364 AND PHE-370.
RX MEDLINE=92340074; PubMed=1634227;
RA Marchetti G., Patrascchini P., Gemmati D., Derosa V., Pinotti M.,
RA Rodorigo G., Casonato A., Girolami A., Bernardi F.;
RT "Detection of two missense mutations and characterization of a repeat
RT polymorphism in the factor VII gene (F7)." ;
RL Hum. Genet. 89:497-502(1992).
RN [12]
RP VARIANT TYR-238.
RX MEDLINE=93372811; PubMed=8364544;
RA Marchetti G., Perrelli M., Patrascchini P., Redaelli R., Bernardi F.;
RT "A missense mutation (178Cys-->Tyr) and two neutral dimorphisms
RT (115His and 333Ser) in the human coagulation factor VII gene." ;
RL Hum. Mol. Genet. 2:1055-1056(1993).
RN [13]
RP VARIANTS.
RX MEDLINE=94061028; PubMed=8242057;
RA Takamiya O., Kembhall-COOK G., Marin D.M.A., Cooper D.N.,
RA von Felten A., Meili E., Hahn I., Prangnell D.R., Lumley H.,
RA Tuddenham E.G.D., McVey J.H.;
RT "Detection of missense mutations by single-strand conformational
RT polymorphism (SSCP) analysis in five dysfunctional variants of
RT coagulation factor VII." ;
RL Hum. Mol. Genet. 2:1355-1359(1993).
RN [14]
RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.
RX MEDLINE=94264305; PubMed=8204879;
RA Ching S., Clatire B., Srihara S., Chu K., Friedman P., Vandusen W.,
RA Roberts H.R., Blajchman W., Monroe D.M., High K.A.;
RT "Severe factor VII deficiency caused by mutations abolishing the
RT cleavage site for activation and altering binding to tissue factor." ;
RL Blood 83:3524-3535(1994).
RN [15]
RP VARIANT VAL-354.
RX MEDLINE=95072589; PubMed=7981691;
RA Bernardi F., Castaman G., Redaelli R., Pinotti M., Lunghi B.,
RA Rodeghiero F., Marchetti G.;
RT "Topologically equivalent mutations causing dysfunctional coagulation
RT factors VII (294Ala-->Val) and X (334Ser-->Pro)." ;
RL Hum. Mol. Genet. 3:1175-1177(1994).
RN [16]
RP VARIANT MET HIS-307.
RX MEDLINE=95064662; PubMed=7973436;

RA Ohlwa M., Hayashi T., Wada H., Minamiyama K., Shitakawa S.,
RA Suzuki K. ;
RT "Factor VIIa: homozygous asymptomatic type I deficiency caused by
RT an amino acid substitution of His (C4C) for Arg(247) (CGC) in the
RT catalytic domain." ;
RL Thromb. Haemost. 71:773-777(1994).
RN [17]
RP VARIANT MET-419.
RX MEDLINE=96247510; PubMed=8652821;
RA Ardini A.A., Mannucci P.M., Bauer K.A. ;
RT "A Thr359Met mutation in factor VII of a patient with a hereditary
RT deficiency causes defective secretion of the molecule." ;
RL Blood 87:5085-5094(1996).
RN [18]
RP VARIANTS W-283; K-325; V-358; Q-364; E-402 AND Q-413.
RX MEDLINE=97001216; PubMed=8844208;
RA Bernardi F., Castaman G., Pinotti M., Ferraresi P., di Isello M.G.,
RA Lunghi B., Rodeghiero F., Marchetti G. ;
RT "Mutation pattern in clinically asymptomatic coagulation factor VII
RT deficiency." ;
RL Hum. Mutat. 8:108-115(1996).
RN [19]
RP VARIANT VAL-304.
RX MEDLINE=97037613; PubMed=8883260;
RA Tanary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N.,
RA Brenner B., Paz M., Luder A.S., Blau O., Korostilshvsky M.,
RA Zaizov R., Seligsohn U. ;
RT "Ala244Val is a common, probably ancient mutation causing factor VII
RT deficiency in Moroccan and Iranian Jews." ;
RL Thromb. Haemost. 76:283-291(1996).
RN [20]
RP VARIANTS MALTA THR-194 AND VAL-304.
RX MEDLINE=98112461; PubMed=9452082;
RA Alshinawi C., Scerif C., Galdies R., Aguilina A., Felice A.E. ;
RT "Two new missense mutations (P134T and A244V) in the coagulation
RT factor VII gene." ;
RL Hum. Mutat. Suppl. 1:S189-S191(1998).
CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
CC CONVERTED TO FACTOR VIIa BY FACTOR Xa, FACTOR XIa, FACTOR IXa, OR
CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.
CC -1- CATALYTIC ACTIVITY: Hydrolyses one Arg-Ile bond in factor X to
CC form factor Xa.
CC -1- SUBUNIT: HEMODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
CC BY A DISULFIDE BOND.
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; A (shown here) and B; are
CC produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- PMR: THE VITAMIN K-DEPENDENT, ENZYMIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM.
CC -1- DISEASE: DEFECTS IN F7 CAN CAUSE COAGULOPATHY.
CC -1- PHARMACEUTICAL: Available under the names Niasase or Novoseven
CC (Novo Nordisk). Used for the treatment of bleeding episodes in
CC hemophilia A or B patients with antibodies to coagulation factors
CC VIII or IX.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO PEPTIDIN FAMILY S1, ALSO KNOWN AS THE
CC TRYPSIN FAMILY.

```

Query Match      67.5%; Score 131; DB 1; Length 466;
Best Local Similarity 54.5%; Pred. No. 8.5e-16;
Matches 24; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

OY 1 ANGFLXLLRPGSLRXRCRXRLCSFXAXHIFPNXXRTQFWMSY 44
    ||| ||||| | | | | | | | | | | | | | | | |
Db 61 ANAFLEELRPGSLERECKEEOCSFEAREIDFADAEYTKLFWISY 104

RESULT 4
      PRTC_MOUSE

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ID	PRNC_MOUSE	STANDARD:	PRT:	461 AA.
AC	P33587	035498		
DT	01-FEB-1994	(Rel. 28, Created)		
DT	01-FEB-1994	(Rel. 28, Last sequence update)		
DT	16-OCT-2001	(Rel. 40, Last annotation update)		
DE	Vitamin-K dependent protein C precursor (EC 3.4.21.65)			
DE	(Autoproteolysin IIa) (Anticoagulant protein C) (Blood coagulation factor XIV).			
GN	PROC.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euteletia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver:			
RX	MEDLINE=92316897; PubMed=1618739;			
RA	Tada N., Sato M., Tsujimura A., Iwase R., Hashimoto-Gotoh T.;			
RL	"Isolation and characterization of a mouse protein C cDNA.";			
RN	J. Biochem. 111:491-495(1992).			
RP	(2)			
RC	SEQUENCE FROM N.A.			
RX	STRAIN=129/SV7;			
RA	MEDLINE=98152576; PubMed=9493582;			
RL	Jaibert L.R., Rosen E.D., Lissens A., Carmeliet P., Collen D.,			
RT	Castellino F.J.;			
RN	"Nucleotide structure and characterization of the murine gene encoding			
RL	anticoagulant protein C.";			
RT	Thromb. Haemost. 79:310-316(1998).			
RP	(3)			
RC	SEQUENCE OF 274-434 FROM N.A.			
RX	STRAIN=BALE/C;			
RA	MEDLINE=94318474; PubMed=8043441;			
RL	Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Nihio Y.;			
RT	"A comparative study of partial primary structures of the catalytic			
CC	region of mammalian protein C.";			
CC	Br. J. Haematol. 86:590-600(1994).			
CC	-1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT			
CC	REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA			
CC	IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.			
CC	-1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va			
CC	and VIIa.			
CC	-1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED			
CC	INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE			
CC	BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A			
CC	TETRAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN, THIS			
CC	REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS			
CC	STRONGLY PROMOTED BY THROMBOMODULIN.			
CC	-1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.			
CC	-1- PM: THE VITAMIN K-DEPENDENT, ENZYMIC CARBOXYLATION OF SOME			
CC	GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.			
CC	-1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO			
CC	ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING			
CC	SITE IS NECESSARY FOR THE RECOGNITION OF THE			
CC	THROMBIN-THROMBOMODULIN COMPLEX.			
CC	-1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.			
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. ALSO KNOWN AS THE			
CC	TRYPsin FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on ways			
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CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: D10445; BAA01235.1; -			
DR	EMBL: AF034569; AAC33795.1; -			
DR	EMBL: D43755; BAA07812.1; -			
DR	PIR: J02010; J02010.			
DR	HSSP: P04070; IPCU.			
DR	MEROPS: S01.218; -			

DR	MGD; MGI:97771; Proc.	
DR	InterPro: IPR000152; Asx_hydroxyl.	
DR	InterPro: IPR001314; Chymotrypsin.	
DR	InterPro: IPR000561; EGF-like.	
DR	InterPro: IPR001881; EGF Ca.	
DR	InterPro: IPR002383; GLA_blood.	
DR	InterPro: IPR001254; trypsin.	
DR	pfam: PF00008; g1a; 1.	
DR	pfam: PF00008; EGF; 2.	
DR	pfam: PF00054; g1a; 1.	
DR	PRINTS; PR00722; CHYMOTRYPsin.	
DR	PRINTS; PR00001; GLABLOOD.	
DR	SMART: SM00179; EGF_CA; 1.	
DR	SMART: SM00001; EGF-like; 1.	
DR	SMART: SM00069; GLA; 1.	
DR	SMART: SM00020; TRYP_Spc; 1.	
DR	PROSITE; PS00010; ASX_HYDROXIL; 1.	
DR	PROSITE; PS00022; EGF_1; 1.	
DR	PROSITE; PS01186; EGF_2; 2.	
DR	PROSITE; PS01187; EGF_CA; 1.	
DR	PROSITE; PS00011; GLU_CARBOXYLATION; 1.	
DR	PROSITE; PSS0240; TRYPSIN_DOM; 1.	
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.	
DR	PROSITE; PS00135; TRYPSIN_SER; 1.	
KV	Blood coagulation; Glycoprotein; Serine protease;	
KV	Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;	
KV	EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.	
FT	SIGNAL	1 33
FT	PROPEP	34 41
FT	CHAIN	42 196
FT	CHAIN	199 461
FT	PEPTIDE	199 212
FT	SITE	212 213
FT	DOMAIN	96 131
FT	DOMAIN	135 175
FT	DOMAIN	213 461
FT	MOD_RES	47 47
FT	MOD_RES	48 48
FT	MOD_RES	55 55
FT	MOD_RES	57 57
FT	MOD_RES	60 60
FT	MOD_RES	61 61
FT	MOD_RES	66 66
FT	MOD_RES	67 67
FT	MOD_RES	70 70
FT	MOD_RES	112 112
FT	ACT_SITE	253 253
FT	ACT_SITE	299 299
FT	ACT_SITE	402 402
FT	DISULFID	58 63
FT	DISULFID	91 110
FT	DISULFID	100 105
FT	DISULFID	104 119
FT	DISULFID	121 130
FT	DISULFID	139 150
FT	DISULFID	146 159
FT	DISULFID	161 174
FT	DISULFID	182 319
FT	DISULFID	238 254
FT	DISULFID	373 387
FT	DISULFID	398 426
FT	CARBOHD	214 214
FT	CARBOHD	290 290
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).	

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FT CARBOHYD 355 355 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 328 328 MISSING (IN REF. 2).
FT CONFLICT 393 393 N -> D (IN REF. 2).
SQ SEQUENCE 461 AA: 51945 MW: 53FAAD085B194D6E CRC64;

Query Match 59.3%; Score 115; DB 1; Length 461;
Best Local Similarity 47.7%; Pred. No. 6.3e-13;
Matches 21; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

OY 1 ANGFLXXLRPGSLKRXCRXXLCSEFXAHXIFRNXXTRQFWASY 44
Db 42 ANSFLFEMRGSLERECMEICDFEEAGELFQVVEDTLAWIY 85

RESULT 5
FA_MOUSE 5
ID FA_MOUSE STANDARD; PRT; 446 AA.
AC P70375;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
  conversion accelerator).
GN F7 OR CF7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:97127167; PubMed:8972017;
RA Idusoglu E., Rosen E.D., Carmeliet P., Collen D., Castellino F.J.;
RT "Nucleotide structure and characterization of the murine blood
  coagulation factor VII gene."
RL Thromb. Haemost. 76:957-964(1996).
CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZMOGEN FORM. FACTOR VII IS
  CONVERTED TO FACTOR VIIA BY FACTOR XIa, FACTOR XIIa, FACTOR IXa, OR
  THROMBIN BY MINOR PROTEOLISIS. IN THE PRESENCE OF TISSUE FACTOR
  AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
  BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
  FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
  SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Hydrolyses one Arg-1-Ile bond in factor X to
  form factor Xa.
CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
  BY A DISULFIDE BOND (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
  GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
  CALCIUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO 2 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
  TRYPSIN FAMILY.
CC -----
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  or send an email to license@sib-sib.ch).
CC -----
DR EMBL: U66079; AAC33796.1; -.
DR HSSP: P08709; 1BF9.
DR MEROPS: S01.215; -.
DR MGD: MGI:109325; F7.
DR InterPro: IPR000152; ASX_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF-2.
DR InterPro: IPR001881; EGF-Ca.
DR InterPro: IPR002383; GLA_blood.

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DR InterPro: IPR001254; Trypsin.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF-Ca; 1.
DR SMART: SM00001; EGF-like; 1.
DR SMART: SM00069; GLA; 1.
DR SMART: PS00020; TRYP_Spc; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01187; EGF-CA; 1.
DR PROSITE: PS01187; EGF-CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS02040; TRYPSIN_DOM; 1.
DR PROSITE: PS00135; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
KW EGF-like domain; Repeat; Signal; Hydroxylation.
FT SIGNAL 1 24
FT PROPEP 25 41
FT CHAIN 42 193
FT CHAIN 194 446
FT DOMAIN 47 76
FT DOMAIN 87 123
FT DOMAIN 128 169
FT DOMAIN 194 446
FT SITE 193 194
FT ACT_SITE 234 234
FT ACT_SITE 283 283
FT ACT_SITE 385 385
FT BINDING 379 379
FT DISULFID 58 63
FT DISULFID 91 102
FT DISULFID 96 111
FT DISULFID 113 122
FT DISULFID 132 143
FT DISULFID 139 153
FT DISULFID 155 168
FT DISULFID 176 303
FT DISULFID 200 205
FT DISULFID 219 235
FT DISULFID 351 370
FT DISULFID 381 409
FT MOD_RES 47 47
FT MOD_RES 48 48
FT MOD_RES 55 55
FT MOD_RES 57 57
FT MOD_RES 60 60
FT MOD_RES 61 61
FT MOD_RES 66 66
FT MOD_RES 67 67
FT MOD_RES 70 70
FT MOD_RES 76 76
FT MOD_RES 104 104
FT CARBOHYD 186 186
FT CARBOHYD 244 244
SQ SEQUENCE 446 AA: 50276 MW: 2512E44A45CB96E CRC64;

Query Match 58.8%; Score 114; DB 1; Length 446;
Best Local Similarity 50.0%; Pred. No. 9.1e-13;
Matches 22; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

OY 1 ANGFLXXLRPGSLKRXCRXXLCSEFXAHXIFRNXXTRQFWASY 44
Db 42 ANSFLFEMRGSLERECMEICDFEEAGELFQVVEDTLAWIY 85

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RESULT	6
PRTE_PIG	STANDARD: PRT; 459 AA.
AC	Q9GLP2; 16-OCT-2001 (Rel. 40, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	Vitamin-K dependent protein C precursor (EC 3.4.21.69)
DE	(Antiproteinase IIIA) (Anticoagulant protein C) (Blood coagulation factor XIV).
DE	PROC.
GN	Sus scrofa (Pig).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX	NCBI_TaxID:9823;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Liver.
RA	Grimm D.R., Colter M.B., Kim H.K.W.;
RT	"Cloning of the complete cDNA sequences encoding porcine factor V and protein C.";
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC	-1- FUNCTION: Protein C is a vitamin K-dependent serine protease that regulates blood coagulation by inactivating factors Va and VIIIa in the presence of calcium ions and phospholipide.
CC	-1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va and VIIIa.
CC	-1- SUBUNIT: Synthesized as a single chain precursor, which is cleaved into a light chain and a heavy chain held together by a disulfide bond. The enzyme is then activated by thrombin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reaction, which occurs at the surface of endothelial cells, is strongly promoted by thrombomodulin.
CC	-1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
CC	-1- PM: The vitamin K-dependent, enzymatic carboxylation of some Glu residues allows the modified protein to bind calcium.
CC	-1- MISCELLANEOUS: Calcium also binds, with stronger affinity to another site, beyond the Gla domain. This Gla-independent binding site is necessary for the recognition of the thrombin-thrombomodulin complex.
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPsin FAMILY.
CC	-1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC	-----
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CC	-----
DR	EMBL, AF191307; AAC28380.1; -
DR	InterPro: IPR0000152; Asx_Hydroxyl.
DR	InterPro: IPR001314; Chymotrypsin.
DR	InterPro: IPR000561; EGF-like.
DR	InterPro: IPR001881; EGF Ca.
DR	InterPro: IPR002383; Gla_blood.
DR	InterPro: IPR001254; Trypsin.
DR	InterPro: IPR000294; VitK_dep_GLA.
DR	Pfam: PF00089; trypsin. 1.
DR	PRINTS: PR00722; CHYMOTRYPsin.
DR	PRINTS: PR00001; GLABLOOD.
DR	SMART: SM00181; EGF_2.
DR	SMART: SM00001; EGF_Like; 2.
DR	SMART: SM00069; GLA_1.
DR	SMART: SM00020; Tryp_spec; 1.
DR	PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR	PROSITE: PS0240; TRYPSIN_DOM; 1.
KW	Blood coagulation; glycoprotein; serine protease;
KW	Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
KW	EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
FT	SIGNAL 1 18 BY SIMILARITY.

FT	PROPEP	19	41	BY SIMILARITY
FT	CHAIN	42	459	VITAMIN K-DEPENDENT PROTEIN C.
FT	CHAIN	42	196	PROTEIN C LIGHT CHAIN (BY SIMILARITY).
FT	CHAIN	199	459	PROTEIN C HEAVY CHAIN (BY SIMILARITY).
FT	PEPTIDE	199	213	ACTIVATION PEPTIDE (BY SIMILARITY).
FT	SITE	213	214	CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
FT	DOMAIN	96	131	EGF-LIKE 1.
FT	DOMAIN	135	175	EGF-LIKE 2.
FT	DOMAIN	214	459	SERINE PROTEASE.
FT	MOD_RES	47	47	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	48	48	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	55	55	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	57	57	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	60	60	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	61	61	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	66	66	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	67	67	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	70	70	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	112	112	HYDROXYLATION (BY SIMILARITY).
FT	ACT_SITE	255	255	CHARGE RELAY SYSTEM.
FT	ACT_SITE	301	301	CHARGE RELAY SYSTEM.
FT	ACT_SITE	400	400	CHARGE RELAY SYSTEM.
FT	DISULFID	58	63	BY SIMILARITY.
FT	DISULFID	91	110	BY SIMILARITY.
FT	DISULFID	100	105	BY SIMILARITY.
FT	DISULFID	104	119	BY SIMILARITY.
FT	DISULFID	121	130	BY SIMILARITY.
FT	DISULFID	139	150	BY SIMILARITY.
FT	DISULFID	146	159	BY SIMILARITY.
FT	DISULFID	161	174	BY SIMILARITY.
FT	DISULFID	182	321	INTERCHAIN (BY SIMILARITY).
FT	DISULFID	240	256	BY SIMILARITY.
FT	DISULFID	371	385	BY SIMILARITY.
FT	DISULFID	396	424	BY SIMILARITY.
FT	CARBOHYD	138	138	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	292	292	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	353	353	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	459 AA;	51866 MW;	8541AAC14CC16D09 CRC64;

Query Match 56.7%; Score 110; DB 1; Length 459;

Best Local Similarity 47.7%; Pred. No. 4.9e-12;

Matches 21; Conservative 2; Mismatches 21; Indels 0; Gaps 0;

OY	1	ANGFLXILRPGSLRXRCRXILCSFXAXHIFENXNRRTRQFWWSY	44
DB	42	ANSFLELRPSLSERCKEETCFEPAEREIFONTENTMAFWMSKY	85

RESULT 7

TMG1_HUMAN

ID TMG1_HUMAN STANDARD; PRT; 218 AA.

AC 01468;

DT 01-MAR-2002 (Rel. 41, Created)

DT 01-MAR-2002 (Rel. 41, Last sequence update)

DE 01-MAR-2002 (Rel. 41, Last annotation update)

DE Transmembrane gamma-carboxyglutamic acid protein 1 precursor (proline-rich gla protein 1) (Proline-rich gamma-carboxyglutamic acid protein 1).

DE PRRC1 OR TMG1 OR PRGP1.

GN Homo sapiens (Human).

OS

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97404347; PubMed=9256434;
 RA Kulman J.D., Harris J.E., Haldeman B.A., Davie E.W.:
 RT "Primary structure and tissue distribution of two novel proline-rich
 RT gamma-carboxyglutamic acid proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997).
 CC -1- TISSUE SPECIFICITY: Highly expressed in the spinal cord.
 CC -1- PTM: Glutamic acid residues are produced after subsequent posttranslational
 CC modifications of glutamic acid by a vitamin K-dependent gamma-
 CC carboxylase.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF009242; AAB67070.1; -.
 DR MIM: 604428; -.
 DR HSSP: P00740; ICFH.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR InterPro: IPR002383; GLA_blood.
 DR Pfam: PF00594; gla; 1.
 DR PRINTS: PRO0001; GLABLOOD.
 DR SMART: SM00069; GLA; 1.
 DR PROSITE: PS00011; GLU-CARBOXYLATION; 1.
 KW Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
 FT PROPEP 1 20
 FT CHAIN 21 218
 FT PROTEIN 1.
 FT TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
 FT DOMAIN 84 106 POTENTIAL.
 FT DOMAIN 107 218 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 24 61 GLA-RICH.
 FT DOMAIN 131 135 POLY-PRO.
 SQ SEQUENCE 218 AA; 24947 MW; 26538A61AB0AEB98 CRC64;

Query Match 55.2%; Score 107; DB 1; Length 218;
 Best local Similarity 38.6%; Pred. No. 8e-12;
 Matches 17; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

OY 1 ANGFLLXLRPGSLKRXCRXALCSFXAHXIFRXXRTROWASY 44
 DB 21 ANGFEEIRGNIERCKEETFEERAEAFENNEKTRFWSY 64

RESULT 8
 ID PRTC_RAT STANDARD: PRT; 461 AA.
 AC P31394;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
 DE (Autocrothrombin IIA) (Anticoagulant protein C) (Blood coagulation
 DE factor XIV).
 GN PROC.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Liver;
 RX MEDLINE=92329550; PubMed=1627650;
 RA Okafuji T., Maekawa K., Nawa K., Marumoto Y.;

RT "The cDNA cloning and mRNA expression of rat protein C.";
 RL Biochim. Biophys. Acta 1131:329-332(1992).
 CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
 CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
 CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
 CC and VIIIA.
 CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
 CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
 CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
 CC TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN. THIS
 CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
 CC STRONGLY PROMOTED BY THROMBOMODULIN.
 CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
 CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
 CC THROMBIN-THROMBOMODULIN COMPLEX.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 CC -----
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 CC -----
 DR EMBL: X64336; CAA45617.1; -.
 DR PIR: S18994; S18994.
 DR PIR: S24312; S24312.
 DR HSSP: P04070; 1PCU.
 DR MEROPS: S01.218; -.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF-like.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Trypsin.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam: PF00008; EGF; 2.
 DR Pfam: PF00594; gla; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PRO00722; CHYMOTRYPSIN.
 DR PRINTS: PRO0001; GLABLOOD.
 DR SMART: SM00179; EGF_CA; 1.
 DR SMART: SM00001; EGF_Like; 1.
 DR SMART: SM00069; GLA; 1.
 DR SMART: SM00020; TRYP_Spc; 1.
 DR PROSITE: PS00010; ASX-HYDROXYL; 1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF_CA; 1.
 DR PROSITE: PS00011; GLU-CARBOXYLATION; 1.
 DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HTS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Blood coagulation; Glycoprotein; Serine protease;
 KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 KW EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
 FT SIGNAL 1 32
 FT PROPEP 33 41
 FT CHAIN 42 196
 FT CHAIN 199 461
 FT PEPTIDE 199 212
 FT SITE 212 213
 FT DOMAIN 96 131
 FT DOMAIN 135 175
 FT DOMAIN 213 461
 EGF-LIKE 1.
 EGF-LIKE 2.
 SERINE PROTEASE.

RA Messler T.L., Pittman D.D., Long G.L., Kaufman R.J., Church W.R.;
RT "Cloning and expression in COS-1 cells of a full-length cDNA encoding
RT human coagulation factor X.";
RL Gene 99:291-294(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87026600; PubMed=3768336;
RA Leytus S.P., Foster D.C., Kurachi K., Davie E.W.;
RT "Gene for human factor X: a blood coagulation factor whose gene
RT organization is essentially identical with that of factor IX and
RT protein C.";
RL Biochemistry 25:5098-5102(1986).
RN [3]
RP SEQUENCE OF 13-488 FROM N.A.
RX MEDLINE=85216545; PubMed=2582420.
RA Fung M.R., Hay C.W., McGillivray R.T.A.;
RT "Characterization of an almost full-length cDNA coding for human
RT blood coagulation factor X.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).
RN [4]
RP SEQUENCE OF 19-488 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=86221713; PubMed=3011603;
RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;
RT "Isolation and characterization of human blood-coagulation factor X
RT cDNA.";
RL Gene 41:311-314(1986).
RN [5]
RP SEQUENCE OF 41-179.
RX MEDLINE=83257207; PubMed=6871167;
RA Mcullen B.A., Fujikawa K., Kistiel W., Sasagawa T., Howald W.N.,
RA Kwa E.Y., Weinstein B.;
RT "Complete amino acid sequence of the light chain of human blood
RT coagulation factor X: evidence for identification of residue 63 as
RL beta-hydroxyaspartic acid.";
RN Biochemistry 22:2875-2884(1983).
RP [6]
RP SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=Liver;
RX MEDLINE=84222026; PubMed=5587384;
RA Leytus S.P., Chung D.W., Kistiel W., Kurachi K., Davie E.W.;
RT "Characterization of a cDNA coding for human factor X.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702(1984).
RN [7]
RP SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=94062825; PubMed=8243461;
RA Inoue K., Morita T.;
RT "Identification of O-linked oligosaccharide chains in the activation
RT peptides of blood coagulation factor X. The role of the carbohydrate
RT moieties in the activation of factor X.";
RL Eur. J. Biochem. 218:153-163(1993).
RN [8]
RP SEQUENCE OF 1-23 FROM N.A.
RX MEDLINE=90128299; PubMed=2612918;
RA Jagadeeswaran P., Reddy S.V., Rao K.J., Hamsabhusanam K., Lyman G.;
RT "Cloning and characterization of the 5' end (exon 1) of the gene
RT encoding human factor X.";
RL Gene 84:517-519(1989).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.
RX MEDLINE=93360277; PubMed=8355279;
RA Padmanabhan K., Padmanabhan K.P., Tulinsky A., Park C.H., Bode W.,
RA Huber R., Blankenship D.T., Cardin A.D., Kistiel W.;
RT "Structure of human des(1-45) factor Xa at 2.2-A resolution.";
RL J. Mol. Biol. 232:947-966(1993).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.
RX MEDLINE=98283982; PubMed=9618463;
RA Kanata K., Kawamoto H., Honma T., Iwama T., Kim S.H.;
RT "Structural basis for chemical inhibition of human blood coagulation
RT factor Xa.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).
CC -1- FUNCTION: FACTOR XA IS A VITAMIN K-DEPENDENT GLYCOPROTEIN THAT

CC CONVERTS PROTHROMBIN TO THROMBIN IN THE PRESENCE OF FACTOR VA,
CC CA⁺⁺, AND PHOSPHOLIPID DURING BLOOD CLOTTING.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
CC Arg-|-Ile bonds in prothrombin to form thrombin.
CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
CC MORE DISULFIDE BONDS.
CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM.
CC -1- PTM: N- AND O-GLYCOSYLATED.
CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
CC -----
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CC -----
CC EMBL: K03194; AAAS2490.1; -;
CC EMBL: M57285; AAAS2421.1; -;
CC EMBL: L29433; AAAS2764.1; -;
CC EMBL: L00390; AAAS2764.1; JOINED.
CC EMBL: L00391; AAAS2764.1; JOINED.
CC EMBL: L00392; AAAS2764.1; JOINED.
CC EMBL: L00393; AAAS2764.1; JOINED.
CC EMBL: L00394; AAAS2764.1; JOINED.
CC EMBL: L00395; AAAS2764.1; JOINED.
CC EMBL: L00396; AAAS2764.1; JOINED.
CC EMBL: M22613; AAAS1984.1; -;
CC EMBL: K01886; AAAS2486.1; -;
CC EMBL: M33297; AAAS2636.1; -;
CC PIR: A00924; EXHU.
CC PIR: A25853; A25853.
CC PIR: A24478; A24478.
CC PDB: 1HCG; 08-MAY-95.
CC PDB: 1EAX; 29-OCT-97.
CC PDB: 1EXY; 17-JUN-98.
CC PDB: 1XKA; 23-MAR-99.
CC MEROPS: S01_216; -;
CC CarBank: CCSD:29393; -;
CC GlycoSuiteDB: P00742; -;
CC MIM: 134530; -;
CC MIM: 227600; -;
CC InterPro: IPR000152; Asx_hydroxyl.
CC InterPro: IPR001314; Chymotrypsin.
CC InterPro: IPR000561; EGF-like.
CC InterPro: IPR000742; EGF_2.
CC InterPro: IPR001881; EGF_CA.
CC InterPro: IPR002383; GLA_blood.
CC InterPro: IPR001254; Trypsin.
CC InterPro: IPR000294; VitK_dep_GLA.
CC Pfam: PF00008; EGF_2.
CC Pfam: PF00594; gla_1.
CC Pfam: PF00089; trypsin_1.
CC PRINTS: PR00722; CHYMOTRYPSIN.
CC PRINTS: PR00001; GLABLOOD.
CC SMART: SM00179; EGF_CA; 1.
CC SMART: SM00001; EGF_like; 1.
CC SMART: SM00069; GLA_1.
CC SMART: SM00020; TYP_Spc; 1.
CC PROSITE: PS00010; ASX_HYDROXYL; 1.
CC PROSITE: PS00022; EGF_1; 1.
CC PROSITE: PS01186; EGF_2; 2.
CC PROSITE: PS01187; EGF_CA; 1.

Query	1	ANGFLXLRPGSLRXRCRXSLCSFXAHXIFRNKXPRFQWVS	44
Db	41	ANSFLKMKKGLHRECEMEETCYEAREVVEDSDKRNEMFNKY	84
Query Match		48.5%: Score 94; DB 1; Length 488;	
Best Local Similarity		36.4%: Pred. No. 3.9e-09;	
Matches	16;	Conservative	7; Mismatches 21; Indels 0; Gaps
Result	12		
PRTC_RABIT			
AC	Q28661	STANDARD;	PRT; 458 AA.
DT	15-DEC-1998	(Rel. 37, Created)	
DT	15-DEC-1998	(Rel. 37, Last sequence update)	
DT	16-OCT-2001	(Rel. 40, Last annotation update)	
DE	Vitamin-K dependent protein C precursor (BC 3.4.21.69)		
DE	(Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation factor XIV) (Fragment).		
GN	PROC.		
OS	Oryctolagus cuniculus (Rabbit).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.		
OX	NCBI_TaxID=9986;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Liver;		
RA	Shen L., He X., Dahlback B.;		
RL	Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.		
CC	FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.		

CC	-1- CATALYTIC ACTIVITY:	Degradation of blood coagulation factors Va and VIII.
CC	-1- SUBUNIT:	SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS STRONGLY PROMOTED BY THROMBOMODULIN.
CC	-1- TISSUE SPECIFICITY:	PLASMA; SYNTHESIZED IN THE LIVER.
CC	-1- PTM:	THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC	-1- MISCELLANEOUS:	CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING SITE IS NECESSARY FOR THE RECOGNITION OF THE THROMBIN-THROMBOMODULIN COMPLEX.
CC	-1- SIMILARITY:	CONTAINS 2 EGF-LIKE DOMAINS.
CC	-1- SIMILARITY:	BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
CC		-----
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CC		-----
DR	EMBL;	P04933; AAA92956.1; -.
DR	HSSP;	P04070; IPCU.
DR	MEROPS;	S01.218; -.
DR	InterPro;	IPR00010152; Asx_hydroxyl.
DR	InterPro;	IPR0000561; EGF-like.
DR	InterPro;	IPR001881; EGF_Ca.
DR	InterPro;	IPR001254; Trypsin.
DR	InterPro;	IPR000294; VitK_dep_GLA.
DR	Pfam;	PF00008; EGF_2.
DR	Pfam;	PF00594; gla_1.
DR	Pfam;	PF00089; trypsin_1.
DR	SMART;	SMO0181; EGF_2.
DR	SMART;	SMO0069; GLA_1.
DR	SMART;	SMO0020; TRYP_spec_1.
DR	PROSITE;	PS00010; ASX_HYDROXYL_1.
DR	PROSITE;	PS00022; EGF_1; 1.
DR	PROSITE;	PS01186; EGF_2; 2.
DR	PROSITE;	PS00187; GLU_CARBOXYLATON; 1.
DR	PROSITE;	PS50240; TRYPSIN_DOM_1.
DR	PROSITE;	PS00134; TRYPSIN_HIS_1.
DR	PROSITE;	PS00135; TRYPSIN_SER_1.
KW	Blood coagulation;	Glycoprotein; Serine protease;
KW	Gamma-carboxyglutamic acid;	Calcium-binding; Vitamin K; Hydroxylation;
KW	EGF-like domain;	Repeat; Endothelial cell; Hydrolase; Signal.
FT	NON_TER	1
FT	SIGNAL	<1 27
FT	PROPEP	28 36
FT	CHAIN	37 458
FT	CHAIN	37 192
FT	CHAIN	195 458
FT	PEPTIDE	195 209
FT	SITE	209 210
FT	DOMAIN	91 126
FT	DOMAIN	130 170
FT	DOMAIN	210 458
FT	MOD_RES	42 42
FT	MOD_RES	43 43
FT	MOD_RES	50 50
FT	MOD_RES	52 52
FT	MOD_RES	55 55

FT	MOD_RES	56	56	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	61	61	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	62	62	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	65	65	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	107	107	HYDROXYLATION (BY SIMILARITY).
FT	ACT_SITE	250	250	CHARGE RELAY SYSTEM.
FT	ACT_SITE	296	296	CHARGE RELAY SYSTEM.
FT	ACT_SITE	399	399	CHARGE RELAY SYSTEM.
FT	DISULFID	53	58	BY SIMILARITY.
FT	DISULFID	85	100	BY SIMILARITY.
FT	DISULFID	96	105	BY SIMILARITY.
FT	DISULFID	95	100	BY SIMILARITY.
FT	DISULFID	99	114	BY SIMILARITY.
FT	DISULFID	116	125	BY SIMILARITY.
FT	DISULFID	134	145	BY SIMILARITY.
FT	DISULFID	141	154	BY SIMILARITY.
FT	DISULFID	156	169	BY SIMILARITY.
FT	DISULFID	177	316	INTERCHAIN (BY SIMILARITY).
FT	DISULFID	235	251	BY SIMILARITY.
FT	DISULFID	370	384	BY SIMILARITY.
FT	DISULFID	395	423	BY SIMILARITY.
FT	CARBOHYD	133	133	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	287	287	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	352	352	N-LINKED (GLCNAC. . .) (POTENTIAL)
EQ	SEQUENCE	458 AA;	51087 MW;	D7545F890C8F29D7 CRC64;

Query Match	47.4%	Score 92;	DB 1;	Length 458;
Best Local Similarity	43.2%	Pred. No. 8.4e-09;		
Matches 19;	Conservative 3;	Mismatches 22;	Indels 0;	Gaps 0;

QY 1 ANGFLXXLRPGSLXRXCRRXXLCSEFXAXHIFRNXRXRTQFWVSY 44
 ||||| ||||| :||| :||| |
 Db 37 ANSFLEELRPSSLERECEVEEVCDDLEAKEIFQSVDDTLAFWYKY 80

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RESULT 13
FALO_RABBIT STANDARD; PRT; 490 AA.
ID FALO_RABBIT
AC 019045;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
GN F10.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_Taxid=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97256311; Pubmed=9101642;
RA Pendurthi U.R., Anderson K.D., James H.L.;
RT "Characterization of a full-length cDNA for rabbit factor X.";
RL Thromb. Res. 85:503-514 (1997).
CC -1- FUNCTION: FACTOR XA IS A VITAMIN K-DEPENDENT GLYCOPROTEIN THAT
CC CONVERTS PROTHROMBIN TO THROMBIN IN THE PRESENCE OF FACTOR VA,
CC Ca++, AND PHOSPHOLIPID DURING BLOOD CLOTTING.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-1-Thr and then
CC Arg-1-Ile bonds in prothrombin to form thrombin.
CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
CC MORE DISULFIDE BONDS.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM (BY SIMILARITY).
CC -1- PTM: N- AND O-GLYCOSYLATED (BY SIMILARITY).
CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY)
CC (BY SIMILARITY).

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CC	-1	MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC	-1	ANOTHER SITE, BEYOND THE GLA DOMAIN.
CC	-1	SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC	-1	SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC		TRYPsin FAMILY.
CC		-----
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration
CC		between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC		the European Bioinformatics Institute. There are no restrictions on its
CC		use by non-profit institutions as long as its content is in no way
CC		modified and this statement is not removed. Usage by and for commercial
CC		entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC		or send an email to license@isb-sib.ch).
CC		-----
DR	EMBL:	AF003200; AAB62542.1; -
DR	HSSP:	P00742; 1HCG.
DR	InterPro:	IPR0001052; Asx_hydroxyl-
DR	InterPro:	IPR001314; Chymotrypsin.
DR	InterPro:	IPR000561; EGF-like.
DR	InterPro:	IPR000742; EGF_2.
DR	InterPro:	IPR001881; EGF_Ca.
DR	InterPro:	IPR002383; GLA_blood.
DR	InterPro:	IPR001254; Trypsin.
DR	InterPro:	IPR000294; Vitk_dep_GLA.
DR	Pfam:	PF00008; EGF; 2.
DR	Pfam:	PF00594; gla; 1.
DR	Pfam:	PF00089; trypsin; 1.
DR	PRINTS:	PR00722; CHYMOTRYPSIN.
DR	PRINTS:	PR00001; GLABLOOD.
DR	SMART:	SM00179; EGF_CA; 1.
DR	SMART:	SM00001; EGF_like; 1.
DR	SMART:	SM00069; GLA; 1.
DR	SMART:	SM00020; TRYP_sec; 1.
DR	PROSITE:	PS00010; ASX_HYDROXYL; 1.
DR	PROSITE:	PS00022; EGF_1; 1.
DR	PROSITE:	PS01186; EGF_2; 2.
DR	PROSITE:	PS01187; EGF_CA; 1.
DR	PROSITE:	PS00011; GLU_CARBOXYLATION; 1.
DR	PROSITE:	PS50240; TRYPSIN_DOM; 1.
DR	PROSITE:	PS00134; TRYPSIN_HIS; 1.
DR	PROSITE:	PS00135; TRYPSIN_SER; 1.
KW		Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
KW		Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
KM		Signal; Zymogen; EGF-like domain; Repeat.
FT	SIGNAL	1 20 POTENTIAL.
FT	PROPEP	21 40 BY SIMILARITY.
FT	CHAIN	41 180 FACTOR X LIGHT CHAIN.
FT	CHAIN	184 490 FACTOR X HEAVY CHAIN.
FT	PROPEP	184 232 ACTIVATION PEPTIDE.
FT	CHAIN	233 490 ACTIVATED FACTOR XA, HEAVY CHAIN.
FT	DOMAIN	86 122 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	125 165 EGF-LIKE 2.
FT	MOD_RES	233 490 SERINE PROTEASE.
FT	MOD_RES	46 46 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT	MOD_RES	47 47 SIMILARITY).
FT	MOD_RES	54 54 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT	MOD_RES	56 56 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT	MOD_RES	59 59 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT	MOD_RES	60 60 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT	MOD_RES	65 65 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT	MOD_RES	66 66 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT	MOD_RES	69 69 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT	MOD_RES	72 72 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT	MOD_RES	72 72 SIMILARITY).

FT MOD_RES 75 75 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 79 79 SIMILARITY).
FT MOD_RES 103 103 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT ACT_SITE 274 274 SIMILARITY).
FT ACT_SITE 320 320 HYDROXYLATION (BY SIMILARITY).
FT ACT_SITE 417 417 CHARGE RELAY SYSTEM.
FT ACT_SITE 417 417 CHARGE RELAY SYSTEM.
FT DISULFID 90 101 BY SIMILARITY.
FT DISULFID 95 110 BY SIMILARITY.
FT DISULFID 112 121 BY SIMILARITY.
FT DISULFID 129 140 BY SIMILARITY.
FT DISULFID 136 149 BY SIMILARITY.
FT DISULFID 151 164 BY SIMILARITY.
FT DISULFID 172 340 INTERCHAIN (BY SIMILARITY).
FT DISULFID 239 244 BY SIMILARITY.
FT DISULFID 259 275 BY SIMILARITY.
FT DISULFID 388 402 BY SIMILARITY.
FT DISULFID 413 441 BY SIMILARITY.
FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 490 AA: 53965 MW: 3A39FA85AF2A6D11 CRC64;

Query Match 47.4%; Score 92; DB 1; Length 490;
Best Local Similarity 38.6%; Pred. No. 9e-09;
Matches 17; Conservative 7; Mismatches 20; Indels 0; Caps 0;

QY 1 ANFLXLRGSLRXRCXKXLCSEFXAHXFRXXRRPFWASY 44
DB 41 ANSFLBELKGNLERCEMEBNCSEYEEALEVEDEKNEFWNKY 84

RESULT 14
PRTC_HUMAN
ID PRTC_HUMAN STANDARD; PRT; 461 AA.
AC P04070; Q16001; Q15190; Q15189;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
DE (Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV).
GN PROC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=85270390; PubMed=2991887;
RA Foster D.C., Yoshitake S., Davie E.W.;
RT "The nucleotide sequence of the gene for human protein C";
RL Proc. Natl. Acad. Sci. U.S.A. 82:4673-4677(1985).
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=85269639; PubMed=2991859;
RA Beckmann R.J., Schmidt R.J., Santerre R.F., Plutsky J., Crabtree G.R.,
RA Long G.L.;
RT "The structure and evolution of a 461 amino acid human protein C
RT precursor and its messenger RNA, based upon the DNA sequence of
RT cloned human liver cDNAs.";
RL Nucleic Acids Res. 13:5233-5247(1985).
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=86120978; PubMed=3511471;
RA Plutsky J., Hoskins J.A., Long G.L., Crabtree G.R.;
RT "Evolution and organization of the human protein C gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986).
RN
RP SEQUENCE OF 106-461 FROM N.A.
RX MEDLINE=84272714; PubMed=6589623;

RA Foster D.C., Davie E.W.;
RT "Characterization of a cDNA coding for human protein C.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984).
RN
RP CARBOHYDRATE-LINKAGE SITE ASN-371.
RX MEDLINE=90293094; PubMed=1694179;
RA Miletch J.P., Broze G.J., Jr.;
RT "Beta protein C is not glycosylated at asparagine 329. The rate of
RT translation may influence the frequency of usage at asparagine-X-
RT cysteine sites.";
RL J. Biol. Chem. 265:11397-11404(1990).
RN
RP HYDROXYLATION.
RX MEDLINE=92184750; PubMed=1544894;
RA Harris R.J., Ling V.T., Spellman M.W.;
RT "O-linked fucose is present in the first epidermal growth factor
RT domain of factor XII but not protein C.";
RL J. Biol. Chem. 267:5102-5107(1992).
RN
RP 3D-STRUCTURE MODELING OF 175-450.
RX MEDLINE=94272342; PubMed=8003977;
RA Fisher C.L., Greengard J.S., Griffin J.H.;
RT "Models of the serine protease domain of the human antithrombotic
RT plasma factor activated protein C and its zymogen.";
RL Protein Sci. 3:588-599(1994).
RN
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 84-461.
RX MEDLINE=97157472; PubMed=9003757;
RA Mather T., Oganessian V., Hof P., Huber R., Foundling S., Esmon C.,
RA Bode W.;
RT "The 2.8 A crystal structure of Gla-domainless activated protein C.";
RL EMBO J. 15:6822-6831(1996).
RN
RP REVIEW ON PROC VARIANTS.
RX MEDLINE=93190290; PubMed=8446940;
RA Reitsma P.H., Poort S.R., Bernardi F., Gandrille S., Long G.L.,
RA Sala N., Cooper D.N.;
RT "Protein C deficiency: a database of mutations. For the Protein C & S
RT Subcommittee of the Scientific and Standardization Committee of the
RT International Society on Thrombosis and Haemostasis.";
RL Thromb. Haemost. 69:77-84(1993).
RN
RP VARIANT CYS-444.
RX MEDLINE=87204221; PubMed=2437584;
RA Romeo G., Hassan H.J., Staempfli S., Roncuzzi L., Cianetti L.,
RA Leonardi A., Vicente V., Mannucci P.M., Bertina R.M., Peschle C.,
RA Cortese R.;
RT "Hereditary thrombophilia: identification of nonsense and missense
RT mutations in the protein C gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:2829-2832(1987).
RN
RP VARIANT TRP-211 (LONDON-1).
RX MEDLINE=90098906; PubMed=2602169;
RA Grundy C.B., Chittolie A., Talbot S., Bevan D., Kakkar V.V.,
RA Cooper D.N.;
RT "Protein C London 1: recurrent mutation at Arg-169 (CGG->TGG) in
RT the protein C gene causing thrombosis.";
RL Nucleic Acids Res. 17:10513-10513(1989).
RN
RP VARIANT CYS-272.
RX MEDLINE=91329836; PubMed=1868249;
RA Reitsma P.H., Poort S.R., Allaart C.F., Briet E., Bertina R.M.;
RT "The spectrum of genetic defects in a panel of 40 Dutch families with
RT symptomatic protein C deficiency type I: heterogeneity and founder
RT effects.";
RL Blood 78:890-894(1991).
RN
RP VARIANTS ALA-62 (VERMONT-1) AND MET-76.
RX MEDLINE=92190481; PubMed=1347706;
RA Bovill E.G., Tomczak J.A., Grant B., Bhushan F., Pillemer E.,
RA Rainville I.R., Long G.L.;
RT "Protein C Vermont: symptomatic type II protein C deficiency
RT associated with two Gla domain mutations.";

BL Blood 79:1456-1465(1992).
 [14]
 RP VARIANT ASP-418 (HONG KONG-2).
 RX MEDLINE=92305321; PubMed=1611081;
 RA Sugahara Y., Miura O., Yuen P., Aoki N.;
 RT "Protein C deficiency Hong Kong 1 and 2: hereditary protein C
 RT deficiency caused by two mutant alleles, a 5-nucleotide deletion and
 RT a missense mutation.";
 RL Blood 80:126-133(1992).
 RN [15]
 RP VARIANT LEU-289.
 RX MEDLINE=92380660; PubMed=1511988;
 RA Grundy C.B., Chisholm M., Kakkar V.V., Cooper D.N.;
 RT "A novel homozygous missense mutation in the protein C (PROC) gene
 RT causing recurrent venous thrombosis.";
 RL Hum. Genet. 89:683-684(1992).
 RN [16]
 RP VARIANTS GLN-220 AND TRP-220.
 RX MEDLINE=92380661; PubMed=1511989;
 RA Grundy C.B., Schulman S., Tengborn L., Kakkar V.V., Cooper D.N.;
 RT "Two different missense mutations at Arg 178 of the protein C (PROC)
 RT gene causing recurrent venous thrombosis.";
 RL Hum. Genet. 89:685-686(1992).
 RN [17]
 RP VARIANT GLN-220.
 RX MEDLINE=93250852; PubMed=1301959;
 RA Gandrille S., Vidard M., Alach M., Alhenc-Gelas M., Fischer A.M.,
 RA Gouault-Heilman M., Toulon P., Flessinger J.N., Coossens M.;
 RT "Two novel mutations responsible for hereditary type I protein C
 RT deficiency: characterization by denaturing gradient gel
 RT electrophoresis.";
 RL Hum. Mutat. 1:491-500(1992).
 RN [18]
 RP VARIANT SER-334.
 RX MEDLINE=92276939; PubMed=1593215;
 RA Yanamoto K., Matsushita T., Sugiura I., Takamatsu J., Iwasaki E.,
 RA Wada H., Deguchi K., Shirakawa S., Saito H.;
 RT "Homozygous protein C deficiency: identification of a novel missense
 RT mutation that causes impaired secretion of the mutant protein C.";
 RL J. Lab. Clin. Med. 119:682-689(1992).
 RN [19]
 RP VARIANTS TRP-38; CYS-42; HIS-42; GLN-271 AND ASN-294.
 RX MEDLINE=9313192; PubMed=832421;
 RA Gandrille S., Alhenc-Gelas M., Gaussem P., Allaud M.-F., Dupuy E.,
 RA Juhan-Vague I., Alach M.;
 RT "Five novel mutations located in exons III and IX of the protein C
 RT gene in patients presenting with defective protein C anticoagulant
 RT activity.";
 RL Blood 82:159-168(1993).
 RN [20]
 RP VARIANTS G-14; Q-211; Y-244; Q-253; L-321; C-328; I-385; T-388 AND
 RP V-388.
 RX MEDLINE=93271391; PubMed=8499565;
 RA Poort S.R., Pabinger-Fasching I., Mannhalter C., Reitsma P.H.,
 RA Bertina R.M.;
 RT "Twelve novel and two recurrent mutations in 14 Austrian families
 RT with hereditary protein C deficiency.";
 RL Blood Coagul. Fibrinolysis 4:273-280(1993).
 RN [21]
 RP VARIANT TRP-57.
 RX MEDLINE=93271396; PubMed=8499568;
 RA Millar D.S., Grundy C.B., Biggell P., Moffat E.H., Martin R.,
 RA Kakkar V.V., Cooper D.N.;
 RT "A Gla domain mutation (Arg 15-->Tyr) in the protein C (PROC) gene
 RT causing type 2 protein C deficiency and recurrent venous
 RT thrombosis.";
 RL Blood Coagul. Fibrinolysis 4:345-347(1993).
 RN [22]
 RP VARIANTS R-145; L-210; W-211; T-243; L-321; M-340 AND Y-426.
 RX MEDLINE=94122329; PubMed=8529730;
 RA Tsay W., Greenard J.S., Montgomery R.R., McPherson R.A., Pucci J.C.,
 RA Koepfer M.A., Coughlin J., Griffin J.H.;
 RT "Genetic mutations in ten unrelated American patients with

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RT symptomatic type 1 protein C deficiency";
RL Blood Coagul. Fibrinolysis 4:791-796(1993).
RN [23]
RP VARIANT SER-423.
RX MEDLINE=94001606; PubMed=8398832;
RA Marchetti G., Patracchini P., Gemmati D., Castaman G., Rodeghiero F.,
RA Wacey A., Cooper D.N., Tuddenham E.G., Bernardi F.;
RT "Symptomatic type II protein C deficiency caused by a missense
RT mutation (Gly 381->Ser) in the substrate-binding pocket.";
RL Br. J. Haematol. 84:285-289(1993).
RN [24]
RP SEQUENCE OF 43-64 FROM N.A., AND VARIANT GLY-57 (YONAGO).
RX MEDLINE=92237511; PubMed=8477066;
RA Minuro J., Muramatsu S., Kaneko M., Yoshitake S., Iijima K.,
RA Nakamura K., Sakata Y., Matsuda M.;
RT "An abnormal protein C (protein C Yonago) with an amino acid
RT substitution of Gly for Arg-15 caused by a single base mutation of C
RT
Query Match 45.9%; Score 89; DB 1; Length 461;
Best Local Similarity 46.3%; Pred. NO. 2.9e+08;
Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;
Oy 1 ANGFLLRPGSLXRRCRXXLCSFXAHXHPNXXRTQFW 41
Db 43 ANSFLEELRHSSLERECEIEICDFEAKETIFQVDDTLAFW 83
RESULT 15
FA10_BOVIN
ID FA10_BOVIN STANDARD; PRT; 492 AA.
AC P00743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
GN F10.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE OF 1-487 FROM N.A.
RX MEDLINE=84247315; PubMed=6330671;
RA Fung M.R., Campbell R.M., McGillyray R.T.A.;
RT "Blood coagulation factor X mRNA encodes a single polypeptide chain
RT containing a prepro leader sequence.";
RL Nucleic Acids Res. 12:4481-4492(1984).
RN [2]
RP SEQUENCE OF 41-180.
RX MEDLINE=80130563; PubMed=6766735;
RA Enfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
RA Titani K.;
RT "Amino acid sequence of the light chain of bovine factor XI (Stuart
RT factor).";
RL Biochemistry 19:659-667(1980).
RN [3]
RP REVISION TO 103.
RX MEDLINE=83308813; PubMed=6685826;
RA McMillen B.A., Fujikawa K., Kistiel W.;
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
RT K-dependent blood coagulation zymogens.";
RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
RN [4]
RP SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RX MEDLINE=76053069; PubMed=1059093;
RA Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,
RA Neurath H.;
RT "Bovine factor XI (Stuart factor): amino-acid sequence of heavy
RT chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).
RN [5]
RP SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.

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RX MEDLINE-94062825; PubMed=8243461;
 RA Inoue K., Morita T.;
 RT "Identification of O-linked oligosaccharide chains in the activation
 RT peptides of blood coagulation factor X. The role of the carbohydrate
 RT moieties in the activation of factor X.";
 RL Eur. J. Biochem. 218:153-163(1993).
 RN [6]
 RP ACTIVE SITE.
 RA MEDLINE-73053314; PubMed=4264286;
 RA Titani K., Hermanson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
 RA Neureath H., Davie E.W.;
 RT "Bovine factor X Ia (activated Stuart factor). Evidence of homology
 RT with mammalian serine proteases.";
 RL Biochemistry 11:489-490(1972).
 RN [7]
 RP PROCESSING.
 RX MEDLINE-76053121; PubMed=1059122;
 RA Fujikawa K., Titani K., Davie E.W.;
 RT "Activation of bovine factor X (Stuart factor): conversion of factor
 RT Xa-alpha to factor Xa-beta.";
 RL Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
 RN [8]
 RP CALCIUM-BINDING DATA.
 RX MEDLINE-84185716; PubMed=6546930;
 RA Sugo T., Bjork I., Holmgren A., Stenflo J.;
 RT "Calcium-binding properties of bovine factor X lacking the gamma-
 RT carboxyglutamic acid-containing region.";
 RL J. Biol. Chem. 259:5705-5710(1984).
 RN [9]
 RP SULFATION.
 RX MEDLINE-86140210; PubMed=3949800;
 RA Morita T., Jackson C.M.;
 RT "Localization of the structural difference between bovine blood
 RT coagulation factors XI and X2 to tyrosine 18 in the activation
 RT peptide.";
 RL J. Biol. Chem. 261:4008-4014(1986).
 RN [10]
 RP STRUCTURE BY NMR OF 85-126.
 RX MEDLINE-91084483; PubMed=2261466;
 RA Selander M., Persson E., Stenflo J., Drakenberg T.;
 RT "1H NMR assignment and secondary structure of the Ca2(+)-free form of
 RT the amino-terminal epidermal growth factor like domain in coagulation
 RT factor X.";
 RL Biochemistry 29:8111-8118(1990).
 RN [11]
 RP STRUCTURE BY NMR OF 85-126.
 RX MEDLINE-92329412; PubMed=1627540;
 RA Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,
 RA Telemann O.;
 RT "Three-dimensional structure of the apo form of the N-terminal
 RT EGF-like module of blood coagulation factor X as determined by NMR
 RT spectroscopy and simulated folding.";
 RL Biochemistry 31:5974-5983(1992).
 RN [12]
 RP STRUCTURE BY NMR OF 85-126.
 RX MEDLINE-92406922; PubMed=1527084;
 RA Selander M., Sunnerhagen M., Ullner M., Persson E., Telemann O.,
 RA Stenflo J., Drakenberg T.;
 RT "How an epidermal growth factor (EGF)-like domain binds calcium. High
 RT resolution NMR structure of the calcium form of the NH2-terminal EGF-
 RT like domain in coagulation factor X.";
 RL J. Biol. Chem. 267:19642-19649(1992).
 RN [13]
 RP STRUCTURE BY NMR OF 41-126.
 RX MEDLINE-96387194; PubMed=8794734;
 RA Sunnerhagen M., Olah G.A., Stenflo J., Forsen S., Drakenberg T.,
 RA Trehubella J.;
 RT "The relative orientation of Glu and EGF domains in coagulation
 RT factor X is altered by Ca2+ binding to the first EGF domain. A
 RT combined NMR-small angle X-ray scattering study.";
 RL Biochemistry 35:11547-11559(1996).
 CC -1- FUNCTION: FACTOR XA IS A VITAMIN K-DEPENDENT GLYCOPROTEIN THAT
 CC CONVERTS PROTHROMBIN TO THROMBIN IN THE PRESENCE OF FACTOR VA,

CC CAA++, AND PHOSPHOLIPID DURING BLOOD CLOTTING.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-1-Thr and then
 CC Arg-1-Ile bonds in prothrombin to form thrombin.
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 CC MORE DISULFIDE BONDS.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC -1- PTM: N- AND O-GLYCOSYLATED.
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 CC -----
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 CC or send an email to license@sib.ch).
 CC -----
 CC EMBL: X00673; CAA25286.1; -.
 CC PIR: A00925; EXBO.
 CC PDB: LAPO: 31-JAN-94.
 CC PDB: ICCF: 31-MAY-94.
 CC PDB: IMHE: 15-MAY-97.
 CC PDB: IMHE: 15-MAY-97.
 CC MEROPS: S01.216; -.
 CC Carbank: CCSD:7747; -.
 CC Carbank: CCSD:7899; -.
 CC Carbank: CCSD:11506; -.
 CC Carbank: CCSD:11508; -.
 CC GlycosultEDB: P00743; -.
 CC InterPro: IPR000152; Asx_hydroxyl.
 CC InterPro: IPR001314; Chymotrypsin.
 CC InterPro: IPR000561; EGF-like.
 CC InterPro: IPR000742; EGF-2.
 CC InterPro: IPR001881; EGF-Ca.
 CC InterPro: IPR002383; GLA_blood.
 CC InterPro: IPR001254; Trypsin.
 CC InterPro: IPR000294; Vitk_dep_GLA.
 CC Pfam: PF00008; EGF: 2.
 CC Pfam: PF00594; gla: 1.
 CC Pfam: PF00089; trypsin: 1.
 CC PRINTS: PR00722; CHYMOTRYPSIN.
 CC PRINTS: PR00001; GLABLOOD.
 CC SMART: SM00179; EGF_CA: 1.
 CC SMART: SM00001; EGF_Like: 1.
 CC SMART: SM00059; GLA: 1.
 CC SMART: SM00020; tryp_Spec: 1.
 CC PROSITE: PS00010; ASX_HYDROXYL: 1.
 CC PROSITE: PS00022; EGF_1: 1.
 CC PROSITE: PS01186; EGF_2: 2.
 CC PROSITE: PS01187; EGF_CA: 1.
 CC PROSITE: PS00011; GLU-CARBOXYLATION: 1.
 CC PROSITE: PS00240; TRYPSIN_DOM: 1.
 CC PROSITE: PS00134; TRYPSIN_HIS: 1.
 CC PROSITE: PS00135; TRYPSIN_SER: 1.
 CC GlycoSite: Hydroxylase: Serine protease; Plasma: Blood coagulation;
 CC Gamma-carboxyglutamic acid: Hydroxylation; Calcium-binding; Vitamin K;
 CC Signal; Zymogen; EGF-like domain; Repeat; Sulfation; 3D-structure.
 CC SIGNAL: 1 23
 CC FT SIGNAL: 24 40
 CC FT PROPEP 180
 CC FT CHAIN 183 492
 CC FT CHAIN 183 233
 CC FT CHAIN 234 492
 CC FT CHAIN 234 492
 CC FT PROPEP 476
 CC FACTOR X LIGHT CHAIN.
 CC FACTOR X HEAVY CHAIN.
 CC ACTIVATION PEPTIDE.
 CC ACTIVATED FACTOR XA, HEAVY CHAIN.
 CC MAY BE REMOVED BUT IS NOT NECESSARY FOR

FT DOMAIN 86 122 ACTIVATION.
 FT DOMAIN 125 165 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
 FT ACT_SITE 234 492 EGF-LIKE 2.
 FT ACT_SITE 275 492 SERINE PROTEASE.
 FT ACT_SITE 321 418 CHANGE RELAY SYSTEM.
 FT ACT_SITE 418 418 CHANGE RELAY SYSTEM.
 FT MOD_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID.
 Query Match 45.9%; Score 89; DB 1; Length 492;
 Best Local Similarity 36.4%; Pred. No. 3.1e-08;
 Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Qy 1 ANGFLXLRPSLRKXRCXRLCSFXAHXIRNXXRTQFVSVY 44
 Db 41 ANSFLKLVKGNLEKLEECLEAREVEDEAQTDEFWSKY 84

RESULT 16
 ID FA9_HUMAN STANDARD; PRT; 461 AA.
 AC P00740;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor IX precursor (EC 3.4.21.22) (Christmas factor).
 GN F9.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86000558; PubMed=2994716;
 RA Yoshitake S., Schach B.G., Foster D.C., Davie E.W., Kurachi K.;
 RT "Nucleotide sequence of the gene for human factor IX (antithemophilic
 factor B).";
 RL Biochemistry 24:3736-3750(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85190593; PubMed=3857619;
 RA McGraw R.A., Davis L.M., Noyes C.M., Lundblad R.L., Roberts H.R.,
 RT "Evidence for a prevalent dimorphism in the activation peptide of
 human coagulation factor IX.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:2847-2851(1985).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84236100; PubMed=6329734;
 RA Anson D.S., Choo K.H., Rees D.J.G., Giannelli F., Gould K.G.,
 RT "The gene structure of human anti-haemophilic factor IX.";
 RL EMBO J. 3:1053-1060(1984).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83220788; PubMed=6687940;
 RA Jaye M., de la Salle H., Schamber F., Ballard A., Kohli V.,
 RT "Isolation of a human anti-haemophilic factor IX cDNA clone using a
 unique 5'-base synthetic oligonucleotide probe deduced from the amino
 acid sequence of bovine factor IX.";
 RL Nucleic Acids Res. 11:2325-2335(1983).
 RN [5]
 RP SEQUENCE OF 36-326 FROM N.A.
 RC TISSUE-Liver;
 RX MEDLINE=84300526; PubMed=6089357;
 RA Jagadeeswaran P., Lavelle D.E., Kaul R., Mohandas T., Warren S.T.;
 RT "Isolation and characterization of human factor IX cDNA:
 RT Identification of Tag I polymorphism and regional assignment.";
 RL Somat. Cell Mol. Genet. 10:465-473(1984).
 RN [6]

RP SEQUENCE OF 290-359 FROM N.A.
 RX MEDLINE=88127096; PubMed=3340835;
 RA Stoflet E.S., Koeberl D.D., Sarker G., Sommer S.S.;
 RT "Genomic amplification with transcript sequencing.";
 RL Science 239:491-494(1988).
 RN [7]
 RP SEQUENCE OF 444-461 FROM N.A.
 RX MEDLINE=94054330; PubMed=8236150;
 RA de la Salle C., Charmantier J.L., Baas M.J., Schwartz A.,
 RT "A deletion located in the 3' non translated part of the factor IX
 gene responsible for mild haemophilia B.";
 RL Thromb. Haemost. 70:370-371(1993).
 RN [8]
 RP SEQUENCE OF 47-461 (VARIANT NAGOYA).
 RX MEDLINE=90078229; PubMed=2592373;
 RA Suehiro K., Kawabata S.-I., Miyata T., Takeya H., Takamatsu J.,
 RA Ogata K., Kamliya T., Saito H., Niho Y., Iwanaga S.;
 RT "Blood clotting factor IX BM Nagoya. Substitution of arginine 180 by
 tryptophan and its activation by alpha-chymotrypsin and rat mast cell
 chymase.";
 RL J. Biol. Chem. 264:21257-21265(1989).
 RN [9]
 RP HYDROXYLATION OF ASP-110.
 RX MEDLINE=83308813; PubMed=6688526;
 RA McMullen B.A., Fujikawa K., Kistiel W.;
 RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
 K-dependent blood coagulation zymogens.";
 RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
 RN [10]
 RP PROCESSING, ACTIVE SITE, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=78194509; PubMed=6596613;
 RA di Scipio R.G., Kurachi K., Davie E.W.;
 RT "Activation of human factor IX (Christmas factor).";
 RL J. Clin. Invest. 61:1528-1538(1978).
 RN [11]
 RP CALCIUM-BINDING DATA.
 RX MEDLINE=84185715; PubMed=6425296;
 RA Morita T., Isaacs B.S., Esmon C.T., Johnson A.E.;
 RT "Derivatives of blood coagulation factor IX contain a high affinity
 Ca2+-binding site that lacks gamma-carboxyglutamic acid.";
 RL J. Biol. Chem. 259:5698-5704(1984).
 RN [12]
 RP ERRATUM.
 RA Morita T., Isaacs B.S., Esmon C.T., Johnson A.E.;
 RL J. Biol. Chem. 260:2583-2583(1985).
 RN [13]
 RP SIGNAL SEQUENCE CLEAVAGE SITE.
 RX MEDLINE=86189947; PubMed=3009023;
 RA Bentley A.K., Rees D.J.G., Rizza C., Brownlee G.G.;
 RT "Defective propeptide processing of blood clotting factor IX caused
 by mutation of arginine to glutamine at position -4.";
 RL Cell 45:343-348(1986).
 RN [14]
 RP STRUCTURE OF CARBOHYDRATE ON SER-99.
 RX MEDLINE=90062160; PubMed=2511201;
 RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T., Takao T.,
 RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
 (Xyl2-Glc) O-glycosidically linked to a serine residue in the first
 epidermal growth factor-like domain of human factors VII and IX and
 protein Z and bovine protein Z.";
 RL J. Biol. Chem. 264:20320-20325(1989).
 RN [15]
 RP STRUCTURE OF CARBOHYDRATE ON SER-99.
 RX MEDLINE=91344709; PubMed=2129367;
 RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;
 RT "A new trisaccharide sugar chain linked to a serine residue in the
 first EGF-like domain of clotting factors VII and IX and protein Z.";
 RL Adv. Exp. Med. Biol. 281:121-131(1990).
 RN [16]
 RP STRUCTURE OF CARBOHYDRATE ON SER-107.
 RX MEDLINE=92388094; PubMed=1517205;

RA Nishimura H., Takeo T., Hase S., Shimonishi Y., Iwanaga S.;
RT "Human factor IX has a tetrasaccharide O-glycosidically linked to
RL serine 61 through the fucose residue.";
RN J. Biol. Chem. 267:17520-17525(1992).
RN [17]
RP PHOSPHORYLATION OF SER-114.
RA Harris R.J., Papac D.I., Truong L., Smith K.J.;
RT "Partial phosphorylation of serine-68 in EGF-1 of human factor IX."
RL (in) Abstracts of Xith International conference on methods in protein
structure analysis, pp.50-50, Anney (1996).
RN [18]
RP POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE-20575397; PubMed-11133752;
RA Arruda V.R., Hagstrom J.N., Dellich J., Helman-Patterson T.,
RA Camarile R.M., Chu K., Fields P.A., Herzog R.W., Couto L.B.,
RA Larson P.J., High K.A.;
RT "Posttranslational modifications of recombinant myotube-synthesized
RL human factor IX";
RN Blood 97:130-138(2001).
RN [19]
RP STRUCTURE BY NMR OF 47-93.
RX MEDLINE-95229607; PubMed-713897;
RA Freedman S.J., Furie B.C., Furie B., Baleja J.D.;
RT "Structure of the metal-free gamma-carboxyglutamic acid-rich
RL binding region of factor IX by two-dimensional NMR spectroscopy.";
RN J. Biol. Chem. 270:7980-7987(1995).
RN [20]
RP STRUCTURE BY NMR OF 47-93.
RX MEDLINE-96032604; PubMed-7547952;
RA Freedman S.J., Furie B.C., Furie B., Baleja J.D.;
RT "Structure of the calcium ion-bound gamma-carboxyglutamic acid-rich
RL domain of factor IX.";
RN Biochemistry 34:12126-12137(1995).
RN [21]
RP STRUCTURE BY NMR OF 47-93.
RX MEDLINE-96279169; PubMed-8663165;
RA Freedman S.J., Blostein M.D., Baleja J.D., Jacobs M., Furie B.C.,
RA Furie B.;
RT "Identification of the phospholipid binding site in the vitamin K-
RL dependent blood coagulation protein factor IX";
RN J. Biol. Chem. 271:16227-16236(1996).
RN [22]
RP STRUCTURE BY NMR OF 47-93.
RX MEDLINE-97199336; PubMed-9047312;
RA Li L., Darden T.A., Freedman S.J., Furie B.C., Furie B., Baleja J.D.,
RA Smith H., Hickey R.G., Pedersen L.G.;
RT "Refinement of the NMR solution structure of the
RL gamma-carboxyglutamic acid domain of coagulation factor IX using
molecular dynamics simulation with initial Ca²⁺ positions determined
by a genetic algorithm.";
RN Biochemistry 36:2132-2138(1997).
RN [23]
RP STRUCTURE BY NMR OF 91-133.
RX MEDLINE-91308127; PubMed-1854745;
RA Huang L.H., Cheng H., Pardi A., Tam J.P., Sweeney W.V.;
RT "Sequence-specific 1H NMR assignments, secondary structure, and
RL location of the calcium binding site in the first epidermal growth
factor like domain of blood coagulation factor IX.";
RN Biochemistry 30:7402-7409(1991).
RN [24]
RP STRUCTURE BY NMR OF 92-130.
RX MEDLINE-93284090; PubMed-1304885;
RA Baron M., Norman D.G., Harvey T.S., Handford P.A., Mayhew M.,
RA Tse A.G.D., Brownlee G.G., Campbell I.D.C.;
RT "The three-dimensional structure of the first EGF-like module of
RL human factor IX: comparison with EGF and TGF-alpha.";
RN Protein Sci. 1:81-90(1992).
RN [25]
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 92-130.
RX MEDLINE-95330802; PubMed-7606779;
RA Rao Z., Handford P., Mayhew M., Knott V., Brownlee G.G., Stuart D.;
RT "The structure of a Ca(2+)-binding epidermal growth factor-like
RL domain: its role in protein-protein interactions.";

RL Cell 82:131-141(1995).
RN [26]
RP MOLECULAR PATHOLOGY OF HEMOPHILIA B.
RN [27]
Query Match 44.8%; Score 87; DB 1; Length 461;
Best Local Similarity 39.5%; Pred. No. 6.7e-08;
Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;
QY 2 NGFLXXLRPGLXRCRXXLCSPFXAHXIFRNXXRTQFVWVSY 44
DB 49 SGKLEEFVGNLRECEMEKCSFEFAREVENTERTTEFWKQY 91
RESULT 17
FA9_BOVIN STANDARD; PRT; 416 AA.
ID FA9_BOVIN
AC P00741;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Coagulation factor IX (EC 3.4.21.22) (Christmas factor).
GN F9.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID:9913;
RN [1]
RP SEQUENCE.
RX MEDLINE-80056619; PubMed-291916;
RA Katayama K., Ericsson L.H., Enfield D.L., Walsh K.A., Neurath H.,
RA Davie E.W., Tildan K.;
RT "Comparison of amino acid sequence of bovine coagulation Factor IX
RL (Christmas Factor) with that of other vitamin K-dependent plasma
RT proteins.";
RN Proc. Natl. Acad. Sci. U.S.A. 76:4990-4994(1979).
RN [2]
RP REVISION TO 64.
RX MEDLINE-83308813; PubMed-6688526;
RA McMullen B.A., Fujikawa K., Kisiel W.;
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
RL K-dependent blood coagulation zymogens.";
RN Biochem. Biophys. Res. Commun. 115:8-14(1983).
RN [3]
RP SEQUENCE OF 51-111 FROM N.A.
RX MEDLINE-82272386; PubMed-6287289;
RA Choo K.H., Gould K.G., Rees D.J.G., Brownlee G.G.;
RT "Molecular cloning of the gene for human anti-thrombophilic factor IX";
RN Nature 299:178-180(1982).
RN [4]
RP STRUCTURE OF CARBOHYDRATE ON SER-53.
RX MEDLINE-89213999; PubMed-3149637;
RA Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T.,
RA Miyata T., Iwanaga S., Takeo T., Shimonishi Y., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in bovine
RL blood coagulation factors VII and IX";
RN J. Biochem. 104:867-868(1988).
RN [5]
RP STRUCTURE OF CARBOHYDRATE ON SER-53.
RX MEDLINE-91344709; PubMed-2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in the
RL first EGF-like domain of clotting factors VII and IX and protein Z.";
RN Adv. Exp. Med. Biol. 281:121-131(1990).
RN [6]
RP STRUCTURE OF CARBOHYDRATE ON SER-53.
RX MEDLINE-90130422; PubMed-2105311;
RA Hase S., Nishimura H., Kawabata S., Iwanaga S., Ikenaka T.;
RT "The structure of (xylose)2glucose-O-serine 53 found in the first
RL epidermal growth factor-like domain of bovine blood clotting factor
RT IX.";
RN J. Biol. Chem. 265:1858-1861(1990).
CC -I- FUNCTION: FACTOR IX IS A VITAMIN K-DEPENDENT PLASMA PROTEIN THAT

CC PARTICIPATES IN THE INTRINSIC PATHWAY OF BLOOD COAGULATION BY
 CC CONVERTING FACTOR X TO ITS ACTIVE FORM IN THE PRESENCE OF CA++
 CC IONS, PHOSPHOLIPIDS, AND FACTOR VIIIA.
 CC -1- CATALYTIC ACTIVITY: Hydrolyses one Arg-I-Ile bond in factor X to
 CC form factor Xa.
 CC -1- SUBUNIT: FACTOR IX IS ACTIVATED BY FACTOR XIA, WHICH EXCISES THE
 CC ACTIVATION PEPTIDE AND THUS PRODUCES A MOLECULE CONSISTING OF 2
 CC CHAINS HELD TOGETHER BY ONE OR MORE DISULFIDE BONDS.
 CC -1- MISCELLANEOUS: CALCIUM BINDS TO THE GAMMA-CARBOXYGLUTAMIC ACID
 CC (GLA) RESIDUES AND, WITH STRONGER AFFINITY, TO ANOTHER SITE,
 CC BEYOND THE GLA DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: J00007; AAA30520.1; -
 CC PIR: A00923; KFB0.
 CC HSSP: P00740; ICFH.
 CC MEROPS: S01.214; -
 CC GlycosultedB: P00741; -
 CC InterPro: IPR000152; Asx_hydroxyl.
 CC InterPro: IPR001312; Chymotrypsin.
 CC InterPro: IPR000561; EGF-like.
 CC InterPro: IPR000742; EGF-2.
 CC InterPro: IPR001881; EGF_Ca.
 CC InterPro: IPR001438; EGF_II.
 CC InterPro: IPR002383; GLA_blood.
 CC InterPro: IPR001254; Trypsin.
 CC InterPro: IPR000294; VitK_dep_GLA.
 CC Pfam: PF00008; EGF_2.
 CC Pfam: PF00594; gla; 1.
 CC Pfam: PF00089; trypsin; 1.
 CC PRINTS: PR00722; CHYMOTRYPSIN.
 CC PRINTS: PR00010; EGFBL00D.
 CC PRINTS: PR00001; GLABLOD.
 CC SMART: SM00179; EGF_CA; 1.
 CC SMART: SM00001; EGF_Like; 1.
 CC SMART: SM00059; GLA; 1.
 CC SMART: SM00020; TRYP_Spc; 1.
 CC PROSITE: PS00010; ASX_HYDROXYL; 1.
 CC PROSITE: PS00022; EGF_1; 1.
 CC PROSITE: PS01186; EGF_2; 2.
 CC PROSITE: PS01187; EGF_CA; 1.
 CC PROSITE: PS00011; GLU_CARBOXYLATION; 1.
 CC PROSITE: PS00240; TRYPSIN_DOM; 1.
 CC PROSITE: PS00134; TRYPSIN_HIS; 1.
 CC PROSITE: PS00135; TRYPSIN_SER; 1.
 CC Blood coagulation: Plasma: Serine protease: Calcium-binding;
 CC Hyaluronase, Glycoprotein; Vitamin K; Gamma-carboxyglutamic acid;
 CC Hemophilin; Hydroxylation; Zymogen; EGF-like domain.
 CC CHAIN 1 146 FACTOR IXA (ACTIVE FORM) LIGHT CHAIN.
 CC PROPEP 147 181 ACTIVATION PEPTIDE.
 CC CHAIN 182 416 FACTOR IXA (ACTIVE FORM) HEAVY CHAIN.
 CC DOMAIN 47 83 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
 CC DOMAIN 84 125 EGF-LIKE 2.
 CC SITE 182 416 SERINE PROTEASE.
 CC SITE 146 147 CLEAVAGE (BY FACTOR XIA).
 CC MOD_RES 7 8 GAMMA-CARBOXYGLUTAMIC ACID.
 CC MOD_RES 8 7 GAMMA-CARBOXYGLUTAMIC ACID.
 CC MOD_RES 15 15 GAMMA-CARBOXYGLUTAMIC ACID.
 CC MOD_RES 17 17 GAMMA-CARBOXYGLUTAMIC ACID.
 CC MOD_RES 20 20 GAMMA-CARBOXYGLUTAMIC ACID.
 CC MOD_RES 21 21 GAMMA-CARBOXYGLUTAMIC ACID.
 CC MOD_RES 26 26 GAMMA-CARBOXYGLUTAMIC ACID.

FT MOD_RES 27 27 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 30 30 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 33 33 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 36 36 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 40 40 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 64 64 GAMMA-CARBOXYGLUTAMIC ACID.
 FT DISULFID 18 23 BY SIMILARITY.
 FT DISULFID 51 62 BY SIMILARITY.
 FT DISULFID 56 71 BY SIMILARITY.
 FT DISULFID 73 82 BY SIMILARITY.
 FT DISULFID 88 99 BY SIMILARITY.
 FT DISULFID 95 109 BY SIMILARITY.
 FT DISULFID 111 124 BY SIMILARITY.
 FT CARBOHYD 53 53 O-LINKED (GLC. .).
 FT CARBOHYD 158 158 /FTID-CAR_000008.
 FT CARBOHYD 168 168 N-LINKED (GLCNC. .).
 FT CARBOHYD 173 173 N-LINKED (GLCNC. .).
 FT CARBOHYD 261 261 N-LINKED (GLCNC. .).
 FT ACT_SITE 222 222 CHARGE RELAY SYSTEM.
 FT ACT_SITE 270 270 CHARGE RELAY SYSTEM.
 FT ACT_SITE 366 366 CHARGE RELAY SYSTEM.
 FT VARIANT 64 64 D -> T (IN REF. 1).
 SQ SEQUENCE 416 AA; 46785 MW; 34A7DEE916330662 CRC64;
 Query Match 44.3%; Score 86; DB 1; Length 416;
 Best Local Similarity 37.2%; Pred. No. 9,1e-08;
 Matches 16; Conservative 6; Mismatches 21; Indels 0; Gaps 0;
 QY 2 NGLFLXLRGSLXRXKXLLCSFXMHLXFRXXRFRQWVAY 44
 DB 3 SKLEEFVRGNLECKEKCSEAREVEWTEKTERWKQY 45
 RESULT 18
 ID FA9_CANFA STANDARD; PRT; 452 AA.
 AC P19540;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Coagulation factor IX precursor (EC 3.4.21.22) (Christmas factor).
 GN F9.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN 11
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=90311364; PubMed=2367529;
 RA Axelrod J.H., Read M.S., Brinkhous K.M., Verma I.M.;
 RT "Phenotypic correction of factor IX deficiency in skin fibroblasts of
 RT hemophilic dogs";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:5173-5177(1990).
 RN 12
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=8932338; PubMed=2752110;
 RA Evans J.P., Matzke H.H., Ware J.L., Stafford D.W., High K.A.;
 RT "Molecular cloning of a cDNA encoding canine factor IX";
 RL Blood 74:207-212(1989).
 RN 13
 RP VARIANT HEMOPHILIA B G104-418.
 RX MEDLINE=9009303; PubMed=2481310;
 RA Evans J.P., Brinkhous K.M., Brayer G.D., Reisner H.M., High K.A.;
 RT "Canine hemophilia B resulting from a point mutation with unusual
 RT consequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:10095-10099(1989).
 CC -1- FUNCTION: FACTOR IX IS A VITAMIN K-DEPENDENT PLASMA PROTEIN THAT
 CC PARTICIPATES IN THE INTRINSIC PATHWAY OF BLOOD COAGULATION BY
 CC CONVERTING FACTOR X TO ITS ACTIVE FORM IN THE PRESENCE OF CA++

CC CA++ AND PHOSPHOLIPID DURING BLOOD CLOTTING.
 CC -1- FUNCTION: VAP CLEAVES THE FUSION PROTEINS OF SENDAI VIRUS, NDV,
 CC AND INFLUENZA VIRUS A AT A SPECIFIC SINGLE ARGININE-CONTAINING
 CC SITE, AND PLAYS A KEY ROLE IN THE VIRAL SPREADING IN THE ALLANTOIC
 CC SAC.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-1-Thr and then
 CC Arg-1-Ile bonds in prothrombin to form thrombin.
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 CC MORE DISULFIDE BONDS.
 CC -1- TISSUE SPECIFICITY: LIVER AND CHORIOALLANTOIC MEMBRANE.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: D00844; BAA00724.1; -
 CC PIR: S15838; S15838.
 CC HSSP: P00742; 1HCG.
 CC MEROPS: S01.216; -
 CC Interpro: IPR000132; Asx_hydroxyl.
 CC Interpro: IPR001314; Chymotrypsin.
 CC Interpro: IPR000561; EGF-like.
 CC Interpro: IPR000742; EGF_2.
 CC Interpro: IPR001881; EGF-ca.
 CC Interpro: IPR001438; EGF-IT.
 CC Interpro: IPR002383; GLA_blood.
 CC Interpro: IPR001254; Trypsin.
 CC Interpro: IPR000294; VitK_dep_GLA.
 CC Pfam: PF00008; EGF_2.
 CC Pfam: PF00594; gla_1.
 CC Pfam: PF00089; trypsin_1.
 CC PRINTS: PR00722; CHYMOTRYPSIN.
 CC PRINTS: PR00010; EGFblood.
 CC PRINTS: PR00001; GLABLOOD.
 CC SMART: SM00179; EGF_CA; 1.
 CC SMART: SM00069; GLA; 1.
 CC SMART: SM00020; TYP_SPC; 1.
 CC PROSITE: PS00010; ASX_HYDROXYL; 1.
 CC PROSITE: PS00022; EGF_1; 1.
 CC PROSITE: PS01186; EGF_2; 2.
 CC PROSITE: PS01187; EGF_CA; 1.
 CC PROSITE: PS00011; GLU_CARBOXYLATION; 1.
 CC PROSITE: PS50240; TRYPSIN_DOM; 1.
 CC PROSITE: PS00134; TRYPSIN_HIS; 1.
 CC PROSITE: PS00135; TRYPSIN_SER; 1.
 CC Glycoprotein: Hydrolase: Serine protease: Plasma: Blood coagulation;
 CC Gamma-carboxyglutamic acid: Hydroxylation: Calcium-binding: Vitamin K;
 CC Signal: Zymogen: EGF-like domain: Repeat.
 CC SIGNAL: 1 20 OR 30, OR 31 (POTENTIAL).
 CC PROPEP 21 40
 CC CHAIN 41 180 FACTOR X LIGHT CHAIN.
 CC CHAIN 186 475 FACTOR X HEAVY CHAIN.
 CC PROPEP 186 475
 CC CHAIN 241 475 ACTIVATION PEPTIDE.
 CC CHAIN 242 475 ACTIVATED FACTOR XA, HEAVY CHAIN.
 CC DOMAIN 86 122 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
 CC DOMAIN 125 168 EGF-LIKE 2.
 CC DOMAIN 241 475 SERINE PROTEASE.
 CC MOD_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID
 CC MOD_RES 46 46 (BY SIMILARITY).
 CC MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID

FT MOD_RES 54 54 (BY SIMILARITY).
 FT MOD_RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID
 FT MOD_RES 59 59 (BY SIMILARITY).
 FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID
 FT MOD_RES 65 65 (BY SIMILARITY).
 FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID
 FT MOD_RES 69 69 (BY SIMILARITY).
 FT MOD_RES 72 72 GAMMA-CARBOXYGLUTAMIC ACID
 FT MOD_RES 79 79 GAMMA-CARBOXYGLUTAMIC ACID
 FT MOD_RES 103 103 (BY SIMILARITY).
 FT ACT_SITE 282 282 HYDROXYLATION (BY SIMILARITY).
 FT ACT_SITE 328 328 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 425 425 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 90 101 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 95 110 BY SIMILARITY.
 FT DISULFID 112 121 BY SIMILARITY.
 FT DISULFID 129 140 BY SIMILARITY.
 FT DISULFID 136 152 BY SIMILARITY.
 FT DISULFID 154 167 BY SIMILARITY.
 FT DISULFID 175 348 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 247 252 BY SIMILARITY.
 FT DISULFID 267 283 BY SIMILARITY.
 FT DISULFID 396 410 BY SIMILARITY.
 FT DISULFID 421 449 BY SIMILARITY.
 FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SSEQUENCE 475 AA; 53142 MW; 570BF84956C574D CRC64;
 Query Match 41.8%; Score 81; DR 1; Length 475;
 Best Local Similarity 34.1%; Pred. No. 8.2e-07;
 Matches 15; Conservative 7; Mismatches 22; Indels 0; Gaps 0;
 Qy 1 ANGFLXLRPGSLXRCXKXLCSEFXAHXIFRNXXRPPWVSY 44
 Db 41 ANSLFEMKGNIERECNERCSNEAREAFEDNEKTEEFWNIT 84
 RESULT 21
 ID TMG2_HUMAN STANDARD; PRT; 202 AA.
 AC 014669;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Transmembrane gamma-carboxyglutamic acid protein 2 precursor (Proline-
 DE rich Gla protein 2) (Proline-rich gamma-carboxyglutamic acid protein
 DE 2).
 GN PRKG2 OR TMG2 OR PRGP2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9740347; PubMed=9256434;
 RA Kulman J.D., Harris J.E., Haldeman B.A., Davie E.W.;
 RT "Primary structure and tissue distribution of two novel proline-rich
 RT gamma-carboxyglutamic acid proteins".
 RL Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

```
CC -!- TISSUE SPECIFICITY: Highly expressed in the thyroid.
CC -!- PTM: Glu residues are produced after subsequent posttranslational
CC modifications of glutamic acid by a vitamin K-dependent gamma-
CC carboxylase.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF009243; AAB67071.1; -.
DR MIM: 604429; -.
DR HSSP: P00740; ICFH.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00594; gla; 1.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00069; GLA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
KW Gamma-carboxyglutamic acid; Vitamin K; Transmembrane; Signal.
FT SIGNAL 1 23
FT PROPEP 24 49
FT CHAIN 50 202
FT DOMAIN 50 109 TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
FT TRANSMEM 110 132 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 133 202 POTENTIAL.
FT DOMAIN 54 91 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 161 173 GLA-RICH.
FT DOMAIN 191 194 POLY-PRO.
FT SO SEQUENCE 202 AA; 22393 MW; BC79400C98492060 CRC64;

Query Match 40.7%; Score 79; DB 1; Length 202;
Best Local Similarity 40.0%; Pred. No. 7.9e-07;
Matches 16; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

OY 5 LXXLRGSLXRXCRXXLCSPXAXHXIFRNXXXTROFWWSY 44
DB 55 LELTPGNLERCELERCSEAREYFEDNTLTLEFWESEY 94

RESULT 22
TMG4_HUMAN STANDARD: PRT; 226 AA.
AC Q9B2D6;
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Transmembrane gamma-carboxyglutamic acid protein 4 precursor.
GN TMG4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN NCB1_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=21117044; PubMed=11171957;
RA Kulman J.D., Harris J.E., Xie L., Davie E.W.;
RT "Identification of two novel transmembrane gamma-carboxyglutamic acid
RT proteins expressed broadly in fetal and adult tissues.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:1370-1375(2001).
RN [12]
RP SEQUENCE FROM N.A.
RX TISSUE=Placenta;
RA Strausberg R.;
RN Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in lung, liver, kidney, pancreas and
CC placenta.
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CC -!- PTM: Glu residues are produced after subsequent posttranslational
CC modifications of glutamic acid by a vitamin K-dependent gamma-
CC carboxylase.
CC -----
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CC -----
DR EMBL: AF326351; AAK00956.1; -.
DR EMBL: BC010052; AAH10052.1; -.
DR HSSP: P00740; ICFH.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR000294; VitK_dep_GLA.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00069; GLA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
KW Gamma-carboxyglutamic acid; Vitamin K; Transmembrane; Signal.
FT SIGNAL 1 17
FT PROPEP 18 49
FT CHAIN 50 226
FT DOMAIN 50 113 TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
FT TRANSMEM 114 134 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 135 226 POTENTIAL.
FT DOMAIN 56 93 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 203 208 GLA-RICH.
FT SO SEQUENCE 226 AA; 25403 MW; 45C783E3825797EE CRC64;

Query Match 40.2%; Score 78; DB 1; Length 226;
Best Local Similarity 37.5%; Pred. No. 1.3e-06;
Matches 15; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

OY 5 LXXLRGSLXRXCRXXLCSPXAXHXIFRNXXXTROFWWSY 44
DB 57 LELTPGNLERCELERCSEAREYFEDNTLTLEFWESEY 96

RESULT 23
THRB_HUMAN STANDARD: PRT; 622 AA.
AC P00734;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Prothrombin precursor (EC 3.4.21.5) (Coagulation factor II).
GN F2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN NCB1_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=88077877; PubMed=2825773;
RA Degen S.J.F., Davie E.W.;
RT "Nucleotide sequence of the gene for human prothrombin.";
RL Biochemistry 26:6165-6177(1987).
RN [2]
RP SEQUENCE OF 8-622 FROM N.A.
RX MEDLINE=83231469; PubMed=6305407;
RA Degen S.J.F., McGillivray R.T.A., Davie E.W.;
RT "Characterization of the complementary deoxyribonucleic acid and gene
RT coding for human prothrombin.";
RL Biochemistry 22:2087-2097(1983).
RN [3]
RP SEQUENCE OF 44-314.
RX MEDLINE=77193964; PubMed=266717;
RA Walz D.A., Hewett-Emmett D., Seegers W.H.;
RT "Amino acid sequence of human prothrombin fragments 1 and 2.";
```

RL Proc. Natl. Acad. Sci. U.S.A. 74:1969-1972(1977).
 RN [4]
 RP SEQUENCE OF 315-622.
 RX MEDLINE=77207112; Pubmed=873923;
 RA Butkowski R.J., Elton J., Downing M.R., Mann K.G.;
 RT "Primary structure of human prothrombin 2 and alpha-thrombin.";
 RL J. Biol. Chem. 252:4942-4957(1977).
 RN [5]
 RP PROCESSING.
 RX MEDLINE=87008532; Pubmed=3759958;
 RA Rabiet M.J., Blaschill A., Furie B., Furie B.C.;
 RT "Prothrombin fragment 1 x 2 x 3, a major product of prothrombin
 activation in human plasma.";
 RL J. Biol. Chem. 261:13210-13215(1986).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=90059942; Pubmed=2583108;
 RA Bode W., Mayr I., Baumann U., Huber R., Stone S.R., Hofsteenge J.;
 RT "The refined 1.9 Å crystal structure of human alpha-thrombin:
 interaction with D-Phe-Pro-Arg chloromethylketone and significance of
 the Tyr-Pro-Pro-Tyr insertion segment.";
 RL EMBO J. 8:3467-3475(1989).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE=90327074; Pubmed=2374926;
 RA Rydel T.J., Ravichandran K.G., Tulinsky A., Bode W., Huber R.,
 RA Rolsch C., Fenton J.W. II;
 RT "The structure of a complex of recombinant hirudin and human alpha-
 thrombin.";
 RL Science 249:277-280(1990).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=94350942; Pubmed=8071320;
 RA Rydel T.J., Yin M., Padmanabhan K.P., Blankenship D.T., Cardin A.D.,
 RA Correa P.E., Fenton J.W. II, Tulinsky A.;
 RT "Crystallographic structure of human gamma-thrombin.";
 RL J. Biol. Chem. 269:22000-22006(1994).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE=97357286; Pubmed=9214615;
 RA van de Lochte A., Bode W., Huber R., le Bonniec B.F., Stone S.R.,
 RA Esmen C.T., Stubbs M.T.;
 RT "The thrombin E192D-BPTI complex reveals gross structural
 rearrangements: implications for the interaction with antithrombin
 and thrombomodulin.";
 RL EMBO J. 16:2977-2984(1997).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 328-601.
 RX MEDLINE=99162521; Pubmed=10051558;
 RA Quinto E.R., Caccia S., Rose T., Fuetterer K., Waksman G., di Cera E.;
 RT "Unexpected crucial role of residue 225 in serine proteases.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:1852-1857(1999).
 RN [11]
 RP VARIANT BARCELONA.
 RX MEDLINE=87033739; Pubmed=3771562;
 RA Rabiet M.-J., Furie B.C., Furie B.;
 RT "Molecular defect of prothrombin Barcelona. Substitution of cysteine
 for arginine at residue 273.";
 RL J. Biol. Chem. 261:15045-15048(1986).
 RN [12]
 RP VARIANT FRANKFURT.
 RX MEDLINE=95313001; Pubmed=7792730;
 RA Degen S.J.F., McDowell S.A., Sparks L.M., Scharer I.;
 RT "Prothrombin Frankfurt: a dysfunctional prothrombin characterized by
 substitution of Glu-466 by Ala.";
 RL Thromb. Haemost. 73:203-209(1995).
 RN [13]
 RP VARIANTS HIMI-1 AND HIMI-2.
 RX MEDLINE=93043342; Pubmed=1421398;
 RA Morishita E., Saito M., Kumabashiri I., Asakura H., Matsuda T.,
 RA Yamaguchi K.;
 RT "Prothrombin Himi: a compound heterozygote for two dysfunctional
 prothrombin molecules (Met-337-->Thr and Arg-388-->His).";

RL Blood 80:2275-2280(1992).
 RN [14]
 RP VARIANT PADUA-1.
 RX MEDLINE=95169898; Pubmed=7865694;
 RA James H.L., Kim D.J., Zheng D.-Q., Girolami A.;
 RT "Prothrombin Padua I: incomplete activation due to an amino acid
 substitution at a factor Xa cleavage site.";
 RL Blood Coagul. Fibrinolysis 5:841-844(1994).
 RN [15]
 RP VARIANT QUICK-1.
 RX MEDLINE=89207504; Pubmed=3242619;
 RA Henriksen R.A., Mann K.G.;
 RT "Identification of the primary structural defect in the dyschrombin
 thrombin Quick I: substitution of cysteine for arginine-382.";
 RL Biochemistry 27:9160-9165(1988).
 RN [16]
 RP VARIANT QUICK-2.
 RX MEDLINE=89247398; Pubmed=2719946;
 RA Henriksen R.A., Mann K.G.;
 RT "Substitution of valine for glycine-558 in the congenital dyschrombin
 thrombin Quick II alters primary substrate specificity.";
 RL Biochemistry 28:2078-2082(1989).
 RN [17]
 RP VARIANT SALAKTA.
 RX MEDLINE=92378975; Pubmed=1354985;
 RA Miyata T., Aruga R., Uneyama H., Bezeaud A., Guillin M.-C.,
 RA Iwanaga S.;
 RT "Prothrombin Salakta: substitution of glutamic acid-466 by alanine
 reduces the fibrinogen clotting activity and the esterase activity.";
 RL Biochemistry 31:7457-7462(1992).
 RN [18]
 RP VARIANT TOKUSHIMA.
 RX MEDLINE=87185407; Pubmed=3567158;
 RA Miyata T., Morita T., Inomoto T., Kawauchi S., Shirakami A.,
 RA Iwanaga S.;
 RT "Prothrombin Tokushima, a replacement of arginine-418 by tryptophan
 that impairs the fibrinogen clotting activity of derived thrombin
 Tokushima.";
 RL Biochemistry 26:1117-1122(1987).
 RN [19]
 RP VARIANT TOKUSHIMA.
 RX MEDLINE=87101511; Pubmed=3801671;
 RA Inomoto T., Shirakami A., Kawauchi S., Shigekyo T., Salto S.,
 RA Miyoshi K., Morita T., Iwanaga S.;
 RT "Prothrombin Tokushima: characterization of dysfunctional thrombin
 derived from a variant of human prothrombin.";
 RL Blood 69:565-569(1987).
 RN [20]
 RP VARIANT TOKUSHIMA.
 RX MEDLINE=92256895; Pubmed=1349838;
 RA Iwahana H., Yoshimoto K., Shigekyo T., Shirakami A., Salto S.,
 RA Itakura M.;
 RT "Detection of a single base substitution of the gene for prothrombin
 Tokushima. The application of PCR-SSCP for the genetic and molecular
 analysis of dysprothrombinemia.";
 RL Int. J. Hematol. 55:93-100(1992).
 RN [21]
 RP VARIANT TYPE-3.
 RX MEDLINE=83204687; Pubmed=6405779;
 RA Board P.G., Shaw D.C.;
 RT "Determination of the amino acid substitution in human prothrombin
 type 3 (157 Glu leads to Lys) and the localization of a third
 thrombin cleavage site.";
 RL Br. J. Haematol. 54:245-254(1983).
 CC -1- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG 6 LYS, CONVERTS
 FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,
 AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: SYNTHESIZED IN THE LIVER, FOUND IN PLASMA.
 CC -1- PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
 RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL
 ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES
 ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY

CC CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
CC OF PROTHROMBIN TO THROMBIN.
CC -1- DISEASE: DEFECTS IN F2 ARE THE CAUSE OF VARIOUS FORMS OF
CC DYSFIBRINOGENEMIA.
CC -1- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A
CC PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &
CC FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES
CC THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &
CC HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR
CC V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
CC THROMBIN.
CC -1- MISCELLANEOUS: IT IS NOT KNOWN WHETHER 1 OR 2 SMALLER ACTIVATION
CC PEPTIDES, WITH ADDITIONAL CLEAVAGE AFTER 314-ARG, ARE RELEASED IN
CC NATURAL BLOOD CLOTTING.
CC -1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL
CC FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
CC BY FACTOR XA.
CC -1- MISCELLANEOUS: THE CLEAVAGE AFTER R-198, OBSERVED IN VITRO, DOES
CC NOT OCCUR IN PLASMA.
CC -1- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC
Query Match 40.2%; Score 78; DB 1; Length 622;
Best Local Similarity 36.4%; Pred. No. 3,7e-06;
Matches 16; Conservative 4; Mismatches 24; Indels 0; Gaps 0;
Oy 1 ANGFLXXLRPGSLXRCXKXLCSPFXAXHIFRNXXRTQFWVSY 44
Db 44 ANTFLEVRKGNLEKREVEEYECSTIEAFEALESSTADVFMAKY 87
RESULT 24
FA10.TROCA STANDARD; PRT; 376 AA.
AC P81428;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Coagulation factor X (EC 3.4.21.6) (Trocarnin prothrombin activator).
OS Trophedechis carinatus (Australian rough-scaled snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylidae; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Trophedechis.
ON NCBI_TaxID=100989;
RN [1]
RP SEQUENCE AND CHARACTERIZATION.
RC TISSUE-Venom.
RX MEDLINE=99326314; PubMed=10397729;
RA Joseph J.S., Chung M.C.M., Jeyaseelan K., Kini R.M.;
RT "Amino acid sequence of trocarnin, a prothrombin activator from
RT Trophedechis carinatus venom: its structural similarity to coagulation
RT factor Xa."
RT Blood 94:621-631(1999).
RL -1- FUNCTION: FACTOR XA IS A VITAMIN K-DEPENDENT GLYCOPROTEIN THAT
CC CONVERTS PROTHROMBIN TO THROMBIN IN THE PRESENCE OF FACTOR VA,
CC CALCIUM, AND PHOSPHOLIPID DURING BLOOD CLOTTING. ACTS AS A TOXIN
CC IN VENOM.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-1-Thr and then
CC Arg-1-Ile bonds in prothrombin to form thrombin.
CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
CC AND ARE HELD TOGETHER BY 1 OR MORE DISULFIDE BONDS.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM.
CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.

DR HSSP: P00742; 1HCG.
DR MEROPS: S01.216; -
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF 2.
DR InterPro: IPR001881; EGF Ca.
DR InterPro: IPR001438; EGF-IT.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Trypsin.
DR InterPro: IPR000294; VitK_dep_GLA.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00010; EGBLOOD.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00001; EGF_Like; 1.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; TRYP_SPE; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
KW Zymogen; EGF-like domain; Repeat.
FT CHAIN 1 141
FT NON_CONS 141 142
FT CHAIN 142 376
FT CHAIN 142 376
FT DOMAIN 50 81
FT DOMAIN 89 124
FT DOMAIN 142 376
FT MOD_RES 6 6
FT MOD_RES 7 7
FT MOD_RES 14 14
FT MOD_RES 16 16
FT MOD_RES 19 19
FT MOD_RES 20 20
FT MOD_RES 25 25
FT MOD_RES 26 26
FT MOD_RES 29 29
FT MOD_RES 32 32
FT MOD_RES 35 35
FT MOD_RES 63 63
FT ACT_SITE 183 183
FT ACT_SITE 229 229
FT ACT_SITE 326 326
FT ACT_SITE 326 326
FT DISULFID 17 22
FT DISULFID 50 61
FT DISULFID 55 70
FT DISULFID 72 81
FT DISULFID 89 100
FT DISULFID 96 109
FT DISULFID 111 124
FT DISULFID 132 249
FT DISULFID 148 153
FT DISULFID 168 184
FT DISULFID 297 311
FT DISULFID 322 350
FT CARBOHYD 52 52
FT CARBOHYD 186 186
SQ SEQUENCE 376 AA; 42455 MW; F5A5CFE9BA561C1 CRC64;
Query Match 39.7%; Score 77; DB 1; Length 376;
Best Local Similarity 31.8%; Pred. No. 3,4e-06;
Matches 14; Conservative 7; Mismatches 23; Indels 0; Gaps 0;
Oy 1 ANGFLXXLRPGSLXRCXKXLCSPFXAXHIFRNXXRTQFWVSY 44

DB 1 SNLSFEIRGNIERECIEKCKSEAREVFEEDNEKTEFWNY 44

RESULT 25

THRB_RAT STANDARD: PRT: 617 AA.

ID THRB_RAT

AC P18292:

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Prothrombin precursor (EC 3.4.21.5).

GN F2.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;

RX MEDLINE=90332426; PubMed=2377469;

RA Dhanich M., Monard D.;

RT "cDNA sequence of rat prothrombin.";

RL Nucleic Acids Res. 18:4251-4251(1990).

RN [2]

RP SEQUENCE OF 383-617 FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=92212913; PubMed=1557383;

RA Banfield D.K., Macgillivray R.T.;

RT "Partial characterization of vertebrate prothrombin cDNAs:

RT amplification and sequence analysis of the B chain of thrombin from

RT nine different species.";

RL Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).

CC -1- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS

CC FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,

CC AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.

CC -1- PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,

CC RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL

CC ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES

CC ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY

CC CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION

CC OF PROTHROMBIN TO THROMBIN.

CC -1- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A

CC PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &

CC FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES

CC THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &

CC HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR

CC V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF

CC THROMBIN.

CC -1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL

CC FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION

CC BY FACTOR XA.

CC -1- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE

CC TRYPSIN FAMILY.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL; X52835; CAA37017.1; -

DR EMBL; M81397; AAA42240.1; -

DR PIR: S10511; S10511.

DR HSSP: P00734; LUVS.

DR MEROPS; S01.217;

DR InterPro; IPR001314; Chymotrypsin.

DR InterPro; IPR002383; GLA_blood.

DR InterPro; IPR000001; Kringlein.

DR InterPro; IPR003966; Prothrombin.

DR InterPro; IPR001254; Trypsin.

DR InterPro; IPR000294; VitK_dep_GLA.

DR Pfam; PF00594; gla; 1.

DR Pfam; PF00051; kringle; 2.

DR Pfam; PF00089; trypsin; 1.

DR PRINTS; PR00722; CHYMOTRYPSIN.

DR PRINTS; PR00001; GLABLOOD.

DR PRINTS; PR00018; KRINGLE.

DR SMART; SM00069; GLA; 1.

DR SMART; SM00130; KR; 2.

DR SMART; SM00020; TRYP_SPC; 1.

DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.

DR PROSITE; PS00021; KRINGLE_1; 2.

DR PROSITE; PS50070; KRINGLE_2; 2.

DR PROSITE; PS50240; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; 1.

DR PROSITE; PS00135; TRYPSIN_SER; 1.

KW Blood coagulation; Plasma; Calcium-binding; Glycoprotein; Repeat;

KW Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver;

KW Hydrolyase; Serine protease; Kringle; Signal.

FT SIGNAL 1 24

FT PROPEP 25 43

FT CHAIN 44 617

FT PEPTIDE 44 200

FT PEPTIDE 201 323

FT CHAIN 324 359

FT CHAIN 360 617

FT DOMAIN 109 187

FT DOMAIN 215 292

FT DOMAIN 360 617

FT SITE 200 201

FT SITE 323 324

FT SITE 359 360

FT ACT_SITE 402 402

FT ACT_SITE 458 458

FT ACT_SITE 564 564

FT MOD_RES 50 50

FT MOD_RES 51 51

FT MOD_RES 58 58

FT MOD_RES 60 60

FT MOD_RES 63 63

FT MOD_RES 64 64

FT MOD_RES 69 69

FT MOD_RES 70 70

FT MOD_RES 73 73

FT MOD_RES 76 76

FT CARBOHYD 120 120

FT CARBOHYD 144 144

FT CARBOHYD 412 412

FT CARBOHYD 552 552

FT CARBOHYD 61 66

FT DISULFID 91 104

FT DISULFID 109 187

FT DISULFID 130 170

FT DISULFID 158 182

FT DISULFID 215 292

FT DISULFID 236 276

FT DISULFID 264 287

FT DISULFID 332 478

FT DISULFID 387 403

FT DISULFID 532 546

FT DISULFID 560 590

SO SEQUENCE 617 AA; 70411 MW; AD27D1B71445BD1D CRC64;

Query Match 38.7%; Score 75; DB 1; Length 617;

Best Local Similarity 37.2%; Pred. No. 1.3e-05;

Matches 16; Conservativity 4; Mismatches 23; Indels 0; Gaps 0;

Oy 2 NGFLXLRPGSLXRCXRXLCSPFXAHXIRPNXXRTROFWVSY 44

DB 46 SGFLLELRKGNLRECVEDQCTSEAFEALESQDDIDVFWAKY 88

RESULT 26
THRB_MOUSE STANDARD; PRT: 618 AA.
AC P19221;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Prothrombin precursor (EC 3.4.21.5).
GN F2 OR CF2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC SFRAIN-C57BL/6; TISSUE=Liver;
RX MEDLINE=91025551; PubMed=222810;
RA Flierzer Degen S.J., Schaffer L.A., Jamison C.S., Grant S.G.,
RA Fitzgibbon J.J., Pal J.-A., Chapman V.M., Elliott R.W.,
RT "Characterization of the cDNA coding for mouse prothrombin and
RT localization of the gene on mouse chromosome 2.";
RL DNA Cell Biol. 9:487-498(1990).
RN [2]
RP SEQUENCE OF 384-618 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92212913; PubMed=1557383;
RA Banfield D.R., Macgillivray R.T.;
RT "Partial characterization of vertebrate prothrombin cDNAs:
RT amplification and sequence analysis of the B chain of thrombin from
RT nine different species.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
CC -1- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS
CC FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,
CC AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.
CC -1- PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
CC RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL
CC ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES
CC ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY
CC CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
CC OF PROTHROMBIN TO THROMBIN.
CC -1- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A
CC PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &
CC FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS. FACTOR XA REMOVES
CC THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &
CC HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR
CC V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
CC THROMBIN.
CC -1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL
CC FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
CC BY FACTOR XA.
CC -1- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
CC -----
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CC -----
DR EMBL: X52308; CA36548.1; -;
DR EMBL: M81394; AAA0435.1; -;
DR PIR: A35827; A35827.
DR HSSP: P00734; 1B7X.
DR MEROPS: S01.217; -;
DR MGD: MGI:88380; F2.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR002383; GLA_Blood.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR003966; Prothrombin.

DR InterPro: IPR001254; Trypsin.
DR InterPro: IPR000294; Vitk_dep_GLA.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00051; kringle; 2.
DR PRINTS: PRO0722; CHYMOTRYPSIN.
DR PRINTS: PRO0001; GLABLOOD.
DR PRINTS: PRO0018; KRINGLE.
DR PRINTS: PRO1505; PROTHROMBIN.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00130; KR; 2.
DR SMART: SM00020; Tryp_spec; 1.
DR PROSITE: PS00011; GLU CARBOXYLATION; 1.
DR PROSITE: PS00021; KRINGLE_1; 2.
DR PROSITE: PS50070; TRYPSIN_DOM; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Blood coagulation; Plasma; Calcium-binding; Glycoprotein; Repeat;
KW Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver;
KW Hydrolyase; Serine protease; Kringle; Signal.
FT SIGNAL 1 24
FT PROPEP 25 43
FT CHAIN 44 618
FT PEPTIDE 44 200
FT PEPTIDE 201 324
FT CHAIN 325 360
FT CHAIN 361 618
FT DOMAIN 109 187
FT DOMAIN 115 292
FT DOMAIN 361 618
FT SITE 200 201
FT SITE 324 325
FT SITE 360 361
FT ACT_SITE 403 403
FT ACT_SITE 459 459
FT ACT_SITE 565 565
FT MOD_RES 50 50
FT MOD_RES 51 51
FT MOD_RES 58 58
FT MOD_RES 60 60
FT MOD_RES 63 63
FT MOD_RES 64 64
FT MOD_RES 69 69
FT MOD_RES 70 70
FT MOD_RES 73 73
FT MOD_RES 76 76
FT DISULFID 61 66
FT DISULFID 91 104
FT DISULFID 109 187
FT DISULFID 130 170
FT DISULFID 158 182
FT DISULFID 215 293
FT DISULFID 236 276
FT DISULFID 264 288
FT DISULFID 333 479
FT DISULFID 388 404
FT DISULFID 533 547
FT DISULFID 561 591
FT CARBOHYD 122 122
FT CARBOHYD 144 144
FT CARBOHYD 413 413
FT CARBOHYD 553 553
FT SEQUENCE 618 AA; 70266 MW; B89F719A6FD601E0 CRC64;

Query Match 38.7%; Score 75; DB 1; Length 618;
Best local similarity 37.2%; Pred. No. 1.3e-05;
Matches 16; Conservative 4; Mismatches 23; Indels 0; Gaps 0;
QY 2 NGFLXXLRPGSLRXCRXXHLCFFXXAHXIFRNXXKTRQFWWSY 44
DB 46 SGFLERKGNLRCEVCEQCSYEAFALESPQOTDVFWMKY 88

RESULT 27
 ID PRS_BOVIN STANDARD: PRT: 675 AA.
 AC P07224;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Vitamin K-dependent protein S precursor.
 OS PROS1 OR PROS.
 GN Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-86233400; PubMed-2940598;
 RA Dahlback B., Lundwall A., Stenflo J.;
 RT "Primary structure of bovine vitamin K-dependent protein S.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:4199-4203(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Wydro R., Cohen E., Dackowski W., Stenflo J., Lundwall A.,
 RA Dahlback B.;
 RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 42-141.
 RX MEDLINE-86168236; PubMed-2937765;
 RA Dahlback B., Lundwall A., Stenflo J.;
 RT "Localization of thrombin cleavage sites in the amino-terminal region
 of bovine protein S.";
 RL J. Biol. Chem. 261:5111-5115(1986).
 CC -1- FUNCTION: ANTICOAGULANT PLASMA PROTEIN; IT IS A COFACTOR TO
 ACTIVATED PROTEIN C IN THE DEGRADATION OF COAGULATION FACTORS VA
 AND VIIIA. IT HELP TO PREVENT COAGULATION AND STIMULATING
 FIBRINOLYSIS.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- SIMILARITY: CONTAINS 2 LAMININ G-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 4 EGF-LIKE DOMAINS.
 CC -----
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 CC -----
 DR EMBL: M13044; AAA30757.1; -
 DR EMBL: X12891; CAA31382.1; -
 DR PIR: A24759; A24759.
 DR HSSP: P00740; 1CFH.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001791; Laminin_G.
 DR InterPro: IPR000294; VitK_deep_GLA.
 DR Pfam: PF00008; EGF_4.
 DR Pfam: PF00594; gla_1.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00179; EGF_CA_3.
 DR SMART: SM00069; GLA_1.
 DR SMART: SM00282; LamG_2.
 DR PROSITE: PS00010; ASX_HYDROXYL_4.
 DR PROSITE: PS00022; EGF_1_1.
 DR PROSITE: PS01186; EGF_2_3.
 DR PROSITE: PS01187; EGF_CA_3.
 DR PROSITE: PS00011; GLU_CARBOXYLATION_1.

DR PROSITE: PS00025; LAM_G-DOMAIN; 2.
 KW Plasma; Gamma-carboxyglutamic acid; Calcium; Vitamin K; Zymogen;
 KW Blood coagulation; Hydroxylation; Glycoprotein; Signal; Repeat;
 KW EGF-like domain.
 FT SIGNAL 1 24
 FT PROPEP 25 41
 FT CHAIN 42 675
 FT DOMAIN 42 86
 FT DOMAIN 87 116
 FT DOMAIN 117 155
 FT DOMAIN 157 200
 FT DOMAIN 201 242
 FT DOMAIN 243 283
 FT DOMAIN 289 475
 FT DOMAIN 484 665
 FT MOD_RES 47 47
 FT MOD_RES 48 48
 FT MOD_RES 55 55
 FT MOD_RES 57 57
 FT MOD_RES 60 60
 FT MOD_RES 61 61
 FT MOD_RES 66 66
 FT MOD_RES 67 67
 FT MOD_RES 70 70
 FT MOD_RES 73 73
 FT MOD_RES 77 77
 FT MOD_RES 136 136
 FT MOD_RES 121 134
 FT DISULFID 126 143
 FT DISULFID 145 154
 FT DISULFID 161 175
 FT DISULFID 171 184
 FT DISULFID 186 199
 FT DISULFID 205 217
 FT DISULFID 212 226
 FT DISULFID 228 241
 FT DISULFID 247 256
 FT DISULFID 252 265
 FT DISULFID 267 282
 FT CARBOHYD 499 499
 FT CARBOHYD 509 509
 SO SEQUENCE 675 AA; 75132 MW; CF7EC5BC1C318BE CRC64;
 Query Match 36.1%; Score 70; DB 1; Length 675;
 Best Local Similarity 36.4%; Pred. No. 0.00011;
 Matches 16; Conservative 4; Mismatches 24; Indels 0; Gaps 0;
 Oy 1 ANGFLXXLRPGSLXRCRXKXLCSPFXAHXIFRNXXRTROFWVS 44
 Db 42 ANTLLEETKKGNLERECIEBELCKKEAREIFENNPETEFYPRK 85
 RESULT 28
 ID THRB_BOVIN STANDARD: PRT: 625 AA.
 AC P00735;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Prothrombin precursor (EC 3.4.21.5).
 GN F2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-88245190; PubMed-3379642;
 RA Irwin D.M., Robertson K.A., Macgillivray R.T.A.;
 RT "Structure and evolution of the bovine prothrombin gene";
 RL J. Mol. Biol. 200:31-45(1988).

[12] RN SEQUENCE FROM N.A.
RX MEDLINE=64203525; PubMed=6326805;
RA McGilivray R.T.A., Davie E.W.;
RT "Characterization of bovine prothrombin mRNA and its translation
product.";
RL Biochemistry 23:1626-1634(1984).
[13] RN
RP SEQUENCE OF 44-625, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RA Magnusson S., Sottirup-Jensen L., Petersen T.E., Claess H.;
RL (in) Hemmer H.C., Veltkamp J.J. (eds.);
RP Boehringer symposium on prothrombin and related coagulation factors,
pp.25-46, Leiden University Press, Leiden (1975).
[14] RN
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF ACTIVATION PEPTIDE 1.
RX MEDLINE=66296633; PubMed=3741841;
RA Park C.H., Tulinsky A.;
RT "Three-dimensional structure of the kringle sequence: structure of
prothrombin fragment 1.";
RL Biochemistry 25:3977-3982(1986).
[15] RN
RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF ACTIVATION PEPTIDE 1.
RX MEDLINE=91311686; PubMed=1856869;
RA Seshadri T., Tulinsky A., Skrzypczak-Jankun E., Park C.H.;
RT "Structure of bovine prothrombin fragment 1 refined at 2.25-A
resolution.";
RL J. Mol. Biol. 220:481-494(1991).
[16] RN
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF ACTIVATION PEPTIDE 1.
RX MEDLINE=92190185; PubMed=1547238;
RA Soriano-Garcia M., Padmanabhan K., de Vos A.M., Tulinsky A.;
RT "The Ca2+ ion and membrane binding structure of the Gla domain of Ca-
prothrombin fragment 1.";
RL Biochemistry 31:2534-2566(1992).
[17] RN
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX MEDLINE=92218459; PubMed=1560020;
RA Martin P.D., Robertson W., Turk D., Huber R., Bode W., Edwards B.F.P.;
RT "The structure of residues 7-16 of the A1alpha-chain of human
fibrinogen bound to bovine thrombin at 2.3-A resolution.";
RL J. Biol. Chem. 267:7911-7920(1992).
[18] RN
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX MEDLINE=92389319; PubMed=1518046;
RA Brandstetter H., Turk D., Hoeffken H.W., Grosse D., Stuerzebecher J.,
RT "Refined 2.3 A x-ray crystal structure of bovine thrombin complexes
formed with the benzamidine and arginine-based thrombin inhibitors
NAPAP, 4-TAPAP and MQPA. A starting point for improving
antithrombotics.";
RL J. Mol. Biol. 226:1085-1089(1992).
[19] RN
RP X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF COMPLEX WITH ORNITHODORIN.
RX MEDLINE=97102783; PubMed=8947023;
RA van de Locht A., Stubbs M.T., Bode W., Friedrich T., Bollschweiler C.,
RT Hoeffken W., Huber R.;
RT "The ornithodorin-thrombin crystal structure, a key to the TAP
enzyme?";
RL EMBO J. 15:6011-6017(1996).
[10] RN
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF COMPLEX WITH TRIABIN.
RX MEDLINE=98004486; PubMed=9342325;
RA Fuentes-Prior P., Noeske-Jungblut C., Donner P., Schleuning W.D.,
RT Huber R., Bode W.;
RT "Structure of the thrombin complex with triabin, a lipocalin-like
exosite-binding inhibitor derived from a triatomine bug.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:11845-11850(1997).
[11] RN
RP GENE STRUCTURE.
RX MEDLINE=86077733; PubMed=3000440;
RA Ivin D.M., Ahern K.G., Pearson G.D., McGilivray R.T.A.;
RT "Characterization of the bovine prothrombin gene.";
RL Biochemistry 24:6854-6861(1985).

CC -1- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS
CC FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,
CC AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.
CC
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC
CC -1- TISSUE SPECIFICITY: SYNTHESIZED IN THE LIVER; FOUND IN PLASMA.
CC
CC -1- PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
CC RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOomal
CC ENZYME. THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES
CC ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY
CC CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
CC OF PROTHROMBIN TO THROMBIN.
CC
CC -1- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A
CC PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &
CC FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS: FACTOR XA REMOVES
CC THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &
CC HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR
CC V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
CC THROMBIN.
CC
CC -1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL
CC FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
CC BY FACTOR XA.
CC
CC -1- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
CC
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
CC
CC -1- DATABASE: NAME=Prozyme technical fact sheet:
CC WWW="http://www.prozyme.com/technical/thrombindata.html".
CC
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC
CC EMBL: V00135; CA23451.1; -;
CC EMBL: J00041; AAA0781.1; -;
CC PIR: A00915; TBRO
CC PIR: S02537; S02537.
CC
CC PDB: 1BBR; 31-JAN-94.
CC PDB: 1ETR; 31-JAN-94.
CC PDB: 1ETS; 31-JAN-94.
CC PDB: 1ETT; 31-JAN-94.
CC PDB: 1HRT; 31-JAN-94.
CC PDB: 2PFI; 31-JAN-94.
CC PDB: 2PF2; 31-JAN-94.
CC PDB: 2SPT; 31-MAY-94.
CC PDB: 1MKW; 07-JUL-97.
CC PDB: 1MKX; 07-JUL-97.
CC PDB: 1TBO; 14-OCT-96.
CC PDB: 1TBR; 14-OCT-96.
CC PDB: 1TQC; 23-JUL-97.
CC PDB: 1VIT; 21-APR-97.
CC PDB: 1YCP; 06-MAY-98.
CC PDB: 1A0H; 17-JUN-98.
CC PDB: 1AVG; 16-FEB-99.
CC
CC MEROPS: S01.217; -;
CC InterPro: IPR001314; Chymotrypsin.
CC InterPro: IPR002383; GLA_blood.
CC InterPro: IPR000001; Kringle.
CC InterPro: IPR003966; Prothrombin.
CC InterPro: IPR001254; Trypsin.
CC InterPro: IPR000294; Vitk_dep_GLA.
CC Pfam: PF00594; gla; 1.
CC Pfam: PF00051; kringle; 2.
CC Pfam: PF00089; trypsin; 1.
CC PRINTS: PR00722; CHYMOTRYPSIN.
CC PRINTS: PR00001; GLABLOOD.
CC PRINTS: PR00018; KRINGLE.
CC PRINTS: PR01505; PROTHROMBIN.
CC SMART: SM00069; GLA; 1.
CC SMART: SM00130; KR; 2.
CC SMART: SM00020; Tryp-spec; 1.

ID PRTE-HUMAN STANDARD: PRT; 676 AA.
AC P07225; Q15518;.
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Vitamin K-dependent protein S precursor.
GN PROS1 OR PROS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE:91084444; PubMed:2148110;
RT Schmid D.K., Tatro A.V., Phelps L.G., Tomczak J.A., Long G.L.;
RT "Organization of the human protein S genes";
RL Biochemistry 29:7845-7852(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Ploos van Amstel H.K.;
RL Submitted (Aug-1987) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 27-676 FROM N.A.
RA MEDLINE:91084445; PubMed:2148111;
RT Ploos van Amstel H.K., Reitsma P.H., der Logt C.P., Bertina R.M.;
RT "Intron-exon organization of the active human protein S gene PS alpha
RT and its pseudogene PS beta: duplication and silencing during primate
RT evolution";
RL Biochemistry 29:7853-7861(1990).
RN [4]
RP SEQUENCE OF 1-42 FROM N.A.
RA MEDLINE:88005138; PubMed:2820795;
RT Ploos van Amstel H.K., van der Zanden A.L., Reitsma P.H.,
RT Bertina R.M.;
RT "Human protein S cDNA encodes Phe-16 and Tyr 222 in consensus
RT sequences for the post-translational processing";
RL FEBS Lett. 222:186-190(1987).
RN [5]
RP SEQUENCE FROM N.A.
RA MEDLINE:87092407; PubMed:3467362;
RT Hoskins J., Norman D.K., Beckmann R.J., Long G.L.;
RT "Cloning and characterization of human liver cDNA encoding a protein
RT S precursor";
RL Proc. Natl. Acad. Sci. U.S.A. 84:349-353(1987).
RN [6]
RP SEQUENCE OF 27-676 FROM N.A.
RA MEDLINE:86313649; PubMed:2944113;
RT Lundvall A., Dackowski W., Cohen E., Shaffer M., Mahr A., Dahlback B.,
RT Stenflo J., Wydro R.;
RT "Isolation and sequence of the cDNA for human protein S, a regulator
RT of blood coagulation";
RL Proc. Natl. Acad. Sci. U.S.A. 83:6716-6720(1986).
RN [7]
RP VARIANT HEERLEN.
RA MEDLINE:90335440; PubMed:213091;
RT Coenen R.M., Ploos van Amstel H.K., van Wijngaarden A.,
RT Coenen J., Leenhuis M.P., Deutz-Terlouw P.P., van der Linden I.K.,
RT Reitsma P.H.;
RT "Heerlen polymorphism of protein S, an immunologic polymorphism due
RT to dimorphism of residue 460";
RL Blood 76:338-348(1990).
RN [8]
RP VARIANT SER-258.
RA Cooper D.N.;
RL Unpublished observations (SEP-1993).
RN [9]
RP VARIANT TOKUSHIMA.
RA MEDLINE:94129009; PubMed:8298131;
RT Hayashi T., Nishioaka J., Shigekiyo T., Saito S., Suzuki K.;
RT "Protein S Tokushima: abnormal molecule with a substitution of Glu
RT for Lys-155 in the second epidermal growth factor-like domain of
RT protein S.";

RL Blood 83:683-690(1994).
CC -1- FUNCTION: ANTICOAGULANT PLASMA PROTEIN; IT IS A COFACTOR TO
CC ACTIVATED PROTEIN C IN THE DEGRADATION OF COAGULATION FACTORS VA
CC AND VIIIA. IT HELPS TO PREVENT COAGULATION AND STIMULATING
CC FIBRINOLYSIS.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- DISEASE: DEFECTS IN PROS1 ARE ASSOCIATED WITH AN INCREASED RISK TO
CC DEVELOP THROMBOTIC DISEASE (THROMBOPHILIA).
CC -1- SIMILARITY: CONTAINS 2 LAMININ G-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 4 EGF-LIKE DOMAINS.

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DR EMBL; M57853; AAA60357.1; -
DR EMBL; M57840; AAA60357.1; JOINED.
DR EMBL; M57841; AAA60357.1; JOINED.
DR EMBL; M57842; AAA60357.1; JOINED.
DR EMBL; M57844; AAA60357.1; JOINED.
DR EMBL; M57845; AAA60357.1; JOINED.
DR EMBL; M57846; AAA60357.1; JOINED.
DR EMBL; M57847; AAA60357.1; JOINED.
DR EMBL; M57848; AAA60357.1; JOINED.
DR EMBL; M57849; AAA60357.1; JOINED.
DR EMBL; M57850; AAA60357.1; JOINED.
DR EMBL; M57851; AAA60357.1; JOINED.
DR EMBL; M57852; AAA60357.1; JOINED.
DR EMBL; M57854; AAA60180.1; -
DR EMBL; M36551; AAA60180.1; JOINED.
DR EMBL; M36552; AAA60180.1; JOINED.
DR EMBL; M36553; AAA60180.1; JOINED.
DR EMBL; M36554; AAA60180.1; JOINED.
DR EMBL; M36555; AAA60180.1; JOINED.
DR EMBL; M36556; AAA60180.1; JOINED.
DR EMBL; M36557; AAA60180.1; JOINED.
DR EMBL; M36558; AAA60180.1; JOINED.
DR EMBL; M36559; AAA60180.1; JOINED.
DR EMBL; M36560; AAA60180.1; JOINED.
DR EMBL; M36561; AAA60180.1; JOINED.
DR EMBL; M36563; AAA60180.1; JOINED.
DR EMBL; Y00692; CAA68687.1; -
DR EMBL; Y00693; CAA68688.1; ALT_SEQ.
DR EMBL; M15036; AAA36479.1; -
DR PIR; A35610; A35610.
DR PIR; A26157; A26157.
DR PIR; A25891; A25891.
DR PIR; S02424; S02424.
DR PIR; S09519; S09519.
DR HSSP; P07204; LEGT.
DR MIM; 176880; -
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001791; Laminin_G.
DR Pfam; PF000594; gla; 1.
DR Pfam; PF000594; gla; 4.
DR Pfam; PF00054; laminin_g; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 3.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 4.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS01187; EGF_CA; 3.


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DR PROSITE; PS00011; GLU-CARBOXYLATION; 1.
DR PROSITE; PS50025; LAM G DOMAIN; 2.
KW Plasma; Gamma-carboxyglutamic acid; Calcium; Vitamin K; Zymogen;
KW Blood coagulation; Hydroxylation; Glycoprotein; Signal; Repeat;
KW EGF-like domain; Polymorphism; Disease mutation; Thrombophilia.
FT SIGNAL 1 24
FT PROPEP 25 41
FT CHAIN 42 676
FT DOMAIN 42 86
FT DOMAIN 87 116
FT DOMAIN 117 135
FT DOMAIN 157 200
FT DOMAIN 201 242
FT DOMAIN 243 283
FT DOMAIN 299 475
FT DOMAIN 484 666
FT MOD_RES 47 47
FT MOD_RES 48 48
FT MOD_RES 55 55
FT MOD_RES 57 57
FT MOD_RES 60 60
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FT MOD_RES 66 66
FT MOD_RES 67 67
FT MOD_RES 70 70
FT MOD_RES 73 73
FT MOD_RES 77 77
FT MOD_RES 136 136
FT DISULFID 121 134
FT DISULFID 126 143
FT DISULFID 145 154
FT DISULFID 161 175
FT DISULFID 171 184
FT DISULFID 186 199
FT DISULFID 205 217
FT DISULFID 212 226
FT DISULFID 228 241
FT DISULFID 247 256
FT DISULFID 252 265
FT DISULFID 267 282
FT CARBOHYD 499 499
FT CARBOHYD 509 509
FT CARBOHYD 530 530
FT VARIANT 196 196
FT VARIANT 258 258
FT VARIANT 501 501
FT CONFLICT 11 11
FT CONFLICT 26 26
SQ SEQUENCE 676 AA; 75122 MW; 2B88A04F85403F25 CRC64;

Query Match 35.6%; Score 69; DB 1; Length 676;
Best Local Similarity 34.18; Pred. No. 0.00017;
Matches 15; Conservative 5; Mismatches 24; Indels 0; Gaps 0;

QY 1 ANGFLXLRPGSLXRCXLCSPFXAHXIRNXXRTQFVWSY 44
DB 42 ANSLLEETKQGNLRECEIEELCNKEAREVEFENDEPTDYFPKY 85

RESULT 32
PRTS_RAT STANDARD: PRT; 675 AA.
AC P53813;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Vitamin K-dependent protein S precursor.
GN PROS1 OR PROS.

OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=95332263; PubMed=7608128;
RA Yasuda F., Hayashi T., Tanitame K., Nishioka J., Suzuki K.:
RT "Molecular cloning and functional characterization of rat plasma
RT protein S.";
RL J. Biochem. 117:374-383(1995).
CC -1- FUNCTION: ANTICOAGULANT PLASMA PROTEIN. IT IS A COFACTOR TO
CC ACTIVATED PROTEIN C IN THE DEGRADATION OF COAGULATION FACTORS VA
CC AND VIII. IT HELP TO PREVENT COAGULATION AND STIMULATING
CC FIBRINOLYSIS.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- SIMILARITY: CONTAINS 2 LAMININ G-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 4 EGF-LIKE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; S78744; AAC60704.1; -.
DR HSSP; P00740; IGFH.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF-Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR000294; Vitk_dep_GLA.
DR Pfam; PF00008; EGF; 4.
DR Pfam; PF00054; gla; 1.
DR Pfam; PF00054; laminin_G; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 3.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00282; Lamc; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 4.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS01187; EGF_CA; 3.
DR PROSITE; PS00011; GLU-CARBOXYLATION; 1.
DR PROSITE; PS50025; LAM_G_DOMAIN; 1.
KW Plasma; Gamma-carboxyglutamic acid; Calcium; Vitamin K; Zymogen;
KW Blood coagulation; Hydroxylation; Glycoprotein; Signal; Repeat;
KW EGF-like domain.
FT SIGNAL 1 24
FT PROPEP 25 41
FT CHAIN 42 675
FT DOMAIN 42 86
FT DOMAIN 87 116
FT DOMAIN 117 155
FT DOMAIN 157 200
FT DOMAIN 201 242
FT DOMAIN 243 283
FT DOMAIN 299 475
FT DOMAIN 484 665
FT MOD_RES 47 47
FT MOD_RES 48 48
FT MOD_RES 55 55
FT MOD_RES 57 57

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FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID
FT (BY SIMILARITY).
FT MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID
FT (BY SIMILARITY).
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID
FT (BY SIMILARITY).
FT MOD_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID
FT (BY SIMILARITY).
FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID
FT (BY SIMILARITY).
FT MOD_RES 73 73 GAMMA-CARBOXYGLUTAMIC ACID
FT (BY SIMILARITY).
FT MOD_RES 77 77 GAMMA-CARBOXYGLUTAMIC ACID
FT (BY SIMILARITY).
FT MOD_RES 136 136 HYDROXYLATION (BY SIMILARITY).
FT DISULFID 121 134 BY SIMILARITY.
FT DISULFID 126 143 BY SIMILARITY.
FT DISULFID 145 154 BY SIMILARITY.
FT DISULFID 161 175 BY SIMILARITY.
FT DISULFID 171 184 BY SIMILARITY.
FT DISULFID 186 199 BY SIMILARITY.
FT DISULFID 205 217 BY SIMILARITY.
FT DISULFID 212 226 BY SIMILARITY.
FT DISULFID 228 241 BY SIMILARITY.
FT DISULFID 247 256 BY SIMILARITY.
FT DISULFID 252 265 BY SIMILARITY.
FT DISULFID 267 282 BY SIMILARITY.
FT CAROHYD 499 499 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 509 509 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 675 AA: 74626 MW: 84338756B486075 CRR64;
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Query Match 34.5%; Score 67; DB 1; Length 675;
Best Local Similarity 34.1%; Pred. No. 0.00038;
Matches 15; Conservative 5; Mismatches 24; Indels 0; Gaps 0;
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OY 1 ANGFLXXLRPSLXRCXRXKXLCSEFXAHXIFRXKXRTROFWSY 44
DB 42 ANLTLEETKKNLEKRECELECKKEAREVEFENNPEYDFYPRY 85
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RESULT 33
PRTZ_HUMAN
ID PRTZ_HUMAN STANDARD; PRT: 400 AA.
AC P22891; Q15213;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Vitamin K-dependent protein Z precursor.
GN PROZ.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver;
RC MEDLINE=91058548; PubMed=2244898;
RA Ichinose A., Takeya H., Espling E., Iwanaga S., Kiesel W., Davie E.W.;
RT "Amino acid sequence of human protein Z, a vitamin K-dependent plasma
RT glycoprotein."
RL Biochem. Biophys. Res. Commun. 172:1139-1144(1990).
RN [2]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=98244864; PubMed=9578570;
RA Fujimaki K., Yamazaki T., Tanikawa M., Ichinose A.;
RT "The gene for human protein Z is localized to chromosome 13 at band
RT q34 and is coded by eight regular exons and one alternative exon."
RL Biochemistry 37:6838-6846(1998).
RN [3]
RP SEQUENCE OF 81-400 FROM N.A., AND PARTIAL SEQUENCE OF 63-103.
RX MEDLINE=90386637; PubMed=2403355;
RA Sejima H., Hayashi T., Deyashiki Y., Nishiohara J., Suzuki K.;
```

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RT "Primary structure of vitamin K-dependent human protein Z.";
RL Biochem. Biophys. Res. Commun. 171:661-668(1990).
RN [4]
RP STRUCTURE OF CARBOHYDRATE ON SER-93.
RX MEDLINE=90062160; PubMed=2511201;
RA Nishimura H., Kawabata S., Kiesel W., Hase S., Ikenaka T., Takao T.,
RA Shimomishi Y., Iwanaga S.;
RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first
RT epidermal growth factor-like domain of human factors VII and IX and
RT protein Z and bovine protein Z."
RL J. Biol. Chem. 264:20320-20325(1989).
RN [5]
RP STRUCTURE OF CARBOHYDRATE ON SER-93.
RX MEDLINE=91344709; PubMed=2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Kiesel W., Hase S., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in the
RT first EGF-like domain of clotting factors VII and IX and protein Z.";
RL Adv. Exp. Med. Biol. 281:121-131(1990).
CC -1- FUNCTION: APPEARS TO ASSIST HEMOSTASIS BY BINDING THROMBIN AND
CC PROMOTING ITS ASSOCIATION WITH PHOSPHOLIPID VESICLES.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE) AND 2; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- SIMILARITY: ALTHOUGH HOMOLOGOUS WITH THE VITAMIN K-DEPENDENT
CC CLOTTING FACTORS, IT HAS LOST TWO OF THE ESSENTIAL CATALYTIC
CC RESIDUES AND HAS NO ENZYMATIC ACTIVITY.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL: M55670; AAA36500.1; -.
DR EMBL: M55671; AAA36501.1; -.
DR EMBL: AB033749; BAA85763.1; -.
DR EMBL: AB033749; BAA85764.1; -.
DR EMBL: M59303; AAA36499.1; -.
DR PIR: A36244; A36244.
DR HSSP: P00740; 1CFH.
DR MEROPS: S01.979; -.
DR GlycoSuiteDB: P22891; -.
DR MIM: 176895; -.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF-2.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Trypsin.
DR InterPro: IPR000294; Vitk_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00181; EGF_2.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; TRYP_SPE; 1.
DR PROSITE: PS00010; ASX-HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS00011; GLI_CARBOXYLATION; 1.
DR PROSITE: PS50240; TRYPsin_DOM; 1.
KW Plasma; Glycoprotein; Gamma-carboxyglutamic acid; Hydroxylation;
KW Calcium; Serine protease homolog; Vitamin K; EGF-like domain; Signal;
KW Alternative splicing.
FT SIGNAL 1 23
FT PROPEP 24 40
FT CHAIN 41 400
FT DOMAIN 87 123
FT VITAMIN K-DEPENDENT PROTEIN Z.
FT EGF-LIKE 1.
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FT DOMAIN 125 166 EGF-LIKE 2.
FT MOD_RES 175 400 SERINE PROTEASE.
FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 51 51 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 73 73 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 75 75 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 80 80 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 104 104 HYDROXYLATION (BY SIMILARITY).
FT DISULFID 91 102 BY SIMILARITY.
FT DISULFID 96 111 BY SIMILARITY.
FT DISULFID 113 122 BY SIMILARITY.
FT DISULFID 129 141 BY SIMILARITY.
FT DISULFID 137 150 BY SIMILARITY.
FT DISULFID 152 165 BY SIMILARITY.
FT CARBOHYD 93 93 O-LINKED (GLCNAc. . .).
FT CARBOHYD 99 99 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 225 225 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 233 233 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 236 236 O-LINKED (POTENTIAL).
FT CARBOHYD 306 306 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 315 315 O-LINKED (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT VARSPIC 24 24 V -> ATSLKERHGLHSDSACTGQESL (IN ISOPORM
SQ SEQUENCE 400 AA; 44744 MW; 7EBD2DCC48860268 CRC64;

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Query Match 34.0%; Score 66; DB 1; Length 400;
 Best Local Similarity 32.5%; Pred. No. 0.00034;
 Matches 13; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

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OY 5 LXLPLGSLKRXCRXXICSFYXAHXIFRNXXRTQFWVS 44
DB 46 LEELEFEGNLEKECEYEICVFEAREVEFENVYVDEFWRY 85

RESULT 34
PRTZ_BOVIN STANDARD; PRT; 396 AA.
AC P00744;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Vitamin K-dependent protein Z.
GN PROZ.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Kuminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID:9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=85204370; PubMed=388670;
RA Hoejrup P., Jensen M.S., Petersen T.E.;
RT "Amino acid sequence of bovine protein Z: a vitamin K-dependent
RL FEBS Lett. 184:333-338(1985).
RN [2]
RP STRUCTURE OF CARBOHYDRATE ON SER-53.
RX MEDLINE=90062160; PubMed=2511201;
RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T., Takao T.,
RA Shimomishi Y., Iwanaga S.;
RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first

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RT epidermal growth factor-like domain of human factors VII and IX and
RT protein Z and bovine protein Z."
RL J. Biol. Chem. 264:20320-20325(1989).
RN [3]
RP STRUCTURE OF CARBOHYDRATE ON SER-53.
RX MEDLINE=91344709; PubMed=2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in the
RT first EGF-like domain of clotting factors VII and IX and protein Z."
RL Adv. Exp. Med. Biol. 281:121-131(1990).
CC -1- FUNCTION: APPEARS TO ASSIST HEMOSTASIS BY BINDING THROMBIN AND
CC PROMOTING ITS ASSOCIATION WITH PHOSPHOLIPID VESICLES.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- SIMILARITY: ALTHOUGH HOMOLOGOUS WITH THE VITAMIN K-DEPENDENT
CC CLOTTING FACTORS, IT HAS LOST TWO OF THE ESSENTIAL CATALYTIC
CC RESIDUES AND HAS NO ENZYMATIC ACTIVITY.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
DR HSP; P00740; KXBOZ.
DR MEROPS; S01.979; -.
DR Glycosylatedb; P00744; -.
DR InterPro: IPR00152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Trypsin.
DR InterPro: IPR00294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYP_SPE; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
KW Plasma; Glycoprotein; Gamma-carboxyglutamic acid; Hydroxylation;
KW Calcium; Serine protease homolog; Vitamin K; EGF-like domain.
FT DOMAIN 47 83 EGF-LIKE 1.
FT DOMAIN 85 126 EGF-LIKE 2.
FT DOMAIN 135 357 SERINE PROTEASE.
FT MOD_RES 7 7 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 8 8 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 11 11 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 15 15 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 17 17 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 20 20 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 21 21 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 26 26 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 27 27 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 30 30 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 33 33 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 36 36 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 40 40 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 44 64 HYDROXYLATION.
FT MOD_RES 51 62 BY SIMILARITY.
FT DISULFID 56 71 BY SIMILARITY.
FT DISULFID 73 82 BY SIMILARITY.
FT DISULFID 89 101 BY SIMILARITY.
FT DISULFID 97 110 BY SIMILARITY.
FT DISULFID 112 125 BY SIMILARITY.
FT CARBOHYD 53 53 O-LINKED (GLCNAc. . .).
FT CARBOHYD 59 59 /FTID-CAR_000032.
FT CARBOHYD 191 191 N-LINKED (GLCNAc. . .).
FT CARBOHYD 289 289 N-LINKED (GLCNAc. . .).
FT CARBOHYD 388 388 O-LINKED.
SQ SEQUENCE 396 AA; 43112 MW; 04C5D7A35849B116 CRC64;

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Query Match 32.0%; Score 62; DB 1; Length 396;
Best Local Similarity 30.0%; Pred. No. 0.0018;
Matches 12; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

QY 5 LXXLRGSLXRCRXXLCSEFXAHXIFRNXXRQFWVSY 44
DB 6 LEELEFGHLEKECMERICYEARVEFDEDTDFWRTY 45

RESULT 35
PRTS_MOUSE STANDARD: PRT: 675 AA.

AC 008761; P43483;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Vitamin K-dependent protein S precursor.
CN PROS1 OR PROS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94198297; PubMed=8148380;
RA Chu M.D., Sun J., Bird P.I.;
RT "Cloning and sequencing of a cDNA encoding the murine vitamin K-
RT dependent protein S";
RL Blochm. Biophys. Acta 1217:325-328(1994).
RN [2]
RP SEQUENCE OF 33-675 FROM N.A.
RX MEDLINE=94302659; PubMed=8029814;
RA Lu D., Schmidt D.K., Long G.L.;
RT "Structure of mouse protein S as determined by PCR amplification and
RT DNA sequencing of cDNA";
RL Thromb. Res. Suppl. 74:135-142(1994).
CC -1- FUNCTION: ANTICOAGULANT PLASMA PROTEIN; IT IS A COFACTOR TO
CC ACTIVATED PROTEIN C IN THE DEGRADATION OF COAGULATION FACTORS VA
CC AND VIIIA. IT HELP TO PREVENT COAGULATION AND STIMULATING
CC FIBRINOLYSIS.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- SIMILARITY: CONTAINS 2 LAMININ G-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 4 EGF-LIKE DOMAINS.
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CC -----
DR EMBL: Z55469; CAA0961.1; -;
DR EMBL: L27439; AAA4006.1; -;
DR HSSP: P00740; ICFH.
DR MGD: MGI:1095733; Pros1.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF-CA.
DR InterPro: IPR002363; GLA_blood.
DR InterPro: IPR001791; Laminin_G.
DR InterPro: IPR000294; Vitr_dep_GLA.
DR Pfam: PF00008; EGF; 4.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00054; laminin_G; 1.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 3.
DR SMART: SM00001; EGF_like; 1.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00282; LamG; 2.

DR PROSITE: PS00010; ASX_HYDROXYL; 4.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 3.
DR PROSITE: PS01187; EGF_CA; 3.
DR PROSITE: PS00011; GLU CARBOXYLATION; 1.
DR PROSITE: PS00025; LAM_G_DOMAIN; 2.
KW Plasma; gamma-carboxyglutamic acid; Calcium; Vitamin K; Zymogen;
KW Blood coagulation; Hydroxylation; Glycoprotein; Signal; Repeat;
KW EGF-like domain.
FT SIGNAL 1 24 BY SIMILARITY.
FT PROPEP 25 41 BY SIMILARITY.
FT CHAIN 42 675 VITAMIN K-DEPENDENT PROTEIN S.
FT DOMAIN 42 86 GLA.
FT DOMAIN 87 116 THROMBIN-SENSITIVE.
FT DOMAIN 117 155 EGF-LIKE 1.
FT DOMAIN 157 200 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 201 242 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 243 283 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 289 475 LAMININ G-LIKE 1.
FT DOMAIN 484 665 LAMININ G-LIKE 2.
FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 73 73 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 77 77 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 136 136 MOD_RES
FT DISULFID 121 134 BY SIMILARITY.
FT DISULFID 126 143 BY SIMILARITY.
FT DISULFID 145 154 BY SIMILARITY.
FT DISULFID 161 175 BY SIMILARITY.
FT DISULFID 171 184 BY SIMILARITY.
FT DISULFID 186 199 BY SIMILARITY.
FT DISULFID 205 217 BY SIMILARITY.
FT DISULFID 212 226 BY SIMILARITY.
FT DISULFID 228 241 BY SIMILARITY.
FT DISULFID 247 256 BY SIMILARITY.
FT DISULFID 252 265 BY SIMILARITY.
FT DISULFID 267 282 BY SIMILARITY.
FT CARBOHYD 499 499 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 509 509 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 493 493 F -> L (IN REF. 2).
SQ SEQUENCE 675 AA; 74934 MW; 79D51203B58A31F CRC64;

Query Match 30.9%; Score 60; DB 1; Length 675;
Best Local Similarity 31.8%; Pred. No. 0.0069;
Matches 14; Conservative 4; Mismatches 26; Indels 0; Gaps 0;

QY 1 ANGFLLXLRGSLXRCRXXLCSEFXAHXIFRNXXRQFWVSY 44
DB 42 ANTLFEETMKGNLERECIEELCNKEAREVFENPETDYFPRY 85

RESULT 36
VE1_BP2 STANDARD: PRT: 604 AA.

AC P11298;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Replication protein E1.
GN E1.
OS Bovine papillomavirus type 2.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10560;
RN [1]
RP SEQUENCE FROM N.A.
RL Groff D.E., Mitra R., Lancaster W.D.;
RL submitted (MAY-1988) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ATP-DEPENDENT DNA HELICASE REQUIRED FOR INITIATION OF
CC VIRAL DNA REPLICATION. IT FORMS A COMPLEX WITH THE VIRAL E2
CC PROTEIN. THE E1-E2 COMPLEX BINDS TO THE REPLICATION ORIGIN WHICH
CC CONTAINS BINDING SITES FOR BOTH PROTEINS.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -----
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CC -----
DR EMBL: M20219; AAA66833.1; -
DR PIR: C31169; MWLMB2.
DR InterPro: IPR001177; Papillom_E1.
DR Pfam: PF00519; E1; 1.
DR Pfam: PF00524; E1_N; 1.
KW Early protein; DNA replication; Helicase; ATP-binding; DNA-binding;
KW Nuclear protein.
FT NP_BIND 432 439 ATP (POTENTIAL).
SQ SEQUENCE 604 AA: 68077 MW: D2D7036ADE88A9D CRC64;

Query Match 26.8%; Score 52; DB 1; Length 604;
Best Local Similarity 45.5%; Pred. No. 0.17;
Matches 10; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

OY 21 LCSFXAHXIFRNXXRTQFV 42
DB 171 LCSFHDTRLRKNKTQOQV 192

RESULT 37
VE1_BPV1 STANDARD; PRT; 605 AA.
AC P03116; Q9WMH1;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Replication protein E1.
GN E1.
OS Bovine papillomavirus type 1.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10559;
RN [1]
RP SEQUENCE FROM N.A.
RL MEDLINE=83012974; PubMed=6289124;
RA Chen E.Y., Howley P.M., Levinson A.D., Seeburg P.H.;
RT "The primary structure and genetic organization of the bovine
RT papillomavirus type 1 genome.";
RL Nature 299:529-534(1982).
RN [2]
RP REQUIREMENT FOR REPLICATION.
RX MEDLINE=91122053; PubMed=1846806;
RA Ustav M., Stenlung A.;
RT "Transient replication of BPV-1 requires two viral polypeptides

RT encoded by the E1 and E2 open reading frames.";
RL EMBO J. 10:449-457(1991).
RN [3]
RN CHARACTERIZATION.
RX MEDLINE=93281701; PubMed=8389467;
RA Yang L., Mohr I., Fouts E., Lim D.A., Nohalle M., Botchan M.;
RT "The E1 protein of bovine papilloma virus 1 is an ATP-dependent DNA
RT helicase.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:5086-5090(1993).
CC -1- FUNCTION: ATP-DEPENDENT DNA HELICASE REQUIRED FOR INITIATION OF
CC VIRAL DNA REPLICATION. IT FORMS A COMPLEX WITH THE VIRAL E2
CC PROTEIN. THE E1-E2 COMPLEX BINDS TO THE REPLICATION ORIGIN WHICH
CC CONTAINS BINDING SITES FOR BOTH PROTEINS.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -----
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CC -----
DR EMBL: X02346; CAB46511.1; -
DR PIR: A03663; MWLEB.
DR InterPro: IPR001177; Papillom_E1.
DR Pfam: PF00519; E1; 1.
DR Pfam: PF00524; E1_N; 1.
KW Early protein; DNA replication; Helicase; ATP-binding; DNA-binding;
KW Nuclear protein.
FT NP_BIND 433 440 ATP (POTENTIAL).
SQ SEQUENCE 605 AA: 68190 MW: C8400B7B8F606EB CRC64;

Query Match 26.8%; Score 52; DB 1; Length 605;
Best Local Similarity 45.5%; Pred. No. 0.17;
Matches 10; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

OY 21 LCSFXAHXIFRNXXRTQFV 42
DB 172 LCSFHDTRLRKNKTQOQV 193

RESULT 38
NCAP_IHNV STANDARD; PRT; 413 AA.
ID NCAP_IHNV
AC P19691;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-MAY-1992 (Rel. 22, Last annotation update)
DE Nucleocapsid protein (Nucleoprotein).
GN N.
OS Infectious hematopoietic necrosis virus (strain Round Butte) (IHNV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; unclassified Rhabdoviridae.
OX NCBI_TaxID=11291;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89073771; PubMed=3201758;
RA Gilmore R.D., Jr., Leong J.C.;
RT "The nucleocapsid gene of infectious hematopoietic necrosis virus, a
RT fish rhabdovirus.";
RL Virology 167:644-648(1988).
CL -1- PTM: PHOSPHORYLATED.
CC -1- SIMILARITY: TO VHSV NUCLEOCAPSID PROTEIN.
CC -----
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CC -----
DR EMBL: J04321; AAA6240.1; -.
DR PIR: A31834; VHVNH.
DR Nucleocapsid; Phosphorylation.
KW SEQUENCE . 413 AA; 45700 MW; 5E2AF659BBEE38 CRC64;
SQ
Query Match 26.3%; Score 51; DB 1; Length 413;
Best Local Similarity 32.3%; Pred. No. 0.17;
Matches 10; Conservative 3; Mismatches 18; Indels 0; Gaps 0;
OY 11 GSIXRXCXXLCSFXXAHXIFRNXXRTROPF 41
Db 57 GEGTRRALGLCAFYAIEYVHREARSPNFW 87
RESULT 39
SLT2_YEAST
ID SLT2_YEAST STANDARD: PRT; 484 AA.
AC 000772;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Mitogen-activated protein kinase SLT2/MPK1 (EC 2.7.1.1-) (MAP kinase
MPK1).
GN SLT2 OR MPK1 OR YHR030C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
ON NCBI_TaxID=4932;
RX STRAIN=AB320;
RC MEDLINE=92140049; PubMed=1779770;
RA Torres L., Martin H., Garcia-Saez M.I., Arroyo J., Molina M.,
RA Sanchez M., Nombela C.;
RA "A protein kinase gene complements the lytic phenotype of
RA Saccharomyces cerevisiae lyt2 mutants.";
RL Mol. Microbiol. 5:2845-2854(1991).
(2)
RN SEQUENCE FROM N.A.
RP STRAIN=S288C / AB972;
RC MEDLINE=94378003; PubMed=8091229;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
RA Du Z., Faveille A., Fulton L., Gatlung S., Gelsel C., Kirsten J.,
RA Kucuba T., Hillier L., Jier M., Johnston L., Langston Y.,
RA Latreille P., Louis E.J., Macrl C., Mardis E., Meneses S., Mouser L.,
RA Nham M., Rifkin L., Riles L., St Peter H., Trevasks E., Vaughan K.,
RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
RA Vaudin M.;
RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
RT VII.";
RL Science 265:2077-2082(1994).
(3)
RN CHARACTERIZATION.
RX MEDLINE=94103336; PubMed=8276900;
RA Mazzoni C., Zarzov P., Rambourg A., Mann C.;
RT "The SLT2 (MPK1) MAP kinase homolog is involved in polarized cell
RT growth in Saccharomyces cerevisiae.";
RL J. Cell Biol. 123:1821-1833(1993).
CC -1- FUNCTION: SERINE/THREONINE PROTEIN KINASE INVOLVED IN A SIGNAL
CC TRANSDUCTION PATHWAY THAT PLAY A ROLE IN YEAST CELL MORPHOGENESIS
CC AND CELL GROWTH. THIS PATHWAY SEEMS TO STARTS BY SMP3, THEN
CC INVOLVE THE KINASE PKC1 THAT MAY ACT THE BCK1 KINASE THAT THEN
CC PHOSPHORYLATES MKK1 AND MKK2 WHICH THEMSELVES PHOSPHORYLATE THE
CC MPK1 KINASE WHICH ACTS ON A YET UNKNOWN SUBSTRATE.
CC -1- ENZYME REGULATION: ACTIVATED BY TYROSINE AND THREONINE
CC PHOSPHORYLATION BY MKK1 AND MKK2 (PROBABLY).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE SUBFAMILY.
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CC -----
DR EMBL: X59262; CAA11954.1; -.
DR EMBL: U00062; AAB68912.1; -.
DR PIR: S19051; S19051.
DR PIR: S46743; S46743.
DR HSSP: P2703; 1ERK.
DR SGD: S0001072; SLT2.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS01351; MAPK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 23 318 PROTEIN KINASE.
FT NP_BIND 29 37 ATP (BY SIMILARITY).
FT BINDING 54 54 ATP (BY SIMILARITY).
FT ACT_SITE 153 153 BY SIMILARITY.
FT DOMAIN 370 391 POLY-GLN.
FT MOD_RES 190 190 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 192 192 PHOSPHORYLATION (BY SIMILARITY).
FT CONFLICT 56 56 V -> L (IN REF. 1).
FT CONFLICT 467 467 T -> S (IN REF. 1).
SQ SEQUENCE 484 AA; 55636 MW; 559A3E0D3EBDE5F9 CRC64;
OY 8 LRPGSL--XRXCRXXLCSFXXAHXIFRNXXRTROPFVSY 44
Db 154 LRGNLNVNADQLKICDGLARGYSENVENSQFLTER 192
Query Match 26.3%; Score 51; DB 1; Length 484;
Best Local Similarity 30.8%; Pred. No. 0.2;
Matches 12; Conservative 4; Mismatches 21; Indels 2; Gaps 1;
OY 11 GSIXRXCXXLCSFXXAHXIFRNXXRTROPF 41
Db 57 GEGTRRALGLCAFYAIEYVHREARSPNFW 87
RESULT 40
SPM1_SCHPO
ID SPM1_SCHPO STANDARD: PRT; 422 AA.
AC 092398;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Mitogen-activated protein kinase spm1 (EC 2.7.1.1-) (MAP kinase spm1)
DE (MAP kinase pmk1).
GN SPM1 OR PMK1 OR SPBCL19.08.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
ON NCBI_TaxID=4896;
(1)
RN SEQUENCE FROM N.A.
RP MEDLINE=97098653; PubMed=8943330;
RX Toda T., Dnut S., Supert-Furga G., Gotoh G., Nishida E., Suglura R.,
RA Kuno T.;
RT "The fission yeast pmk1+ gene encodes a novel mitogen-activated
RT protein kinase homolog which regulates cell integrity and functions
RT coordinately with the protein kinase C pathway.";
RL Mol. Cell. Biol. 16:6752-6764(1996).
(2)
RN SEQUENCE FROM N.A.
RP MEDLINE=97280820; PubMed=9135147;
RX Zaitsevskaia-Carter T., Cooper J.A.;
RT "Spm1, a stress-activated MAP kinase that regulates morphogenesis in

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RT 5..pombe.";
RL EMBL J. 16:1318-1331(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Wood V., Rajandream M.A., Barrell B.G., Skelton J., Churcher C.M.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: REGULATES CELL INTEGRITY AND FUNCTIONS COORDINATELY WITH
CC THE PROTEIN KINASE C PATHWAY (PKC1 AND PKC2). INVOLVED THE
CC REGULATION OF WALL ARCHITECTURE, CELL SHAPE, CYTOKINESIS IN
CC EXPONENTIAL AND STATIONARY PHASE, AND METABOLISM OF IONS.
CC -1- ENZYME REGULATION: ACTIVATED BY TYROSINE AND THREONINE
CC PHOSPHORYLATION BY SKH1/PEK1.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE SUBFAMILY.
CC -----
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CC -----
DR EMBL: X98243; CAA66899.1; -.
DR EMBL: U65405; AAC49707.1; -.
DR EMBL: AL022117; CAA17923.1; -.
DR HSSP: Q16539; IMPC.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase.1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS01351; MAPK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Cell cycle; Phosphorylation.
FT DOMAIN 21 314 PROTEIN KINASE.
FT NP_BIND 27 35 ATP (BY SIMILARITY).
FT BINDING 52 52 ATP (BY SIMILARITY).
FT ACT_SITE 149 149 BY SIMILARITY.
FT MOD_RES 186 186 PHOSPHORYLATION (ACTIVATES THE KINASE)
FT MOD_RES 188 188 (BY SIMILARITY).
FT MOD_RES 188 188 PHOSPHORYLATION (ACTIVATES THE KINASE)
FT DOMAIN 389 394 POLY-SER.
FT SEQUENCE 422 AA; 48261 MM; FD02521E64EBB82 CRC64;
SQ
Query Match 23.2%; Score 45; DB 1; Length 422;
Best Local Similarity 28.3%; Pred. No. 2.1;
Matches 13; Conservative 3; Mismatches 28; Indels 2; Gaps 1;
OY 1 ANGFLXLRPGSL--XRXCRXXLCSEFXAHXIFRNXXRTROPWVSX 44
DB 143 ANVHRDLKPGNLVNADECKIKCPGLARGCSENPENPGFMTY 188
RESULT 41
MKC1_CANAL STANDARD: PRT; 501 AA.
ID MKC1_CANAL
AC P43068;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Mitogen-activated protein kinase MKC1 (BC 2.7.1.1-) (MAP kinase MKC1).
GN MKC1.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 64385 / 1001;
RX MEDLINE=95198740; PubMed=7891715;
RA Navarro-Garcia F., Sanchez M., Pla J., Nombela C.;
RL "Functional characterization of the MKC1 gene of Candida albicans,
RT which encodes a mitogen-activated protein kinase homolog related to
RT cell integrity.";
RL Mol. Cell. Biol. 15:2197-2206(1995).
CC -1- ENZYME REGULATION: ACTIVATED BY TYROSINE AND THREONINE
CC PHOSPHORYLATION (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X76708; CAA54129.1; -.
DR HSSP: Q16539; IMPC.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase.1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS01351; MAPK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Cell cycle; Phosphorylation.
FT DOMAIN 28 339 PROTEIN KINASE.
FT NP_BIND 34 42 ATP (BY SIMILARITY).
FT BINDING 74 74 ATP (BY SIMILARITY).
FT ACT_SITE 174 174 BY SIMILARITY.
FT MOD_RES 211 211 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 213 213 PHOSPHORYLATION (BY SIMILARITY).
FT SEQUENCE 501 AA; 58192 MM; DBA9F8B6CB97AB07 CRC64;
SQ
Query Match 23.2%; Score 45; DB 1; Length 501;
Best Local Similarity 28.2%; Pred. No. 2.5;
Matches 11; Conservative 3; Mismatches 23; Indels 2; Gaps 1;
OY 8 LRPGSL--XRXCRXXLCSEFXAHXIFRNXXRTROPWVSX 44
DB 175 LKPGNLVNADECKIKCPGLARGFSENPENAGFMTY 213
RESULT 42
RFB_C_MYXXA STANDARD: PRT; 1275 AA.
ID RFB_C_MYXXA
AC Q50864;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE O-antigen biosynthesis protein rfbC.
GN RFB_C.
OS Myxococcus xanthus.
OC Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
OC Myxococcales; Cystobacteriales; Myxococcaceae; Myxococcus.
OX NCBI_TaxID=34;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DK6640;
RX MEDLINE=96198166; PubMed=8626291;
RA Guo D., Bowden M.G., Pershad R., Kaplan H.B.;
RL "The Myxococcus xanthus rfbABC operon encodes an ATP-binding cassette
RT transporter homolog required for O-antigen biosynthesis and
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RT      multicellular development";
CC      J. Bacteriol. 178:1631-1639(1996).
CC      -1- FUNCTION: INVOLVED IN O-ANTIGEN BIOSYNTHESIS.
CC      -----
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CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: U36795; AAB05019.1; -.
DR      InterPro: IPR001296; Glycosyltransferase_1.
DR      InterPro: IPR001173; Glycosyltransferase_2.
DR      Pfam: PF00534; Glycosyltransferase_1; 1.
DR      Pfam: PF00535; Glycosyltransferase_2; 2.
KM      Lipopolysaccharide biosynthesis.
SQ      SEQUENCE 1275 AA; 139596 MW; 3AF9662A10A140F1 CRC64;

Query Match      23.2%; Score 45; DB 1; Length 1275;
Best Local Similarity 38.5%; Pred. No. 6.5;
Matches 10; Conservative 1; Mismatches 15; Indels 0; Gaps 0;

Oy      3 GFLXLRPGSLRXRCRXLCSPFXAH 28
Db      1144 GMLPAGTALYRCVGLCFMPTRH 1169

RESULT 43
ID      GSHB_BUCAI      STANDARD;      PRT;      320 AA.
AC      P57612;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      01-MAR-2002 (Rel. 41, Last annotation update)
DE      Glutathione synthetase (EC 6.3.2.3) (Glutathione synthase) (GSH
DE      synthetase) (GSH-S) (GSHase).
GN      GSHB OR BU547.
OS      Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OS      symbiotic bacterium).
OC      Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX      NCBI_TaxID=118099;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=TOKYO 1998;
RX      MEDLINE=20445173; PubMed=10993077;
RA      Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT      "Genome sequence of the endocellular bacterial symbiont of aphids
RT      Buchnera sp. AFS."
RL      Nature 407:81-86(2000).
CC      -1- CATALYTIC ACTIVITY: ATP + gamma-L-glutamyl-L-cysteine + glycine =
CC      ADP + phosphate + glutathione.
CC      -1- PATHWAY: Glutathione biosynthesis; second step.
CC      -1- SIMILARITY: BELONGS TO THE PROKARYOTIC GSH SYNTHASE FAMILY.
CC      -----
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CC      -----
DR      EMBL: AF001119; BAB13339.1; -.
KM      Glutathione biosynthesis; Ligase: ATP-binding; Complete proteome.
SQ      SEQUENCE 320 AA; 37022 MW; F4F1B99F3FDCA3 CRC64;

Query Match      22.7%; Score 44; DB 1; Length 320;
Best Local Similarity 29.8%; Pred. No. 2.4;
Matches 14; Conservative 5; Mismatches 22; Indels 6; Gaps 2;

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Oy      3 GFLXLRPGSLRXRCRXLCSPFXAHXIFRN 44
Db      114 GVLIINKPKSL-RDCNEKIFTSWFPDLITDTLVTRNIFQIRQFWEKX 159

RESULT 44
ID      FX10_HUMAN      STANDARD;      PRT;      551 AA.
AC      Q9UK36; Q9UKC3;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      F-box only protein 10 (Fragment).
GN      FBXO10 OR FBX10.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=20003061; PubMed=10531037;
RT      Winston J.T., Koepf D.M., Zhu C., Elledge S.J., Harper J.W.;
RA      "A family of mammalian F-box proteins."
RL      Curr. Biol. 9:1180-1182(1999).
RN      [2]
RP      SEQUENCE OF 1-178 FROM N.A.
RX      MEDLINE=20003060; PubMed=10531035;
RA      Cenciarelli C., Chlaur D.S., Guardavaccaro D., Parks W., Vidal M.,
RA      Pagano M.;
RT      "Identification of a family of human F-box proteins."
RL      Curr. Biol. 9:1177-1179(1999).
CC      -1- FUNCTION: Probably recognizes and binds to some phosphorylated
CC      proteins and promotes their ubiquitination and degradation.
CC      -1- SUBUNIT: PART OF A SCF (SKP1-CULIN-F-BOX) PROTEIN LIGASE COMPLEX
CC      (BY SIMILARITY).
CC      -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
CC      -----
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CC      -----
DR      EMBL: AF176705; AAF03705.1; -.
DR      EMBL: AF174598; AAF04519.1; -.
DR      InterPro: IPR001810; F-box.
DR      Pfam: PF00646; F-box; 1.
DR      SMART: SM00256; FBOX; 1.
DR      PROSITE: PS50181; FBOX; 1.
KM      Ubiquitin conjugation.
FT      NON_TER      1
FT      DOMAIN      16 64      F-BOX.
FT      NON_TER      551
SQ      SEQUENCE 551 AA; 60927 MW; 153437B7BF0E4BB9 CRC64;

Query Match      22.2%; Score 43; DB 1; Length 551;
Best Local Similarity 28.1%; Pred. No. 6.4;
Matches 9; Conservative 4; Mismatches 15; Indels 4; Gaps 1;

Oy      2 NGFLXLRPGSLRXRCRXLCSPFXAHXIFRN 33
Db      226 NGHGVHGPGT-----GVKRCFTKRNTHIFLHN 253

RESULT 45
ID      VG59_HSV11      STANDARD;      PRT;      345 AA.
AC      000138;
DT      01-DEC-1992 (Rel. 24, Created)

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DT 01-DEC-1992 (Rel. 24, Last sequence update)
DE 01-DEC-1992 (Rel. 24, Last annotation update)
DR Hypothetical gene 59 membrane protein.
CN 59.
OS Ictalurid herpesvirus 1 (Channel catfish virus) (CCV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
CC unclassified Herpesviridae.
OX NCBI_TaxID=10401;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AOBURN 1.
RX MEDLINE=92087490; PubMed=1727613;
RA Davison A.J.;
RT "Channel catfish virus: a new type of herpesvirus.";
RL virology 186:9-14(1992).
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CC -----
DR EMBL: M75136; AAA88162.1; -.
DR PIR: F36792; MMBE17.
KM Hypothetical protein; Transmembrane.
FT TRANSMEM 46 63 POTENTIAL.
FT TRANSMEM 101 118 POTENTIAL.
FT TRANSMEM 147 165 POTENTIAL.
FT TRANSMEM 265 286 POTENTIAL.
SQ SEQUENCE 345 AA; 38135 MW; 920CA308157F320E CRC64;

Query Match 21.6%; Score 42; DB 1; Length 345;
Best Local Similarity 30.0%; Pred. No. 6;
Matches 6; Conservative 3; Mismatches 11; Indels 0; Gaps 0;
QY 22 CSFXAXHIFRNXXRTQFW 41
DB 217 CGYGVHLMLESRTRLW 236

RESULT 46
MPK7_ARATH STANDARD; PRT; 368 AA.
AC Q39027;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Mitogen-activated protein kinase homolog 7 (EC 2.7.1.-) (MAP kinase 7)
DE (ACMPK7).
GN MPK7.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA.
RX MEDLINE=94109583; PubMed=8282107;
RA Mizoguchi T., Hayashida N., Yamaguchi-Shinozaki K., Kamada H.,
RA Shinozaki K.;
RT "ATMPs: a gene family of plant MAP kinases in Arabidopsis thaliana.";
RL FEBS Lett. 336:440-444(1993).
CC -1- ENZYME REGULATION: ACTIVATED BY TYROSINE AND THREONINE
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE SUBFAMILY.
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CC -----
DR EMBL: D21843; BAA04870.1; -.
DR HSSP: O16539; IMFC.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR003527; MAP_Kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS001351; MAPK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Multigene family.
FT DOMAIN 32 319 PROTEIN_KINASE.
FT NP_BIND 38 46 ATP (BY SIMILARITY).
FT BINDING 61 61 ATP (BY SIMILARITY).
FT ACT_SITE 158 158 BY SIMILARITY.
FT MOD_RES 191 191 PHOSPHORYLATION (ACTIVATES THE KINASE)
FT MOD_RES 193 193 (BY SIMILARITY).
FT MOD_RES 193 193 PHOSPHORYLATION (ACTIVATES THE KINASE)
FT MOD_RES 193 193 (BY SIMILARITY).
SQ SEQUENCE 368 AA; 42381 MW; 65F41CB/CC37BIOD CRC64;

Query Match 21.6%; Score 42; DB 1; Length 368;
Best Local Similarity 30.4%; Pred. No. 6.4;
Matches 14; Conservative 3; Mismatches 23; Indels 6; Gaps 2;
QY 1 ANGFLXLRPGSL--XRXCRXXLCFFXAXHIFRNXXRTQFWYS 44
DB 152 ANILHRDLKPGNLLVNMNCDLKICDFGLA----RTSGNDEGFMEY 193

RESULT 47
NAPA_DESDE STANDARD; PRT; 755 AA.
AC P81186;
DT 15-JUL-1998 (Rel. 36, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Periplasmic nitrate reductase precursor (EC 1.7.99.4).
GN NAPA OR NAP.
OS Desulfovibrio desulfuricans.
OC Bacteria; Proteobacteria; delta subdivision; Desulfovibrio.
OX NCBI_TaxID=876;
RN [1]
RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RC STRAIN=ATCC 27774;
RX MEDLINE=99220830; PubMed=10368307;
RA Dias J.M., Than M.E., Humm A., Huber R., Bourenkov G.P.,
RA Bartunik H.D., Bursakov S., Calvete J., Caldeira J., Carneiro C.,
RA Moura J.J.G., Moura I., Romao M.J.;
RT "Crystal structure of the first dissimilatory nitrate reductase at 1.9
RT A solved by MAD methods.";
RL Structure 7:65-79(1999).
RN [2]
RP SEQUENCE OF 33-73.
RC STRAIN=ATCC 27774;
RX MEDLINE=98042476; PubMed=9367852;
RA Bursakov S.A., Carneiro C., Almeida M.J., Duarte R.O., Caldeira J.,
RA Moura I., Moura J.J.G.;
RT "Enzymatic properties and effect of ionic strength on periplasmic
RT nitrate reductase (NAP) from Desulfovibrio desulfuricans ATCC
RT 27774.";
RL Biochem. Biophys. Res. Commun. 239:816-822(1997).
RN [3]
RP CHARACTERIZATION.

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RC STRAIN-ATCC 27774;
RA Bursakov S., Liu M.-Y., Payne W.J., Legall J., Moura I., Moura J.J.G.;
RT "Isolation and preliminary characterization of a soluble nitrate
RT reductase from the sulfate-reducing bacterium Desulfovibrio
RT desulfuricans 27774."
RL Anaerobe 1:55-60(1995).
CC -1- FUNCTION: LARGE SUBUNIT OF THE PERIPLASMIC NITRATE REDUCTASE
CC (NMR). ONLY EXPRESSED AT HIGH LEVELS DURING AEROBIC GROWTH. NARAB
CC COMPLEX RECEIVES ELECTRONS FROM THE MEMBRANE-ANCHORED TETRAHEME
CC NADP PROTEIN, THUS ALLOWING ELECTRON FLOW BETWEEN MEMBRANE AND
CC PERIPLASM. ESSENTIAL FUNCTION FOR NITRATE ASSIMILATION AND MAY
CC HAVE A ROLE IN ANAEROBIC METABOLISM.
CC -1- CATALYTIC ACTIVITY: Nitrite + acceptor -> nitrate + reduced
CC acceptor.
CC -1- COFACTOR: MOLYBDENUM (MOLYBDOPTERIN); MAY BIND A 4FE-4S CLUSTER.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Periplasmic.
CC -1- INDUCTION: NITRATE REDUCTASE ACTIVITY IS INDUCED BY POTASSIUM AND
CC SODIUM AND INHIBITED BY MAGNESIUM AND CALCIUM.
CC -1- SIMILARITY: BELONGS TO THE PROKARYOTIC MOLYBDOPTERIN-CONTAINING
CC OXIDOREDUCTASE FAMILY. NASA/NAPV/NARB SUBFAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: Y18045; CAA77019.1; -.
DR PDB: 2NAP; 19-SEP-99.
DR InterPro: IPR001467; Molybdopterin.
DR Pfam: PF00384; molybdopterin; 1.
DR PROSITE: PS00551; MOLYBDOPTERIN_PROK_1; FALSE_NEG.
DR PROSITE: PS00490; MOLYBDOPTERIN_PROK_2; FALSE_NEG.
DR PROSITE: PS00932; MOLYBDOPTERIN_PROK_3; FALSE_NEG.
KW Nitrate assimilation; Oxidoreductase; Electron transport; Molybdenum;
KW Periplasmic; Iron-sulfur; 4Fe-4S; 3D-structure; Signal.
FT SIGNAL 1 32
FT CHAIN 33 755 PERIPLASMIC NITRATE REDUCTASE.
FT METAL 45 45 IRON-SULFUR (4FE-4S).
FT METAL 48 48 IRON-SULFUR (4FE-4S).
FT METAL 52 52 IRON-SULFUR (4FE-4S).
FT METAL 79 79 IRON-SULFUR (4FE-4S).
SQ SEQUENCE 755 AA; 83497 MW; D54BDB9D1FE21DC2 CRC64;

Query Match 21.6%; Score 42; DB 1; Length 755;
Best Local Similarity 26.3%; Pred. No. 13;
Matches 10; Conservative 2; Mismatches 26; Indels 0; Gaps 0;

OY 4 FLXLRPGSLXRCXXLCSEFXAXHXIFRNXXTRQFW 41
DB 301 FLENYRPEKVAELCRVPEQIYGAARAFASATMSLM 338

RESULT 48
ADML_MOUSE
ID ADML_MOUSE STANDARD; PRT; 184 AA.
AC P97297; P97453;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN ADM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN-129/SV;
RX MEDLINE-9702892; PubMed-8938454;
RA Okazaki T., Ogawa Y., Tamura N., Mori Y., Ise N., Aoki T.,
RA Rochelle J.M., Takeo M.M., Seidin M.F., Nakao K.;
RT "Genomic organization, expression, and chromosomal mapping of the
RT mouse adrenomedullin gene."
RL Genomics 37:395-399(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J;
RA Yotsumoto S., Ko M.S.H.;
RT "Expression of mouse adrenomedullin gene in trophoblastic giant
RT cells at the implantation site."
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATOR
CC AGENTS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: D78349; BAA11367.1; -.
DR EMBL: U77630; AAB36535.1; -.
DR MGD; MGI:108058; Adm.
DR InterPro: IPR001710; Adrenomedullin.
DR Pfam: PF02039; Adrenomedullin; 1.
DR PRINTS: PR00801; ADRENOMEDULLIN.
KW Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 21
FT PEPTIDE 22 41 PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
FT PROPEP 45 92 BY SIMILARITY.
FT PEPTIDE 95 144 ADRENOMEDULLIN.
FT PROPEP 151 184 PREPROAM C-TERMINAL FRAGMENT (BY
FT SIMILARITY).
FT DISULFID 108 113 BY SIMILARITY.
FT MOD_RES 41 41 AMIDATION (G-42 PROVIDE AMIDE GROUP)
FT MOD_RES 144 144 (BY SIMILARITY).
FT MOD_RES 144 144 AMIDATION (G-145 PROVIDE AMIDE GROUP)
FT CONFLICT 173 173 A -> G (IN REF. 2).
SQ SEQUENCE 184 AA; 20764 MW; C88C99045A79C898 CRC64;

Query Match 21.4%; Score 41.5; DB 1; Length 184;
Best Local Similarity 34.6%; Pred. No. 3; 9;
Matches 9; Conservative 4; Mismatches 12; Indels 1; Gaps 1;

OY 8 LRFGLXRCXXLCSEFXAXHXIFRNXXTRQFW 32
DB 99 MNGSRSGRCRGCTCTCFORLHQIQ 124

RESULT 49
RPOA_LELV
ID RPOA_LELV STANDARD; PRT; 3859 AA.
AC Q04561;
DT 01-OCT-1993 (Rel. 27; Created)
DT 01-OCT-1993 (Rel. 27; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE POL polyprotein (ORF1A/1B) [Contains: RNA-directed RNA polymerase
DE (EC 2.7.7.48); Helicase; Protease (EC 3.4.21.-)].
GN POL.
OS Lelystad virus (LV) (Porcine reproductive and respiratory syndrome
OS virus).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Arteriviridae; Arterivirus.

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OX NCBI_TaxID=11049;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93297139; PubMed=8517032;
RA Meulenber J.J.M., Hulst M.M., de Meijer E.J., Moonen P.L.J.M.,
den Besten A., de Kluuyver E.P., Moorman R.J.M.;
RT "Leijstad virus, the causative agent of porcine epidemic abortion and
RT respiratory syndrome (PEARS), is related to LDV and EAV.";
RL Virology 192:62-72(1993).
RN [2]
RP REVISION TO 3327.
RA Kroeze M.V., Moorman R.J.M.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 3327-3859 FROM N.A.
RC STRAIN=BOXMEER 10;
RX MEDLINE=93174942; PubMed=8438574;
RA Conzelmann K.K., Vlisser N., van Woensel P., Thiel H.J.;
RT "Molecular characterization of porcine reproductive and respiratory
RT syndrome virus, a member of the arterivirus group.";
RL Virology 193:329-339(1993).
CC -1- FUNCTION: RNA-DIRECTED RNA POLYMERASE & POSSIBLE HELICASE. A
CC ROLE FOR NTP-BINDING PROTEINS IN RNA DUPLICATION UNWINDING HAS BEEN
CC SUGGESTED. ALSO CONTAINS A PROTEASE DOMAIN.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate -> N diphosphate +
CC (RNA)(N).
CC -1- SIMILARITY: WITH THE POLYMERASE PROTEIN OF OTHER CORONAVIRUSES AND
CC OF TOROVIRUSES.
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S32.
CC -----
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CC -----
DR EMBL: M96262; AAA46273.2; -
DR EMBL: M96262; AAA46274.1; -
DR EMBL: L04493; AAA47101.1; -
DR PIR: A36861; A36861.
DR PIR: A45392; A45392.
DR MEROPS: C31.001; -
DR MEROPS: C32.001; -
DR MEROPS: C33.001; -
DR InterPro: IPR000606; Viral_helicase1.
DR Pfam: PF01443; Viral_helicase1.
KW RNA-directed RNA polymerase; Transferase; Helicase; ATP-binding;
KW Hydrolyase; Serine protease; Zinc-finger.
FT CHAIN 1 2396 ORF1A.
FT CHAIN 2397 3859 ORF1B.
FT DOMAIN 262 290 CYS-RICH.
FT DOMAIN 472 525 CYS-RICH.
FT DOMAIN 792 1506 HELICASE.
FT DOMAIN 1203 1284 CYS-RICH.
FT DOMAIN 1724 1830 TRYPsin-LIKE SERINE PROTEASE.
FT DOMAIN 2010 2108 CYS-RICH.
FT DOMAIN 2768 2972 POLYMERASE.
FT ACT_SITE 1732 1732 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 1757 1757 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 1810 1810 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT NP_BIND 2388 2395 ATP (BY SIMILARITY).
FT ZN_FING 3042 3094 BY SIMILARITY.
FT CONFLICT 3506 3506 T -> V (IN REF. 3).
FT CONFLICT 3744 3744 V -> I (IN REF. 3).
SQ SEQUENCE 3859 AA; 421758 MW; 8C5E945AC6895CEE CRC64;

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Query Match 21.1%, Score 41; DB 1; Length 3859;
 Best Local Similarity 25.6%; Pred. No. 1e+02;
 Matches 10; Conservative 4; Mismatches 13; Indels 12; Gaps 2;

```

OY 15 RXXRXXLCSEFXAHX-----IFRNXX---RTRQFW 41
Db 167 QACRQPCFPFEHASSYTRMKFVFTDSLGRSRMM 205
RESULT 50
TSNR_STRLU STANDARD: PRT: 270 AA.
ID TSNR_STRLU
AC P52393.
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE rRNA (adenosine-2'-O-methyltransferase (EC 2.1.1.66) (23S rRNA
DE [AM1067] 2'-O-methyltransferase) (23S rRNA methylase) (Thiostrepton-
DE resistance methylase).
GN TSNR.
OS Streptomyces laurentii.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=39478;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96060853; PubMed=7590303;
RA Smith T.M., Jiang Y.F., Shipley P., Floss H.G.;
RT "The thiostrepton-resistance-encoding gene in Streptomyces laurentii
RT is located within a cluster of ribosomal protein operons.";
RL Gene 164:137-142(1995).
CC -1- FUNCTION: SPECIFICALLY METHYLATED THE ADENOSINE-1067 IN 23S
CC RIBOSOMAL RNA. CONFERS RESISTANCE TO ANTIBIOTIC THIOSTREPTON.
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + RNA -> S-adenosyl-L-
CC homocysteine + RNA containing a single residue of 2'-O-
CC methyladenosine.
CC -1- SIMILARITY: TO S-ACTUOSUS NHS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L39157; AAA9931.1; -
DR InterPro: IPR001537; SpoU_methylase.
DR Pfam: PF00588; SpoU_methylase.
DR ProDom: PD001243; SpoU_methylase; 1.
KW Antibiotic resistance; Transferase; Methyltransferase.
SQ SEQUENCE 270 AA; 28723 MW; 298E871C3DB8BCDCE CRC64;

```

Query Match 20.9%, Score 40.5; DB 1; Length 270;
 Best Local Similarity 25.6%; Pred. No. 8.7;
 Matches 10; Conservative 7; Mismatches 17; Indels 5; Gaps 1;

Search completed: August 30, 2002, 15:45:37
 Job time: 857 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2002, 15:44:05 ; Search time 155.42 Seconds
(without alignments)
48.976 Million cell updates/sec

Title: US-09-302-239-4

Perfect score: 194
Sequence: 1 ANGFLXLLRPGSLXRCXCRXX.....XXAHXIFRNXXRTQFWVSY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :

1: SPREMBL.19:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	131	67.5	701	4	Q96P08
2	115	59.3	460	11	Q91WN8
3	114	58.8	446	11	Q61109
4	109	56.2	460	11	Q99PC6
5	107	55.2	218	4	Q14668
6	99	51.0	231	4	Q9BZD7
7	98	50.5	456	6	Q9TRD0
8	94	48.5	482	11	Q63207
9	91	46.9	481	11	Q88947
10	91	46.9	481	11	Q54740
11	91	46.9	481	11	Q99L32
12	87	44.8	456	4	Q14316
13	87	44.8	461	6	Q95ND7
14	87	44.8	461	6	Q95ND6
15	87	44.8	469	6	Q9GMD9
16	86	44.3	49	6	Q95ME8

17	81	41.8	138	6	Q28994
18	80	41.2	433	13	Q90YK1
19	79	40.7	202	4	Q14669
20	78	40.2	100	4	Q15253
21	78	40.2	226	4	Q9BZD6
22	78	40.2	608	13	Q9PTW7
23	74	38.1	648	6	Q29094
24	73	37.6	399	11	Q9COW3
25	69	35.6	650	4	Q9NSD0
26	69	35.6	650	4	Q16519
27	66	34.0	607	13	Q91001
28	65	33.5	98	13	P82807
29	58	29.9	678	4	Q14393
30	57	29.4	673	11	Q61592
31	57	29.4	674	11	Q99K57
32	56.5	29.1	431	10	Q94EY5
33	56.5	29.1	543	10	Q9MB23
34	56.5	29.1	576	10	Q9C9U4
35	56.5	29.1	589	10	Q91MS2
36	56	28.9	25	11	Q9QVH6
37	55.5	28.6	575	10	Q94E17
38	55.5	28.6	608	10	Q9XF36
39	55	28.4	674	11	Q63772
40	54.5	28.1	594	10	Q9SJC9
41	54.5	28.1	603	10	Q91P67
42	54.5	28.1	606	10	Q94518
43	53.5	27.6	196	10	Q04284
44	53.5	27.6	459	10	Q9SE22
45	53.5	27.6	492	10	Q9SMJ7
46	53.5	27.6	492	10	Q9SPF0
47	53.5	27.6	506	10	Q9SE23
48	53.5	27.6	593	10	Q9LUC3
49	52.5	27.1	510	10	Q9MB22
50	52.5	27.1	619	10	Q9LV37

ALIGNMENTS

RESULT 1
ID Q96P08 PRELIMINARY: PRT: 701 AA.
AC Q96P08:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE FACTOR VII ACTIVE SITE MUTANT IMMUNOCONJUGATE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21477448; PubMed=11593034;
RA Hu Z., Garen A.;
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
RT cells for immunotherapy in mouse models of prostatic cancer.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
DR EMBL: AF272774; AAK58686.1; -
SQ SEQUENCE 701 AA; 77826 MW; 94AC6EBA2CC92F CXC64;

Query Match 67.5%; Score 131; DB 4; Length 701;
Best Local Similarity 54.5%; Pred. No. 2.3e-15;
Matches 24; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 1 ANGFLXLLRPGSLXRCXCRXXLCFFXXAHXIFRNXXRTQFWVSY 44
DB 61 ANAFLELRPGSLERCKEKCSEFARERFDARTKLEWISY 104
RESULT 2
Q91WN8

```
ID Q91N8 PRELIMINARY; PRT; 460 AA.
AC Q91N8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE SIMILAR TO PROTEIN C.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
RL Submitted (Sep-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013896; AAH13896.1; -.
SQ SEQUENCE 460 AA; 51818 MW; 0117F26568FC274 CRC64;

Query Match 59.3%; Score 115; DB 11; Length 460;
Best Local Similarity 47.7%; Pred. No. 1.3e-12;
Matches 21; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXLRPGSLXRCXRXLCSPXAHXIFRNXXRTROFWVS 44
ID 061109 PRELIMINARY; PRT; 446 AA.
AC 061109;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE COAGULATION FACTOR VII.
GN F7 OR FVII.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA MEDLINE; 96276538; Pubmed=8701412;
RA Idusogie E., Rosen E., Geng J.P., Carmeliet P., Collen D.,
RA Castellino F.J.;
RT "Characterization of a cDNA encoding murine coagulation factor VII.";
RL Thromb. Haemost. 75:481-487(1996).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; U44795; AAC52570.1; -.
DR HSSP; P08709; 1FAK.
DR MGD; MGT:109325; F7.
DR InterPro; IPR002086; Aldehyde_dehydr.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF-like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Trypsin.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TYP_SPC; 1.
DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
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DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ SEQUENCE 446 AA; 50318 MW; 482FD09BEFDA6870 CRC64;
```

```
Query Match 58.8%; Score 114; DB 11; Length 446;
Best Local Similarity 50.0%; Pred. No. 1.9e-12;
Matches 22; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANGFLXLRPGSLXRCXRXLCSPXAHXIFRNXXRTROFWVS 44
ID 099PC6 PRELIMINARY; PRT; 460 AA.
AC 099PC6;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ANTICOAGULANT PROTEIN C.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL;
RA Korf I.;
RT "Complete sequence of UC72A01.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AE318182; AAK07918.1; -.
DR HSSP; P04070; 1PCU.
DR InterPro; IPR00152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF-like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Trypsin.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF_2.
DR SMART; SM00001; EGF_like; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TYP_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00135; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KW Hydrolyation; Repeat; Serine protease.
SQ SEQUENCE 460 AA; 51784 MW; 0293BC25E9D3ED16 CRC64;

Query Match 56.2%; Score 109; DB 11; Length 460;
Best Local Similarity 45.5%; Pred. No. 1.6e-11;
```

Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

OY 1 ANGFLXLRPGSLXRCXRLCSFXXAHXIFRNXXRTQFWVS 44
 DB 42 ANSFLEEMRPGSLRECEMEICDELEAOEIFQNVEDTLAFWKY 85

RESULT 5

ID 014668 PRELIMINARY; PRT; 218 AA.
 AC 014668;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PROLINE-RICH GLA PROTEIN 1.
 GN PCP1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=97404347; PubMed=9256434;
 RA Kulman J.D., Harris J.E., Haldeman B.A., Davie E.W.;
 RT "Primary structure and tissue distribution of two novel proline-rich
 gamma-carboxyglutamic acid proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997).
 DR EMBL: AF009242; AAB67070.1; -.
 DR HSSP: P00740; ICFH.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR000294; VltK_dep_GLA.
 DR Pfam: PF00594; gla; 1.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00069; GLA; 1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
 DR SEQUENCE 218 AA; 24947 MM; 26538A61AB0AEB98 CRC64;
 SQ

Query Match 55.2%; Score 107; DB 4; Length 218;
 Best Local Similarity 38.6%; Pred. No. 1.7e-11;
 Matches 17; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

OY 1 ANGFLXLRPGSLXRCXRLCSFXXAHXIFRNXXRTQFWVS 44
 DB 21 ANGFEEIRQGNIRECKEECTFEARAEFENNEKTEFWSTY 64

RESULT 6

ID 09BZD7 PRELIMINARY; PRT; 231 AA.
 AC 09BZD7;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID PROTEIN 3 TMG3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=SPINAL CORD;
 RC MEDLINE=21117044; PubMed=11171957;
 RA Kulman J.D., Harris J.E., Xie L., Davie E.W.;
 RT "Identification of two novel transmembrane gamma-carboxyglutamic acid
 proteins expressed broadly in fetal and adult tissues.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:1370-1375(2001).
 DR EMBL: AF326350; AAK0955.1; -.
 DR HSSP: P00740; ICFH.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR000294; VltK_dep_GLA.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00069; GLA; 1.

DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
 SQ SEQUENCE 231 AA; 25848 MM; 8A373E4848490D81 CRC64;

Query Match 51.0%; Score 99; DB 4; Length 231;
 Best Local Similarity 38.6%; Pred. No. 5.4e-10;
 Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

OY 1 ANGFLXLRPGSLXRCXRLCSFXXAHXIFRNXXRTQFWVS 44
 DB 20 ANEFLEELRQGTIERECMEICSYEVKVEFENKEKTEFWMGY 63

RESULT 7

ID 09TTR0 PRELIMINARY; PRT; 456 AA.
 AC 09TTR0;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PROTEIN C PRECURSOR.
 GN PROC.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP Leeb T., Kopp T., Deppe A., Breen M., Mattis U., Brunberg L.,
 RA Breen B.;
 RT "Molecular characterization and chromosomal assignment of the canine
 protein C gene.";
 RL Mamm. Genome 10:135-139(1999).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=99371952; PubMed=10443005;
 RA Leeb T., Pfeiffer I., Kopp T., Deppe A., Breen B.;
 RT "Analysis of canine protein C gene polymorphisms.";
 RL Anim. Genet. 30:237-238(1999).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 DR EMBL: AJ001979; CA05126.1; -.
 DR HSSP: P04070; IPCU.
 DR MEROPS: S01.218; -.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Trypsin.
 DR InterPro: IPR000294; VltK_dep_GLA.
 DR Pfam: PF00008; EGF; 2.
 DR Pfam: PF00594; gla; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00181; EGF; 2.
 DR SMART: SM00069; GLA; 1.
 DR SMART: SM00020; TRYP_SPE; 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; 1.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF_Ca; 1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 DR Calcium-binding, EGF-like domain; Glycoprotein; Hydrolase;
 KW Hydroxylation; Repeat; Serine protease; Signal.
 FT SIGNAL 1 42
 FT CHAIN 43 192 PROTEIN C LIGHT CHAIN.
 FT CHAIN 193 194 PROTEIN C CONNECTING DIPEPTIDE.
 FT CHAIN 195 456 PROTEIN C HEAVY CHAIN.

SO SEQUENCE 456 AA; 50813 MW; 7AD3A8C1C34E59FF CRC64;

Query Match 50.5%; Score 98; DB 6; Length 456;
Best Local Similarity 43.2%; Pred. No. 1.6e-09;
Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

QY 1 ANGFLXLRGSLXRXCRXXLCSTXXAHXIFRNXXRTROFVSV 44
DB 43 ANSFEIRAGSLERECMEECIDFEAKELIFQNVDDTLAVWSKY 86

RESULT 8

063207 PRELIMINARY; PRT; 482 AA.

AC 063207;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE FACTOR X.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=96093366; PubMed=8578539; Wallin R.;
RA Stanton C., Ross R.P., Hutson S.,
RT "Evidence for competition between vitamin K-dependent clotting factors
RT for intracellular processing by the vitamin K-dependent gamma-
RT carboxylase.";
RL Thromb. Res. 80:63-73(1995).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL: X79807; CA56202.1; -.
DR HSSP: P00742; 1XKA.
DR MEROPS: S01.216; -.
DR Interpro: IPR000152; Asx_hydroxyl.
DR Interpro: IPR001314; Chymotrypsin.
DR Interpro: IPR000561; EGF-like.
DR Interpro: IPR000742; EGF-2.
DR Interpro: IPR001881; EGF_Ca.
DR Interpro: IPR002383; GLA_blood.
DR Interpro: IPR001254; Trypsin.
DR Interpro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF; 2.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00001; EGF_CA; 1.
DR SMART: SM00001; EGF_like; 1.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; TRYP_SPE; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS50240; TRYPsin_DOM; 1.
DR PROSITE: PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KW Hydroxylation; Repeat; Serine protease.

SO SEQUENCE 482 AA; 54265 MW; 0284678E3954A698 CRC64;

Query Match 48.5%; Score 94; DB 11; Length 482;
Best Local Similarity 36.4%; Pred. No. 9.4e-09;
Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLXLRGSLXRXCRXXLCSTXXAHXIFRNXXRTROFVSV 44

DB 41 ANSFEIRKGNLERECVEECISFEAREYFEDNEKTEFWNKY 84

RESULT 9

088947 PRELIMINARY; PRT; 481 AA.

AC 088947;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE COAGULATION FACTOR X PRECURSOR.
GN F10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL6 X CBA; TISSUE=LIVER;
RX MEDLINE=98347933; PubMed=9684791;
RA Liang Z., Cooper A., Deford M.E., Carmeliet P., Collen D.,
RA Castellino F.J., Rosen E.D.;
RT "Cloning and characterization of a cDNA encoding murine coagulation
RT factor X.";
RL Thromb. Haemost. 80:87-91(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129SJ.
RA Cooper A., Liang Z., Castellino F.J., Rosen E.D.;
RT "Cloning and Characterization of the Murine Factor X Gene.";
RL Thromb. Haemost. 0:0-0(2000).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL: AF087644; AAC36345.1; -.
DR EMBL: AF21347; AAC22980.1; -.
DR HSSP: P00742; 1XKA.
DR MEROPS: S01.216; -.
DR MGD: MGI:103107; F10.
DR Interpro: IPR000152; Asx_hydroxyl.
DR Interpro: IPR001314; Chymotrypsin.
DR Interpro: IPR000561; EGF-like.
DR Interpro: IPR000742; EGF-2.
DR Interpro: IPR001881; EGF_Ca.
DR Interpro: IPR002383; GLA_blood.
DR Interpro: IPR001254; Trypsin.
DR Interpro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF; 2.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00001; EGF_CA; 1.
DR SMART: SM00001; EGF_like; 1.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; TRYP_SPE; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS50240; TRYPsin_DOM; 1.
DR PROSITE: PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease; Signal.

FT SIGNAL 1
FT CHAIN 41 481 POTENTIAL FACTOR X.
SO SEQUENCE 481 AA; 54018 MW; 8AC09DE5EF9D271E CRC64;

Query Match 46.9%; Score 91; DB 11; Length 481;
Best Local Similarity 31.8%; Pred. No. 3.3e-08;

Matches 14; Conservative 9; Mismatches 21; Indels 0; Gaps 0;

OY 1 ANGFLXXLRPGSLKRXCRXXLCSEFXAHXIFRNXXRTQFWVS 44
 DB 41 ANSFEEFKKGNLERECMEICSYEEVREIFEDDKETREYWKY 84

RESULT 10
 054740 PRELIMINARY; PRT: 481 AA.

AC 054740;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE COAGULATION FACTOR X PRECURSOR (EC 3.4.21.6).
 GN F10.
 OS Mus musculus (Mouse).
 OG Plasmid pBluescript.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RX MEDLINE-9845493; PubMed-9783672;
 RA Heidmann H.H., Kontermann R.E.;
 RL Thromb. Res. 92:33-41(1998).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
 DR EMBL: AJ222677; CAI10933.1; -.
 DR HSSP: P00742; IYKA.
 DR MEROPS: S01.216; -.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000742; EGF_2.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Trypsin.
 DR InterPro: IPR000294; VltK_dep_GLA.
 DR Pfam: PF00008; EGF_2.
 DR Pfam: PF00594; gla_1.
 DR Pfam: PF00089; trypsin_1.
 DR PRINTS: PRO0722; CHYMOTRYPSIN.
 DR PRINTS: PRO0001; GLABLOOD.
 DR SMART: SM00179; EGF_CA_1.
 DR SMART: SM00069; GLA_1.
 DR SMART: SM00020; TRYPSIN_DOM_1.
 DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF_CA_1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE: PS50240; TRYPSIN_DOM_1.
 DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Plasmid;
 KW Repeat; Serine protease; Signal.
 FT SIGNAL 1 40 POTENTIAL.
 FT CHAIN 41 481 COAGULATION FACTOR X
 SO SEQUENCE 481 AA; 53986 MW; CF702DE5EF9D97AE CMC64;

Query Match 46.9%; Score 91; DB 11; Length 481;
 Best Local Similarity 31.8%; Pred. No. 3.3e-08;
 Matches 14; Conservative 9; Mismatches 21; Indels 0; Gaps 0;

OY 1 ANGFLXXLRPGSLKRXCRXXLCSEFXAHXIFRNXXRTQFWVS 44
 DB 41 ANSFEEFKKGNLERECMEICSYEEVREIFEDDKETREYWKY 84

RESULT 11

ID 099L32 PRELIMINARY; PRT: 481 AA.
 AC 099L32;

DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE COAGULATION FACTOR X.
 GN F10.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RX MEDLINE-9845493; PubMed-9783672;
 RA Heidmann H.H., Kontermann R.E.;
 RL Thromb. Res. 92:33-41(1998).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
 DR EMBL: BC003877; AAH03877.1; -.
 DR HSSP: P00742; IYKA.
 DR MGD: MGI:103107; F10.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000742; EGF_2.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Trypsin.
 DR InterPro: IPR000294; VltK_dep_GLA.
 DR Pfam: PF00008; EGF_2.
 DR Pfam: PF00594; gla_1.
 DR Pfam: PF00089; trypsin_1.
 DR PRINTS: PRO0722; CHYMOTRYPSIN.
 DR PRINTS: PRO0001; GLABLOOD.
 DR SMART: SM00181; EGF_2.
 DR SMART: SM00001; EGF-like; 2.
 DR SMART: SM00069; GLA_1.
 DR SMART: SM00020; TRYPSIN_DOM_1.
 DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF_CA_1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE: PS50240; TRYPSIN_DOM_1.
 DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
 KW Serine protease.
 SO SEQUENCE 481 AA; 54004 MW; BD88E96C8A0B7E7F CMC64;

Query Match 46.9%; Score 91; DB 11; Length 481;
 Best Local Similarity 31.8%; Pred. No. 3.3e-08;
 Matches 14; Conservative 9; Mismatches 21; Indels 0; Gaps 0;

OY 1 ANGFLXXLRPGSLKRXCRXXLCSEFXAHXIFRNXXRTQFWVS 44
 DB 41 ANSFEEFKKGNLERECMEICSYEEVREIFEDDKETREYWKY 84

RESULT 12

ID 014316 PRELIMINARY; PRT: 456 AA.
 AC 014316;

DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-AUG-1999 (TREMBlrel. 11, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE F9 (COAGULATION FACTOR IX (PLASMA THROMBOPLASTIC COMPONENT, CHRISTMAS DISEASE, HAEMOPHILIA B)) (FACTOR IX).

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GN F9 OR FACTOR IX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bird C.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 3-19 FROM N.A.
RX MEDLINE=88327116; PubMed=3416069;
RA Reitsma P.A., Bertina R.M., Ploos van Amstel J.K., Riemens A.,
RA Briet E.;
RT "The putative factor IX gene promoter in hemophilia B Leyden.";
RL Blood 72:1074-1076(1988).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPsin FAMILY.
DR EMBL; AL033403; CAA21954.1; -.
DR EMBL; X55008; CAB38245.2; -.
DR HSSP; P00740; ICFH.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF-2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001438; EGF_II.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Trypsin.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam; PR00008; EGF_2.
DR Pfam; PF00594; gla_1.
DR Pfam; PF00089; trypsin_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFBL00D.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF-2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
KW Calcium-binding; EGF-like domain; glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ
SEQUENCE 436 AA; 51149 MW; 54E20A1B3964E234 CRC64;

Query Match 44.8%; Score 87; DB 4; Length 456;
Best Local Similarity 39.5%; Pred. No. 1.7e-07;
Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

OY 2 NGFLXLRPGSLRXCRXXLCSPFXAHXIFRNXXRTROFWVSY 44
Db 44 SGKLEEFVQGNLRECEMEKCSFEAREVEPENTERTTEFWKQY 86

RESULT 13
O95ND7 PRELIMINARY; PRT; 461 AA.
AC O95ND7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE COAGULATION FACTOR XI.
GN F9.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.

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OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=504;
RA Satta Y.;
RT "Comparison of DNA and protein polymorphisms between humans and
RT chimpanzees.";
RL Genes Genet. Syst. 0:0-0(2001).
DR EMBL; AB062470; BAB58885.1; JOINED.
DR EMBL; AB062458; BAB58885.1; JOINED.
DR EMBL; AB062460; BAB58885.1; JOINED.
DR EMBL; AB062462; BAB58885.1; JOINED.
DR EMBL; AB062464; BAB58885.1; JOINED.
DR EMBL; AB062466; BAB58885.1; JOINED.
DR EMBL; AB062468; BAB58885.1; JOINED.
SQ
SEQUENCE 461 AA; 51764 MW; 30C2F857C0F77F45 CRC64;

Query Match 44.8%; Score 87; DB 6; Length 461;
Best Local Similarity 39.5%; Pred. No. 1.7e-07;
Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

OY 2 NGFLXLRPGSLRXCRXXLCSPFXAHXIFRNXXRTROFWVSY 44
Db 49 SGKLEEFVQGNLRECEMEKCSFEAREVEPENTERTTEFWKQY 91

RESULT 14
O95ND6 PRELIMINARY; PRT; 461 AA.
AC O95ND6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE COAGULATION FACTOR XI.
GN F9.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Satta Y.;
RT "Comparison of DNA and protein polymorphisms between humans and
RT chimpanzees.";
RL Genes Genet. Syst. 0:0-0(2001).
DR EMBL; AB062471; BAB58886.1; JOINED.
DR EMBL; AB062459; BAB58886.1; JOINED.
DR EMBL; AB062461; BAB58886.1; JOINED.
DR EMBL; AB062463; BAB58886.1; JOINED.
DR EMBL; AB062465; BAB58886.1; JOINED.
DR EMBL; AB062467; BAB58886.1; JOINED.
DR EMBL; AB062469; BAB58886.1; JOINED.
SQ
SEQUENCE 461 AA; 51695 MW; 8F5A69A525DF65B5 CRC64;

Query Match 44.8%; Score 87; DB 6; Length 461;
Best Local Similarity 39.5%; Pred. No. 1.7e-07;
Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

OY 2 NGFLXLRPGSLRXCRXXLCSPFXAHXIFRNXXRTROFWVSY 44
Db 49 SGKLEEFVQGNLRECEMEKCSFEAREVEPENTERTTEFWKQY 91

RESULT 15
O9GMD9 PRELIMINARY; PRT; 469 AA.
AC O9GMD9;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)

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DE COAGULATION FACTOR X.
OC Ornithorhynchus anatinus (Duckbill platypus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.
OX NCBI_TaxID=9258;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21015017; PubMed=11132153;
RA Poorafshar M., Aveskogh M., Munday B., Hellman L.;
RT "Identification and structural analysis of four serine proteases in a
RL monotreme, the platypus, Ornithorhynchus anatinus.";
CC Immunogenetics 52:19-28(2000).
CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AF215654; AAC00453.1; -.
DR HSSP; P00742; IAKB.
DR MEROPS; S01.216; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Trypsin.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF_2.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF-like; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR HydroLase; Serine protease.
SQ SEQUENCE 469 AA; 52196 MW; 4C66C230D0758F6A CRC64;

Query Match 44.8%; Score 87; DB 6; Length 469;
Best Local Similarity 34.1%; Pred. No. 1.8e-07;
Matches 15; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

Oy 1 ANGFLXLRPGSLXRCXKXLCSEFXAHXIFRNXXRTQFWVSY 44
Db 41 ANSLFEELKGNLERECNEFTCSFEAREVEFTDKTNEFWNY 84

RESULT 16
ID Q95ME8 PRELIMINARY; PRT; 49 AA.
AC Q95ME8.
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE COAGULATION FACTOR IX (FRAGMENT).
OS Bos taurus (bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizlata M.N., Amaral E.J.;
RT "Partial sequence of bovine F9 coding gene.";
RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF394598; AAK7556.1; -.
FT NON_TER 1 1
FT SEQUENCE 49 AA; 6023 MW; D15C6DE9CCBA4A14 CRC64;

Query Match 44.3%; Score 86; DB 6; Length 49;
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Best Local Similarity 37.2%; Pred. No. 2.6e-08;
Matches 16; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

Oy 2 NGFLXLRPGSLXRCXKXLCSEFXAHXIFRNXXRTQFWVSY 44
Db 6 SGKLEEFVAGNLERECKEKCSEFEAREVEFTDKTNEFWNY 48

RESULT 17
ID Q28994 PRELIMINARY; PRT; 138 AA.
AC Q28994.
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MATURE PORCINE FACTOR IX (FRAGMENT).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=96003866; PubMed=7568220;
RA Brandstetter H., Bauer M., Huber R., Lollar P., Bode W.;
RT "X-ray structure of clotting factor IXa: active site and module
RT structure related to kase activity and hemophilia B.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:9796-9800(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Lollar P.;
RL Submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.
DR EMBL; U51135; AAA96318.1; -.
DR HSSP; P00740; IEDM.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR001438; EGF-II.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00094; gla; 2.
DR PRINTS; PR00010; EGFBLD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
FT NON_TER 1 1
FT NON_TER 138 138
FT SEQUENCE 138 AA; 15515 MW; 793BADE4D5FAFD CRC64;

Query Match 41.8%; Score 81; DB 6; Length 138;
Best Local Similarity 41.2%; Pred. No. 6.2e-07;
Matches 14; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

Oy 11 GSLXRCXKXLCSEFXAHXIFRNXXRTQFWVSY 44
Db 4 GNLRECEIEKCSFEAREVEFTDKTNEFWNY 37

RESULT 18
ID Q90YK1 PRELIMINARY; PRT; 433 AA.
AC Q90YK1.
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
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DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE COAGULATION FACTOR VII.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21353085; PubMed-11459993;
RA Sheehan J., Temple M., Gregory M., Hanumanthiah R., Troyer D.,
RA Phan T., Thankavel B., Jagadeeswaran P.;
RT "Demonstration of the extrinsic coagulation pathway in teleostei:
RT Identification of zebrafish coagulation factor VII."
RL Proc. Natl. Acad. Sci. U.S.A. 98:8768-8773(2001).
DR EMBL; AY040345; AAK74192.1; -.
SQ SEQUENCE 433 AA; 48680 MW; CD9D1B179601BA4C CRC64;

Query Match 41.2%; Score 80; DB 13; Length 433;
Best Local Similarity 32.6%; Pred. No. 3.1e-06;
Matches 14; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

QY 2 NGFLXLRPGSLKRCXKXLCSPFXAHXIFRNXXRTROFWVS 44
DB 40 SGWFEELKTGNLERECLEEKCSYEAREVEFHEATNEFWKTY 82

RESULT 19
ID 014669 PRELIMINARY; PRT; 202 AA.
AC 014669;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE PROLINE-RICH GLA PROTEIN 2.
GN PRGP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-97404347; PubMed-9256434;
RA Kulman J.D., Harris J.E., Haldeman B.A., Davie E.W.;
RT "Primary structure and tissue distribution of two novel proline-rich
RT gamma-carboxyglutamic acid proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997).
DR EMBL; AF009243; AAB67071.1; -.
DR HSSP; P00740; 1CFH.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
SQ SEQUENCE 202 AA; 22393 MW; BC79400C98492060 CRC64;

Query Match 40.7%; Score 79; DB 4; Length 202;
Best Local Similarity 40.0%; Pred. No. 2.1e-06;
Matches 16; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

QY 5 LXXLRGSLKRCXKXLCSPFXAHXIFRNXXRTROFWVS 44
DB 55 LELLTPGNLERECLEEKCSWEAREVEDNTLTERFWESY 94

RESULT 20
ID 015253 PRELIMINARY; PRT; 100 AA.
AC 015253;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
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DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE THROMBIN PRECURSOR (FRAGMENT).
GN F2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-87182874; PubMed-3471151;
RA MacGillivray R.T., Irvine D.M., Guinlo E.R., Stone J.C.;
RT "Recombinant genetic approaches to functional mapping of thrombin."
RL Ann. N. Y. Acad. Sci. 485:73-79(1986).
DR EMBL; M33031; AAA60220.1; -.
DR HSSP; P00735; 2PFL.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
KW SIGNAL.
FT SIGNAL 1 43 POTENTIAL.
FT CHAIN 44 >100 POTENTIAL.
FT NON_TER 100 100
SQ SEQUENCE 100 AA; 11302 MW; FD0B5D0174E1F6FE CRC64;

Query Match 40.2%; Score 78; DB 4; Length 100;
Best Local Similarity 36.4%; Pred. No. 1.6e-06;
Matches 16; Conservative 4; Mismatches 24; Indels 0; Gaps 0;

QY 1 ANGFLXLRPGSLKRCXKXLCSPFXAHXIFRNXXRTROFWVS 44
DB 44 ANTFLEEVKGNLERECVEECTCSYEAFALLESSTADIVWAKY 87

RESULT 21
ID 09BZD6 PRELIMINARY; PRT; 226 AA.
AC 09BZD6;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID PROTEIN 4 TMG4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-2117044; PubMed-11171957;
RA Kulman J.D., Harris J.E., Xie L., Davie E.W.;
RT "Identification of two novel transmembrane gamma-carboxyglutamic acid
RT proteins expressed broadly in fetal and adult tissues."
RL Proc. Natl. Acad. Sci. U.S.A. 98:1370-1375(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-PLACENTA, CHORIOCARCINOMA;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF326351; AAK00956.1; -.
DR EMBL; BC010052; AAH10052.1; -.
DR HSSP; P00740; 1CFH.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR000294; VitK_dep_GLA.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
SQ SEQUENCE 226 AA; 25403 MW; 45C783E3825797EE CRC64;
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Query Match 40.2%; Score 78; DB 4; Length 226;
 Best Local Similarity 37.5%; Pred. No. 3.7e-06;
 Matches 15; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

OY 5 LXXLRPGSLXRCXRXKXLCFFXAXHXIFRNXXRTROFWVS 44
 DB 57 LELFTPGNLERECNEELCNEYEARLEIFVDEKTIAMQRY 96

RESULT 22

O9PTW7 PRELIMINARY; PRT; 608 AA.
 ID O9PTW7;
 AC O9PTW7;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PROTHROMBIN.
 GN OSPT.
 OS Struthio camelus (Ostrich).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Palaeognathae; Struthioniformes; Struthionidae;
 OC Struthio.
 OC NCBI_TaxID=8801;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=20579470; PubMed=1137455;
 RA Frost C., Naude R., Oelofsen W., Muramoto K., Naganuma T., Ogawa T.;
 RT "Purification and characterization of ostrich prothrombin."
 RL Int. J. Biochem. Cell Biol. 32:1151-1159(2000).
 CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 DR EMBL; AB028871; BAA89046.1; -
 DR HSSP; P00734; IUVS.
 DR MEROPS; S01.217; -
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR001254; Trypsin.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam; PF00594; gla; 1.
 DR Pfam; PF00051; kringle; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR PRINTS; PR00018; KRINGLE.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00130; KR; 2.
 DR SMART; SM00020; TRYP_SPE; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS00021; KRINGLE_1; 2.
 DR PROSITE; PS00070; KRINGLE_2; 2.
 DR PROSITE; PS00240; TRYPsin_DOM; 1.
 DR PROSITE; PS00134; TRYPsin_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPsin_SER; 1.
 KW Hydrolase; Serine protease.
 SQ SEQUENCE 608 AA; 69392 MW; 11B974B9AE54EA2 CRC64;

Query Match 40.2%; Score 78; DB 13; Length 608;
 Best Local Similarity 33.3%; Pred. No. 1e-05;
 Matches 14; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

OY 3 GFLXLRPGSLXRCXRXKXLCFFXAXHXIFRNXXRTROFWVS 44
 DB 47 GFLXLRPGSLXRCXRXKXLCFFXAXHXIFRNXXRTROFWVS 88

RESULT 23

O29094 PRELIMINARY; PRT; 648 AA.
 AC O29094;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PROPEIN S (FRAGMENT).
 GN PROS.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 OC NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=95134217; PubMed=7832752;
 RA Greengard J.S., Fernandez J.A., Radtke K.P., Griffin J.H.;
 RT "Identification of candidate residues for interaction of protein S
 with C4b binding protein and activated protein C."
 RL Biochem. J. 305:397-403(1995).
 DR EMBL; L31379; AAA0382.1; -
 DR HSSP; P00740; ICFH.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001791; Laminin_G.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 4.
 DR Pfam; PF00594; gla; 1.
 DR Pfam; PF00054; laminin_G; 1.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 3.
 DR SMART; SM00001; EGF_like; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00282; lang; 2.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS0186; EGF_2; 3.
 DR PROSITE; PS0187; EGF_CA; 3.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
 FT NON_TER
 SQ SEQUENCE 648 AA; 71914 MW; 4BDF9ABBI3872136 CRC64;

Query Match 38.1%; Score 74; DB 6; Length 648;
 Best Local Similarity 36.4%; Pred. No. 5.8e-05;
 Matches 16; Conservative 5; Mismatches 23; Indels 0; Gaps 0;

OY 1 ANGFLXLRPGSLXRCXRXKXLCFFXAXHXIFRNXXRTROFWVS 44
 DB 15 ANSMLEERKQGNLERECIELCSKEAREVFENDPEYFYFAY 58

RESULT 24

O9COW3 PRELIMINARY; PRT; 399 AA.
 ID O9COW3;
 AC O9COW3;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE 1300015B06RIK PROTEIN.
 GN 1300015B06RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=STOMACH, AND LIVER;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,


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FT MOD_RES 20 20 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 25 25 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 26 26 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 29 29 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 32 32 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 35 35 GAMMA-CARBOXYGLUTAMIC ACID.
FT ACT_SITE 91 91 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 17 22 BY SIMILARITY.
FT DISULFID 47 52 BY SIMILARITY.
FT DISULFID 67 7 BY SIMILARITY.
FT NON_TER 98 98 BY SIMILARITY.
SQ SEQUENCE 98 AA; 11270 MW; 6FD398A3608DCFF3 CRC64;

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Query Match 33.5%; Score 65; DB 13; Length 98;
 Best Local Similarity 30.2%; Pred. No. 0.00037;
 Matches 13; Conservative 8; Mismatches 22; Indels 0; Gaps 0;

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QY 1 ANGFLXLRGSLKRXKRXHLCSEFXAHXIFRNXXRTQFWVS 43
Db 1 SNSLFEEIRPGNTERECIEKCSKEAREVFNDEKTXFXIVN 43

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RESULT 29
ID 014393 PRELIMINARY; PRT; 678 AA.
AC 014393;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GROWTH-ARREST-SPECIFIC PROTEIN.
GN GAS6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93330291; PubMed=8336730;
RA Manfioletti G., Brancolini C., Avanzi G., Schneider C.;
RT "The protein encoded by a growth arrest-specific gene (gas6) is a new
RT member of the vitamin K-dependent proteins related to protein S, a
RT negative coregulator in the blood coagulation cascade."
RL Mol. Cell. Biol. 13:4876-4985(1993).
DR EMBL: L13720; AA58494.1; -.
DR HSSP: P00740; ICFH.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001791; Laminin_G.
DR Pfam: PF00008; EGF_4.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00054; laminin_G; 1.
DR PRINTS: PRO0001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 3.
DR SMART: SM00001; EGF_Like; 1.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00282; LamG; 2.
DR PROSITE: PS00010; ASX_HYDROXYL; 4.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS0186; EGF_2; 3.
DR PROSITE: PS0187; EGF_CA; 3.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
SQ SEQUENCE 678 AA; 74925 MW; BB6D8AB0F6C48EA9 CRC64;

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Query Match 29.9%; Score 58; DB 4; Length 678;
 Best Local Similarity 36.1%; Pred. No. 0.052;
 Matches 13; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

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QY 9 RPSGLXRCXRXHLCSEFXAHXIFRNXXRTQFWVS 44
Db 57 KQGLHRECEVEELCSKEAREVFNDEPDTFYFPRY 92

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RESULT 30
ID 061592 PRELIMINARY; PRT; 673 AA.
AC 061592;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GAS6 PROTEIN.
GN GAS6 OR GAS6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Manfioletti G., Brancolini C., Bordo D., Philipson L., Schneider C.;
RT "Growth-arrest is associated with a negative control element in the
RT blood coagulation pathway."
RL Mol. Cell. Biol. 13:0-0(1993).
DR EMBL: X58646; CA042507.1; -.
DR HSSP: P00740; ICFH.
DR MGD: MGI:95660; Gas6.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001791; Laminin_G.
DR InterPro: IPR000294; VltK_dep_GLA.
DR Pfam: PF00008; EGF_4.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00054; laminin_G; 2.
DR PRINTS: PRO0001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 3.
DR SMART: SM00001; EGF_Like; 1.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00282; LamG; 2.
DR PROSITE: PS00010; ASX_HYDROXYL; 4.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS0186; EGF_2; 3.
DR PROSITE: PS0187; EGF_CA; 3.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
SQ SEQUENCE 673 AA; 74512 MW; 6A49B3F004F92815 CRC64;

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Query Match 29.4%; Score 57; DB 11; Length 673;
 Best Local Similarity 33.3%; Pred. No. 0.078;
 Matches 12; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

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QY 9 RPSGLXRCXRXHLCSEFXAHXIFRNXXRTQFWVS 44
Db 54 KQGLHRECEVEELCSKEAREVFNDEPDTFYFPRY 89

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RESULT 31
ID 099K57 PRELIMINARY; PRT; 674 AA.
AC 099K57;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GROWTH ARREST SPECIFIC 6.
GN GAS6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

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RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC005444; AAH05444.1; -.
 DR HSSP: P00740; ICFH.
 DR MGD: MGI:95660; Gas6.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001791; Laminin_G.
 DR InterPro: IPR000294; VltK_dep_GLA.
 DR Pfam: PF00008; EGF_4.
 DR Pfam: PF00594; gla; 1.
 DR Pfam: PF00054; laminin; 2.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00181; EGF_4.
 DR SMART: SM00179; EGF_CA; 4.
 DR SMART: SM00069; GLA; 1.
 DR SMART: SM00282; lang; 2.
 DR PROSITE: PS00010; ASX_HYDROXYL; 4.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE: PS01186; EGF_2; 3.
 DR PROSITE: PS01187; EGF_CA; 3.
 DR PROSITE: PS00011; GLU CARBOXYLATION; 1.
 KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
 SQ SEQUENCE 674 AA; 74609 MW; 7C41F7693903F401 CRC64;

Query Match 29.4%; Score 57; DB 11; Length 674;
 Best Local Similarity 33.3%; Pred. No. 0.079;
 Matches 12; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

Oy 9 RPSGLXRXCRXXLCSEFXAHXIFRNXXRTROFWSY 44
 Db 54 KQGLRECEVECVSKSEAREVFENDPETEYFPRY 89

RESULT 32
 ID 094EY5 PRELIMINARY; PRT; 431 AA.
 AC 094EY5;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE PUTATIVE MAP KINASE.
 GN F25P22.9.
 OS Arabidopsis thaliana (Mouse-ear cress).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eustosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lam B., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
 RA Palm C.J., Bowser L., Jones T., Banh J., Carinuci P., Chen H.,
 RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
 RA Kim C., Lin J., Liu S.X., Natrusaka M., Piam P.K., Sakano H.,
 RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
 RA Ecker J., Theologis A., Davis R.W.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF387019; AAK62464.1; -.
 KW KINASE.
 SQ SEQUENCE 431 AA; 49425 MW; 471AAFE18FD524C4 CRC64;

Query Match 29.1%; Score 56.5; DB 10; Length 431;
 Best Local Similarity 32.6%; Pred. No. 0.061;
 Matches 15; Conservative 5; Mismatches 23; Indels 3; Gaps 2;
 Oy 1 ANGFLXLRPGSL--XRXCRXXLCSEFXAHXIFRNXXRTROFWSY 44
 Db 210 ANVFHRLKPKNIILANADCKIKICDFGLARVSF-NDAPTAIFWTDY 254

RESULT 33
 ID 09MB23 PRELIMINARY; PRT; 543 AA.
 AC 09MB23;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE ATPK8.
 OS Arabidopsis thaliana (Mouse-ear cress).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eustosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA;
 RA Mizoguchi T., Ichimura K., Shinozaki K.;
 RT "Arabidopsi thaliana mRNA for MAP kinase";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB038693; BAA92222.1; -.
 DR HSSP: P24941; IHCL.
 DR InterPro: IPR000719; Euk_kinase.
 DR InterPro: IPR003527; MAP_kin.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR Pfam: PF00069; PKinase; 1.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PS01351; MAPK; UNKNOWN_1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 KW ATP-binding; Transferase.
 SQ SEQUENCE 543 AA; 61513 MW; 60D508FED40A94E9 CRC64;

Query Match 29.1%; Score 56.5; DB 10; Length 543;
 Best Local Similarity 32.6%; Pred. No. 0.078;
 Matches 15; Conservative 5; Mismatches 23; Indels 3; Gaps 2;

Oy 1 ANGFLXLRPGSL--XRXCRXXLCSEFXAHXIFRNXXRTROFWSY 44
 Db 224 ANVFHRLKPKNIILANADCKIKICDFGLARVSF-NDAPTAIFWTDY 268

RESULT 34
 ID 09C9U4 PRELIMINARY; PRT; 576 AA.
 AC 09C9U4;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE PUTATIVE MAP KINASE.
 GN F25P22.9.
 OS Arabidopsis thaliana (Mouse-ear cress).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eustosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV_COLUMBIA;
 RX MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Creasy T.H., Dewar K.,
 RA Dunn P., Etny P., Feldlyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
 RA Miltscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,


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RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC006931; AAD21721.1; -.
DR HSSP: P24941; 1B38.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_Kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS01351; MAPK; UNKNOWN; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR ATP-binding; Kinase; Transferase.
KW SEQUENCE 594 AA; 67275 MW; AEC31DAF90EE871E CRC64;

Query Match 28.1%; Score 54.5; DB 10; Length 594;
Best Local Similarity 30.4%; Pred. No. 0.2;
Matches 14; Conservative 6; Mismatches 23; Indels 3; Gaps 2;

Qy 1 ANGFLXLRPGSL--XRXCRLXCSFYXAHXIFRNXXRTQFVWSY 44
Db 133 ANYYHNDLRKKNILANANCKLKICDFGLARVAF-NDPTTTFWTDX 177

RESULT 41
Q9LPG7 PRELIMINARY; PRT; 603 AA.
AC 09LPG7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, last annotation update)
DE T3F20.17 PROTEIN (MAP KINASE ATPMPK9, PUTATIVE).
GN T3F20.17 OR F22G10.12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lee J.M., Vayberg M., Sakano H., Lenz C., Liu S.X., Pham P.,
RA Toriumi M., Yu G., Chin C., Chlou B., Choi E., Chung M., Gonzalez A.,
RA Homing B., Liu A., Altafi H., Brooks S., Buehler E., Chao Q., Conn L.,
RA Conway A.B., Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B.,
RA Miranda M., Nguyen M., Palm C.J., Shin P., Southwick A., Davis R.W.,
RA Ecker J.R., Federspiel N.A., Theologis A.;
RT "The sequence of BAC T3F20 from Arabidopsis thaliana chromosome 1.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA MEDLINE:21016719; PubMed=1130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Egu P., Feldhym T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultzer L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremetska I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Mafti R., Marshall A.,
RA Miltischer J., Miranda M., Nguyen M., Niernan W.C., Osborne B.I.,
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shin P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vayberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis

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RT thaliana.";
RL Nature 408:816-820(2000).
DR EMBL: AC018748; AAF78438.1; -.
DR EMBL: AC024260; AAG51978.1; -.
DR HSSP: P24941; 1HCL.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_Kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS01351; MAPK; UNKNOWN; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR ATP-binding; Kinase; Transferase.
KW SEQUENCE 603 AA; 67951 MW; DDFDB95CC372489D CRC64;

Query Match 28.1%; Score 54.5; DB 10; Length 603;
Best Local Similarity 30.4%; Pred. No. 0.2;
Matches 14; Conservative 6; Mismatches 23; Indels 3; Gaps 2;

Qy 1 ANGFLXLRPGSL--XRXCRLXCSFYXAHXIFRNXXRTQFVWSY 44
Db 133 ANYYHNDLRKKNILANANCKLKICDFGLARVAF-NDPTTTFWTDX 177

RESULT 42
Q945L8 PRELIMINARY; PRT; 606 AA.
AC 0945L8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, last annotation update)
DE AT2G42880/F7D19.12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin S.X., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis cDNA clones.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF412082; AAL06535.1; -.
SQ SEQUENCE 606 AA; 68774 MW; F36B4BDF6BD78A1 CRC64;

Query Match 28.1%; Score 54.5; DB 10; Length 606;
Best Local Similarity 30.4%; Pred. No. 0.2;
Matches 14; Conservative 6; Mismatches 23; Indels 3; Gaps 2;

Qy 1 ANGFLXLRPGSL--XRXCRLXCSFYXAHXIFRNXXRTQFVWSY 44
Db 145 ANYYHNDLRKKNILANANCKLKICDFGLARVAF-NDPTTTFWTDX 189

RESULT 43
O04284 PRELIMINARY; PRT; 196 AA.
AC 004284;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, last annotation update)
DE MAP KINASE-LIKE PROTEIN (FRAGMENT).
GN SDHN-6R.

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OS Selaginella lepidophylla.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Lycopodiophyta; Isoetes; Selaginellales; Selaginellaceae;
OC Selaginella: 59777;
OX NCBI_TaxID=59777;
RN [1]
RP SEQUENCE FROM N.A.
RA Choi D.-W., Close T.J., Ieturraga G.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U96716; AAB57843.1; -.
DR HSSP: P27703; IERK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_kin.
DR Pfam: PF00069; Pkinase; 1.
DR PROSITE: PS01351; MAPK; UNKNOWN_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; kinase; transferase.
FT NON_TER 196 196
SQ SEQUENCE 196 AA; 22852 MW; 11417FAAE31CF72D CRC64;

Query Match 27.6%; Score 53.5; DB 10; Length 196;
Best Local Similarity 31.1%; Pred. No. 0.097;
Matches 14; Conservative 5; Mismatches 23; Indels 3; Gaps 2;
OY 2 NGFLXLRPGSL--XRCRXXLCSEFXAHXIFRNXXRTROFWSY 44
DB 137 NVFHRDLKPKNIILANSCKIKICDFGLARVAF--NDAPTAIFWTDY 180

RESULT 44
OQ9SE22 PRELIMINARY; PRT: 459 AA.
AC OQ9SE22;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MAP KINASE HOMOLOG.
GN MAPK2.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eubartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Cheong Y.H., Moon B.C., Kim J.K., Cho M.J.;
RL "Novel plant MAP kinases phosphorylate defense-related transcription factors."
RT Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF194416; AAF23903.1; -.
DR HSSP: P24941; IHCL.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS01351; MAPK; UNKNOWN_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; kinase; transferase.
SQ SEQUENCE 459 AA; 53308 MW; EAB944437373057F CRC64;

Query Match 27.6%; Score 53.5; DB 10; Length 459;
Best Local Similarity 30.4%; Pred. No. 0.23;
Matches 14; Conservative 6; Mismatches 23; Indels 3; Gaps 2;
OY 1 ANGFLXLRPGSL--XRCRXXLCSEFXAHXIFRNXXRTROFWSY 44
DB 133 ANVHRDLKPKNIILANSCKIKICDFGLARVAF--NDSPSTIFWTDY 177

RESULT 45
OQ9SMU7 PRELIMINARY; PRT: 492 AA.
AC OQ9SMU7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MAP KINASE PROTEIN (FRAGMENT).
OS Cicer arietinum (Chickpea) (Gardano).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Ciceraceae; Cicer.
OX NCBI_TaxID=3827;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, CASTELLANA; TISSUE=ETIOLATED EPICOTYLS;
RA Dopico B., Esteban R., Labrador E.;
RL "A MAP kinase is expressed in chickpea epicotyls."
RT Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ275316; CAB61750.1; -.
DR HSSP: Q16539; IWFC.
DR InterPro: IPR000719; Euk_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; kinase; transferase.
FT NON_TER 1
SQ SEQUENCE 492 AA; 55638 MW; 8791EF36365A6811 CRC64;

Query Match 27.6%; Score 53.5; DB 10; Length 492;
Best Local Similarity 30.4%; Pred. No. 0.25;
Matches 14; Conservative 6; Mismatches 23; Indels 3; Gaps 2;
OY 1 ANGFLXLRPGSL--XRCRXXLCSEFXAHXIFRNXXRTROFWSY 44
DB 33 ANVHRDLKPKNIILANSCKIKICDFGLARVAF--NDAPTSIFWTDY 77

RESULT 46
OQ9SPF0 PRELIMINARY; PRT: 506 AA.
AC OQ9SPF0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE BLAST AND WOUNDING INDUCED MITOGEN-ACTIVATED PROTEIN KINASE.
GN BMK1.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eubartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2008141; PubMed=10624015;
RA He C., Fong S.H., Yang D., Wang G.L.;
RT "BMK1, a novel MAP kinase induced by fungal infection and mechanical wounding in rice."
RL Mol. Plant Microbe Interact. 12:1064-1073(1999).
DR EMBL: AF177392; AAD52659.1; -.
DR HSSP: P24941; IHCL.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS01351; MAPK; UNKNOWN_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; kinase; transferase.
SQ SEQUENCE 506 AA; 57955 MW; 0CB538FDEB171F0B CRC64;

Query Match 27.6%; Score 53.5; DB 10; Length 506;
Best Local Similarity 30.4%; Pred. No. 0.26;
Matches 14; Conservative 6; Mismatches 23; Indels 3; Gaps 2;

OY 1 ANGFLXXLRPGL--XRXCXXLCSEFXAHXIFRNXXRTROFWVS 44
DB 133 ANVFHDLKPKNILANSCKLKICDGLARVSP-NDAPSAIFWTDY 177

RESULT 47
O9SE23 PRELIMINARY; PRT: 506 AA.

AC O9SE23; 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MAP KINASE HOMOLOG.
GN MAPK1.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Cheong Y.H., Moon B.C., Kim J.K., Cho M.J.;
RT "Novel plant MAP kinases phosphorylate defense-related transcription factors."
RT Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF194415; AAF23902.1; -.
DR HSSP: P24941; 1HCL.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS01351; MAPK; UNKNOWN_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 506 AA; 57945 MW; B05509010B2673C4 CRC64;

Query Match 27.6%; Score 53.5; DB 10; Length 506;
Best Local Similarity 30.4%; Pred. No. 0.26;
Matches 14; Conservative 6; Mismatches 23; Indels 3; Gaps 2;

OY 1 ANGFLXXLRPGL--XRXCXXLCSEFXAHXIFRNXXRTROFWVS 44
DB 133 ANVFHDLKPKNILANSCKLKICDGLARVSP-NDAPSAIFWTDY 177

RESULT 48
O9LUC3 PRELIMINARY; PRT: 593 AA.

AC O9LUC3; 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MITOGEN-ACTIVATED PROTEIN KINASE.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RT Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
SQ SEQUENCE FROM N.A.

RC STRAIN-COLUMBIA;
RX MEDLINE=20277480; PubMed=10819329;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty p1 and TAC RT clones."
RT DNA Res. 7:131-135(2000).
RL EMBL: AB023038; BAB02403.1; -.
DR HSSP: P24941; 1HCL.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS01351; MAPK; UNKNOWN_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 593 AA; 66812 MW; 466BF00A1319D23 CRC64;

Query Match 27.6%; Score 53.5; DB 10; Length 593;
Best Local Similarity 30.4%; Pred. No. 0.3;
Matches 14; Conservative 6; Mismatches 23; Indels 3; Gaps 2;

OY 1 ANGFLXXLRPGL--XRXCXXLCSEFXAHXIFRNXXRTROFWVS 44
DB 140 ANVFHDLKPKNILANACKLKVCDFGLARVSP-NDPTTFVFWTDY 184

RESULT 49
O9MB22 PRELIMINARY; PRT: 510 AA.

AC O9MB22; 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ATPK9.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizoguchi T., Ichimura K., Shinzaki K.;
RT "Arabidopsis thaliana mRNA for MAP kinase."
RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB038694; BAA92223.1; -.
DR HSSP: P27703; 1ERK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS01351; MAPK; UNKNOWN_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Transferase.
SQ SEQUENCE 510 AA; 58440 MW; 496BF0657F53C97 CRC64;

Query Match 27.1%; Score 52.5; DB 10; Length 510;
Best Local Similarity 30.4%; Pred. No. 0.39;
Matches 14; Conservative 6; Mismatches 23; Indels 3; Gaps 2;

OY 1 ANGFLXXLRPGL--XRXCXXLCSEFXAHXIFRNXXRTROFWVS 44
DB 143 ANVFHDLKPKNILANSCKLKICDGLARVSP-NDAPSAIFWTDY 187

RESULT 50

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Q9LV37
ID Q9LV37 PRELIMINARY; PRT; 619 AA.
AC Q9LV37;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MAP KINASE.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_Taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA.
RA Kaneo T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20363099; PubMed=10907853;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety P1,
RT TAC and BAC clones.";
RL DNA Res. 7:217-221(2000).
DR EMBL; AB020749; BAB02016.1; -.
DR HSP; P24941; IHCL.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003527; MAP_kin.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase.1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS01351; MAPK; UNKNOWN_1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 619 AA; 70770 MW; 9AB2B461058ED2DB CRC64;

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Query Match          27.1%; Score 52.5; DB 10; Length 619;
Best Local Similarity 30.4%; Pred. No. 0.48;
Matches 14; Conservative 6; Mismatches 23; Indels 3; Gaps 2;

QY 1 ANGFLLXLRGSL--XRXCRXXLCFXXAHXIFRNXXRTROFWVSY 44
   ||| \ | : : : | : | | | | : | | |
Db 252 ANVFHRLKPKNIANSDCIKLKICDFGIARVSF-NDAPSAIFWTDY 296

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Search completed: August 30, 2002, 15:44:06
Job time: 821 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 3, 2002, 15:01:52 ; Search time 51.38 Seconds
(without alignments)
95.120 Million cell updates/sec

Title: US-09-302-239-3-COPY
Perfect score: 182
Sequence: 1 ANAFLXLRGSLRXCKKX.....XXAXXIFDAXRFLFWISY 44

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 50 summaries

Database : A-Geneseq_032802:*

- 1: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT:*
- 2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT:*
- 3: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT:*
- 4: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT:*
- 5: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT:*
- 6: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT:*
- 7: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT:*
- 8: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT:*
- 9: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT:*
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- 13: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT:*
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- 15: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT:*
- 16: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT:*
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- 18: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT:*
- 19: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT:*
- 20: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	158	86.8	44	20	AAV18310
2	158	86.8	44	20	AAV18311
3	157	86.3	44	20	AAV18312
4	157	86.3	44	20	AAV18305
5	157	86.3	44	22	AAAB36395
6	157	86.3	401	22	AAAB84870
7	157	86.3	401	22	AAAB84871
8	157	86.3	406	14	AAAB35764
9	157	86.3	406	18	AAW14509
10	157	86.3	406	18	AAW14510
11	157	86.3	406	22	AAW52171

X C residues
10 + 28

12	157	86.3	406	22	AAW52172	Mammalian expresse
13	157	86.3	406	22	AAW52181	Human FVII mutant
14	157	86.3	406	22	AAW52182	Human FVII mutant
15	157	86.3	406	22	AAW52183	Human FVII mutant
16	157	86.3	406	22	AAW52184	Human FVII mutant
17	157	86.3	406	22	AAW52185	Human FVII mutant
18	157	86.3	406	22	AAW52186	Human FVII mutant
19	157	86.3	406	22	AAW52187	Human FVII mutant
20	157	86.3	406	22	AAW52188	Human FVII mutant
21	157	86.3	406	22	AAW52189	Human FVII mutant
22	157	86.3	406	22	AAW52190	Human FVII mutant
23	157	86.3	406	22	AAW52191	Human FVII mutant
24	157	86.3	406	22	AAW52192	Human FVII mutant
25	157	86.3	406	22	AAW52193	Human FVII mutant
26	157	86.3	406	22	AAW52194	Human FVII mutant
27	157	86.3	406	22	AAW52195	Human FVII mutant
28	157	86.3	406	22	AAW52196	Human FVII mutant
29	157	86.3	406	22	AAW52197	Human FVII mutant
30	157	86.3	406	22	AAW52198	Human FVII mutant
31	154	84.6	44	20	AAV18302	Modified blood coa
32	153	84.1	406	18	AAW14507	Modified blood coa
33	151	83.0	44	20	AAV18313	Modified blood coa
34	151	83.0	406	18	AAW14508	Modified blood coa
35	147	80.8	406	18	AAW14511	Modified blood coa
36	142	78.0	41	16	AAW11904	Modified blood coa
37	133	73.1	406	18	AAW14506	Modified blood coa
38	121	66.5	44	20	AAV18306	Modified blood coa
39	121	66.5	44	20	AAV18306	Modified blood coa
40	112	61.5	345	22	AAU02959	Factor VII
41	105	57.7	139	17	AAU02959	Factor VII
42	101	55.5	453	7	AAU02959	Factor VII
43	96	52.7	250	12	AAU02959	Factor VII
44	96	52.7	436	13	AAU02959	Factor VII
45	96	52.7	448	14	AAU02959	Factor VII
46	96	52.7	448	14	AAU02959	Factor VII
47	96	52.7	448	19	AAU02959	Factor VII
48	96	52.7	467	19	AAU02959	Factor VII
49	96	52.7	488	13	AAU02959	Factor VII
50	96	52.7	488	13	AAU02959	Factor VII

ALIGNMENTS

RESULT 1	AAV18310	standard: peptide; 44 AA.
ID	AAV18310;	
AC	AAV18310;	
XX		
DE	17-AUG-1999 (first entry)	
XX		
DE	Modified GLA domain of vitamin K-dependent protein.	
XX		
KW	GLA domain; muten; vitamin K-dependent protein; clotting disorder;	
KM	therapy.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
XX		
FT	Key	Location/Qualifiers
FT	Misc-difference 1..44	/note="Xaa" gamma-carboxyglutamic acid, or glutamic acid"
FT		
XX		
XX	WO920767-A1.	
XX	29-APR-1999.	
XX		
XX	20-OCT-1998.	98WO-US22152.
XX		
XX	23-OCT-1997.	97US-0955636.
XX		

Best Local Similarity 95.5%; Pred. No. 5e-20;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ANAFLLXLRXGSLRXCKXXQCSFXAXXIFKDXARTKLFWISY 44
|||||
Db 1 anaflxxlrpgslrxckxxqcsfxaxxfkdxartklfwlsy 44

RESULT 4

AAI18305
ID AAY18305 standard; peptide: 44 AA.

AC AAY18305;

DT 17-NOV-1999 (first entry)

DE Human factor VII GLA domain.

KW GLA domain; vitamin K-dependent protein; clotting disorder;

OS Homo sapiens.

PI Key Location/Qualifiers

FT Misc-difference 1..44
FT /note="Xaa=gamma-carboxyglutamic acid, or glutamic acid"

PN WO9920767-A1.

PD 29-APR-1999.

PF 20-OCT-1998; 98WO-US22152.

PR 23-OCT-1997; 97US-0955636.

PA (MINU) UNIV MINNESOTA.

PI Nelsstuen GL;

DR WPI; 1999-288309/24.

PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
acid domain, useful for treating clotting disorders

PS Disclosure: Page 15; 86pp; English.

CC This sequence is the factor VII GLA (gamma-carboxyglutamic acid)
CC domain. The invention relates to a vitamin K-dependent polypeptide
CC comprising a modified GLA domain containing an amino acid substitution
CC which enhances membrane binding of the modified polypeptide as compared
CC to the native polypeptide. The polypeptide is used to treat a clotting
CC disorder by decreasing or increasing clot formation. Modification of the
CC GLA domain results in a protein which has enhanced membrane binding
CC affinity as compared to the native protein.

SQ Sequence 44 AA;

Query Match 86.3%; Score 157; DB 20; Length 44;
Best Local Similarity 95.5%; Pred. No. 5e-20;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ANAFLLXLRXGSLRXCKXXQCSFXAXXIFKDXARTKLFWISY 44
|||||
Db 1 anaflxxlrpgslrxckxxqcsfxaxxfkdxartklfwlsy 44

RESULT 5

AAI18305
ID AAB36395 standard; peptide: 44 AA.

AC AAB36395;

XX 27-FEB-2001 (first entry)

DE Human factor VII gamma-carboxyglutamic acid domain SEQ ID NO:3.

KW Vitamin K-dependent protein; factor VII; protein C; GLA domain;

KW gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;

KW factor X; prothrombin; enhanced membrane binding affinity;

KW clot formation; thrombolytic; haemostatic; bleeding disorder;

KW thrombosis; clotting disorder; haemophilia A; haemophilia B;

OS Homo sapiens.

PI WO200066753-A2.

PD 09-NOV-2000.

PF 28-APR-2000; 2000WO-US11416.

PR 29-APR-1999; 99US-0302239.

PA (MINU) UNIV MINNESOTA.

PI Nelsstuen GL;

DR WPI; 2001-007226/01.

PT Novel vitamin K-dependent polypeptide useful for treating clotting
disorders such as thrombosis and hemophilia, comprises modified
PT gamma-carboxy glutamic acid domain that enhances membrane binding
PT affinity

PS Disclosure: Page 12; 81pp; English.

CC The present invention describes a vitamin K-dependent polypeptide (I)
CC comprising a modified gamma-carboxy glutamic acid (GLA) domain having
CC at least one amino acid substitution, that enhances membrane binding
CC affinity and the activity of the polypeptide relative to a corresponding
CC native vitamin K-dependent polypeptide and inhibits clot formation.
CC (I) can have thrombolytic and haemostatic activities, and can be used
CC as an inhibitor of clot formation. (I) is useful for decreasing clot
CC formation in a mammal, a factor VII or factor IX containing a modified
CC GLA domain is useful for increasing clot formation and for treating a
CC bleeding disorder, including thrombosis and clotting disorders such as
CC haemophilia A, haemophilia B and liver disease. The present sequence
CC represents a wild type human factor VII GLA domain sequence, given in
CC the exemplification of the present invention.

SQ Sequence 44 AA;

Query Match 86.3%; Score 157; DB 22; Length 44;
Best Local Similarity 95.5%; Pred. No. 5e-20;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ANAFLLXLRXGSLRXCKXXQCSFXAXXIFKDXARTKLFWISY 44
|||||
Db 1 anaflxxlrpgslrxckxxqcsfxaxxfkdxartklfwlsy 44

RESULT 6

AAI18305
ID AAB84870 standard; Protein: 401 AA.

AC AAB84870;

DT 31-JUL-2001 (first entry)

DE Mutant blood coagulant factor VII (FVII-31).

KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;

KW mutant; munein.

```
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key
XX FT MISC-difference 311..317
XX FT /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp
XX FT -Ser-Pro-Asn substituted by Gln-Ala-Ser-Tyr-Pro-Gly-Lys"
XX PN JP2001061479-A.
XX PD 13-MAR-2001.
XX PE 24-AUG-1999; 99JP-0237610.
XX PR 24-AUG-1999; 99JP-0237610.
XX PA (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX DR WPI; 2001-310677/33.
XX DR N-PSDB; AAH19463.
XX PT Mutant of blood coagulant factor VII, used for substitution therapy in
XX PT the treatment of hemophilia -
XX PS Claim 14; Page 20-21; 29pp; Japanese.
XX PS The present invention relates to mutants of blood coagulant factor VII
XX CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
XX CC sequence is one such mutant FVII: VII-31. The mutants can be used as an
XX CC agent for the substitution therapy of haemophilia inhibitor patients.
XX SQ Sequence 401 AA;

Query Match 86.3%; Score 157; DB 22; Length 401;
Best Local Similarity 72.7%; Pred. No. 4.6e-19;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLLXLRXGSLRXKCKXKXQCSFXKXAXIFKDXRRTKLFWISY 44
Db 1 anafleelrpslrekeegcsfeearelfkdaertklfwisy 44

RESULT 7
AAB84871
ID AAB84871 standard; Protein: 401 AA.
XX
AC AAB84871;
XX
DT 31-JUL-2001 (first entry)
XX
DE Mutant blood coagulant factor VII (FVII-39).
XX
XX Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
XX KM mutant; mutlein.
XX OS Homo sapiens.
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX FT MISC-difference 235..239
XX FT /note= "Wild-type Val-Pro-Gly-Thr-Thr substituted by
XX FT Asp-Arg-Lys-Thr-Leu"
XX FT MISC-difference 311..317
XX FT /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp
XX FT -Ser-Pro-Asn substituted by Gln-Ala-Ser-Tyr-Pro-Gly-Lys"
XX PN JP2001061479-A.
XX PD 13-MAR-2001.
XX PE 24-AUG-1999; 99JP-0237610.
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XX PR 24-AUG-1999; 99JP-0237610.
XX PA (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX DR WPI; 2001-310677/33.
XX DR N-PSDB; AAH19464.
XX PT Mutant of blood coagulant factor VII, used for substitution therapy in
XX PT the treatment of hemophilia -
XX PS Claim 16; Page 23-24; 29pp; Japanese.
XX PS The present invention relates to mutants of blood coagulant factor VII
XX CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
XX CC sequence is one such mutant FVII: VII-39. The mutants can be used as an
XX CC agent for the substitution therapy of haemophilia inhibitor patients.
XX SQ Sequence 401 AA;

Query Match 86.3%; Score 157; DB 22; Length 401;
Best Local Similarity 72.7%; Pred. No. 4.6e-19;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLLXLRXGSLRXKCKXKXQCSFXKXAXIFKDXRRTKLFWISY 44
Db 1 anafleelrpslrekeegcsfeearelfkdaertklfwisy 44

RESULT 8
AAR35764
ID AAR35764 standard; Protein: 406 AA.
XX
AC AAR35764;
XX
DT 24-SEP-1993 (first entry)
XX
DE Factor VII (VII).
XX
XX PC; protein C; IX; Factor IX; X; Factor X; PT; prothrombin; VII;
XX KM Factor VII; CT; chymotrypsinogen; SP; serine protease; binding;
XX KM exosite; catalytic activity.
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT Region 1..152 "Factor VII light chain"
XX FT /note= "Factor VII light chain"
XX FT Region 153..406
XX FT /note= "Factor VII heavy chain"
XX FT Peptide 374..388
XX FT /note= "exosite 1"
XX FT Peptide 290..310
XX FT /note= "exosite 2"
XX FT Peptide 290..310
XX FT /note= "pref. PC polypeptide; claim 2, page 136"
XX FT Peptide 374..388
XX FT /note= "pref. PC polypeptide; claim 2, page 136"
XX FT Peptide 289..304
XX FT /note= "pref. PC polypeptide; claim 4, page 137"
XX FT Peptide 290..304
XX FT /note= "pref. PC polypeptide; claim 4, page 137"
XX FT Peptide 245..266
XX FT /note= "claim 9, page 138-139 describes an antibody
XX FT that reacts with Factor VII; fragments
XX FT 289-304, 290-304, 290-310, 374-388 and
XX FT 400-414 but not with fragment 245-266"
XX PN WO9309804-A.
XX PD 27-MAY-1993.
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PF 18-NOV-1992; 92WO-US10242.
 XX
 PR 18-NOV-1991; 91US-0793989.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Griffin JH, Masters RM;
 XX
 DR WPI: 1993-182244/22.
 XX
 XX Serine protease derived-polypeptide(s) and anti-peptide
 PT antibodies - for inhibiting coagulation and assaying for the
 PT presence of serine protease in fluid samples
 XX
 PS Disclosure: Page 133-135; 149pp; English.
 XX
 CC The PC polypeptides indicated in the Features Table inhibit
 CC coagulation (they prevent binding of serine protease to natural
 CC substrates), esp. when admin. to give an intravascular blood
 CC concn. of 0.1-100 (pref. 0.5-10) microm.
 CC NB: Sequences corresp. to SEQ ID NO 6, 7, 8 and 9 are described
 CC in the specification but have not yet been added to the SEQUENCE
 CC LISTING.
 CC
 SQ Sequence 406 AA:
 Query Match 86.3%; Score 157; DB 14; Length 406;
 Best Local Similarity 72.7%; Pred. No. 4,7e-19;
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLRXRCXKCSFFXAXXIFKDXARTKLEWTSY 44
 Db 1 anafleellrpslreecqcsfsearelfkdaertklfwasy 44

RESULT 9
 AAM14509
 ID AAM14509 standard; protein; 406 AA.
 AC AAM14509;
 XX
 DT 14-MAY-1997 (first entry)
 XX
 DE Modified blood coagulation Factor VII (R290S).
 XX
 KW Blood coagulation; factor 7; mutain; mutation; modification;
 KW thrombocytopenia; von Willebrand's disease; plasma substitute.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX
 FT Key Location/Qualifiers
 FT FH 6
 FT Modified-site /label= OTHER
 FT /note= "gamma-carboxylutamic acid"
 FT Modified-site 7
 FT /label= OTHER
 FT /note= "gamma-carboxylutamic acid"
 FT Modified-site 14
 FT /label= OTHER
 FT /note= "gamma-carboxylutamic acid"
 FT Modified-site 16
 FT /label= OTHER
 FT /note= "gamma-carboxylutamic acid"
 FT Modified-site 19
 FT /label= OTHER
 FT /note= "gamma-carboxylutamic acid"
 FT Modified-site 20
 FT /label= OTHER
 FT /note= "gamma-carboxylutamic acid"
 FT Disulfide-bond 17..22
 FT Modified-site 25

FT /label= OTHER
 FT /note= "gamma-carboxylutamic acid"
 FT Modified-site 26
 FT /label= OTHER
 FT /note= "gamma-carboxylutamic acid"
 FT Modified-site 29
 FT /label= OTHER
 FT /note= "gamma-carboxylutamic acid"
 FT Cleavage-site 32..33
 FT /note= "proteolytic site"
 FT Modified-site 35
 FT /label= OTHER
 FT /note= "gamma-carboxylutamic acid"
 FT Cleavage-site 38..39
 FT /note= "proteolytic site"
 FT Cleavage-site 42..43
 FT /note= "proteolytic site"
 FT Cleavage-site 44..45
 FT /note= "proteolytic site"
 FT Disulfide-bond 50..51
 FT Disulfide-bond 55..70
 FT Modified-site 63
 FT /label= OTHER
 FT /note= "beta-hydroxy-aspartic acid"
 FT Disulfide-bond 72..81
 FT /note= "proteolytic site"
 FT Disulfide-bond 91..102
 FT /note= "proteolytic site"
 FT Disulfide-bond 98..112
 FT /note= "proteolytic site"
 FT Disulfide-bond 114..127
 FT /note= "proteolytic site"
 FT Disulfide-bond 135..162
 FT /note= "proteolytic site"
 FT Cleavage-site 143..144
 FT /note= "proteolytic site"
 FT Modified-site 145
 FT /note= "proteolytic site"
 FT Disulfide-bond 159..164
 FT /note= "proteolytic site"
 FT Disulfide-bond 178..194
 FT /note= "proteolytic site"
 FT Active-site 193
 FT Active-site 242
 FT Active-site 344
 FT Cleavage-site 290..291
 FT /note= "proteolytic site in unmodified factor VII"
 FT /note= "proteolytic site in unmodified factor VII"
 FT Misc-difference 290
 FT /note= "native Arg290 has been substituted by Ser to provide a proteolytically more stable peptide bond"
 FT Disulfide-bond 310..329
 FT /note= "proteolytic site"
 FT Cleavage-site 315..316
 FT /note= "proteolytic site"
 FT Modified-site 322
 FT /note= "glycosylation site"
 FT Disulfide-bond 340..368
 FT /note= "proteolytic site"
 FT Cleavage-site 341..342
 FT /note= "proteolytic site"
 FT Cleavage-site 392..393
 FT /note= "proteolytic site"
 FT Cleavage-site 396..397
 FT /note= "proteolytic site"
 FT Cleavage-site 402..403
 FT /note= "proteolytic site"
 FT US580560-A.
 FT PD 03-DEC-1996.
 FT XX
 FT PF 13-NOV-1989; 89US-0434149.
 FT XX
 FT PR 09-AUG-1993; 93US-0104509.
 FT PR 13-NOV-1989; 89US-0434149.
 FT PR 12-JUN-1992; 92US-0898248.
 FT PR 22-AUG-1994; 94US-0293778.
 FT XX
 FT PA (NOVO) NOVO-NORDISK AS.
 FT BI Bjorn SE, Nicolaisen EM, Wiberg FC, Woodbury R;


```

XX Factor VII; FVII: Factor VIIa; FVIIa: haemostatic; thrombolytic;
KW cardiant; hepatotrophic; cerebroprotective; haemophilia; liver disease;
KW myocardial infarction; thrombotic stroke; deep-vein thrombosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 52
FT Modified-site /note= "O-glycosylated"
FT Modified-site 60
FT Modified-site /note= "O-glycosylated"
FT Modified-site 145
FT Modified-site /note= "N-glycosylated"
FT Cleavage-site 152..153
FT /note= "proteolytic cleavage site converting FVII zymogen
FT to an activated form, comprising two chains
FT linked by a single disulphide bridge"
FT Modified-site 322
FT /note= "N-glycosylated"
XX
PN WO200158935-A2.
XX
PD 16-AUG-2001.
XX
PE 12-FEB-2001; 2001WO-DK00094.
XX
PR 11-FEB-2000; 2000DK-0000218.
PR 18-OCT-2000; 2000DK-0001558.
XX
PA (MAXY-) MAXGEN APS.
XX
PI Andersen KV, Pedersen AH, Bornaes C;
XX
DR WPI; 2001-581807/65.
DR N-PSDB; AAI99983.
XX
PT New conjugate, useful for treating Factor VIIa related diseases or
PT disorders such as haemophilia, liver disease, myocardial infarction and
PT deep-vein thrombosis, comprises non-polypeptide group covalently
PT attached to polypeptide group -
XX
PS Disclosure; Page 85-86; 89pp; English.
XX
XX The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
CC polypeptide conjugates, comprising at least one non-polypeptide group
CC covalently attached to a polypeptide, where the amino acid sequence of
CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
CC least one amino acid residue containing an attachment group for the
CC non-polypeptide group has been introduced or removed. The FVIIa
CC conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and
CC cerebroprotective activity and are useful for treating FVIIa/VF-related
CC diseases or disorders such as haemophilia, liver disease, myocardial
CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
CC have increased functional in vivo half life and/or increased plasma half
CC life, increased bioavailability and/or reduced sensitivity to proteolytic
CC degradation. Consequently medical treatment using the conjugates has a
CC number of advantages over currently available such as longer duration
CC between injections.
XX
SQ Sequence 406 AA;

```

```

Query Match 86.3%; Score 157; DB 22; Length 406;
Best Local Similarity 72.7%; Pred. NO. 4.7e-19;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

```

```

OY 1 ANAFLLXLRGSLCKRXKXXQCSPXAXIFKDXRRTKLFRTSY 44
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 anafllelrpplslerckeegcsfearelfkdaerklwisyy 44

```

RESULT 13

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AAM52181
ID AAM52181 standard; Protein; 406 AA.
XX
XX AAM52181;
AC
XX
DT 07-FEB-2002 (first entry)
XX
DE Human FVII mutant T106N.
XX
KW Factor VII; FVII; Factor VIIa; FVIIa: haemostatic; thrombolytic;
KW cardiant; hepatotrophic; cerebroprotective; haemophilia; liver disease;
KW myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;
KW mucin.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT MISC-difference 6
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT MISC-difference 7
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT MISC-difference 14
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT MISC-difference 16
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT MISC-difference 19
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT MISC-difference 20
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT MISC-difference 25
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT MISC-difference 26
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT MISC-difference 29
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT MISC-difference 35
FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Modified-site 52
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Modified-site 60
FT /note= "O-glycosylated"
FT MISC-difference 106
FT /note= "O-glycosylated"
FT Modified-site 145
FT /note= "Wild-type Thr substituted by Asn"
FT Cleavage-site 152..153
FT /note= "proteolytic cleavage site converting FVII zymogen
FT to an activated form, comprising two chains
FT linked by a single disulphide bridge"
FT Modified-site 322
FT /note= "N-glycosylated"
XX
XX WO200158935-A2.
XX
PD 16-AUG-2001.
XX
PE 12-FEB-2001; 2001WO-DK00094.
XX
PR 11-FEB-2000; 2000DK-0000218.
PR 18-OCT-2000; 2000DK-0001558.
XX
PA (MAXY-) MAXGEN APS.

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XX Andersen KV, Pedersen AH, Bornaes C;
 XX WPI: 2001-581807/65.
 XX
 XX New conjugate, useful for treating Factor VIIa related diseases or
 PT disorders such as haemophilia, liver disease, myocardial infarction and
 PT deep-vein thrombosis, comprises non-polypeptide group covalently
 PT attached to polypeptide group -
 XX
 PS Example 3; Page -: 89pp; English.
 XX
 CC The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
 CC polypeptide conjugates, comprising at least one non-polypeptide group
 CC covalently attached to a polypeptide, where the amino acid sequence of
 CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
 CC least one amino acid residue containing an attachment group for the
 CC non-polypeptide group has been introduced or removed. The FVIIa
 CC conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and
 CC cerebroprotective activity and are useful for treating FVIIa/TF-related
 CC diseases or disorders such as haemophilia, liver disease, myocardial
 CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
 CC have increased functional in vivo half life and/or increased plasma half
 CC life, increased bioavailability and/or reduced sensitivity to proteolytic
 CC degradation. Consequently medical treatment using the conjugates has a
 CC number of advantages over currently available such as longer duration
 CC between injections. The present sequence is that of a human FVII mutant,
 CC having an addition in vivo glycosylation site and tested for its
 CC amidolytic activity.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from the human wild-type FVII sequence shown in SEQ ID NO 1
 CC (AAM52171).
 XX
 SQ Sequence 406 AA:

Query Match 86.3%; Score 157; DB 22; Length 406;
 Best Local Similarity 95.5%; Pred. NO. 4.7e-19;
 Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ANAFLXXLRXGSLRXKXGXGCFXXAXIFKDXRRTKLEWISY 44
 |||||||
 Db 1 anaflxxlrpyslrxckxxgcsfxaxrxifkdxrtklfwisy 44

RESULT 14
 AAM52182
 ID AAM52182 standard; Protein: 406 AA.
 XX
 AC AAM52182;
 XX
 DT 07-FEB-2002 (first entry)
 XX
 DE Human FVII mutant K143N/N145T.
 XX
 KW Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
 KW cardiant; hepatotrophic; cerebroprotective; haemophilia; liver disease;
 KW myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;
 KW mutlein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 6 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT Misc-difference 7 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT Misc-difference 14 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT

FT Misc-difference 16 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT Misc-difference 19 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT Misc-difference 20 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT Misc-difference 25 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT Misc-difference 26 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT Misc-difference 29 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT Misc-difference 35 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT Modified-site 52 /note= "OTHER = gamma carboxyglutamic acid"
 FT Modified-site 60 /note= "O-glycosylated"
 FT Misc-difference 143 /note= "O-glycosylated"
 FT Misc-difference 145 /note= "Wild-type Lys substituted by Asn"
 FT Misc-difference 152..153 /note= "Wild-type Asn substituted by Thr"
 FT Cleavage-site /note= "proteolytic cleavage site converting FVII zymogen
 FT to an activated form, comprising two chains
 FT linked by a single disulphide bridge"
 FT Modified-site 322 /note= "N-glycosylated"
 FT
 PN WO200158935-A2.
 XX
 PD 16-AUG-2001.
 XX
 XX 12-FEB-2001; 2001WO-DK00094.
 XX
 XX 11-FEB-2000; 2000DK-0000218.
 PR 18-OCT-2000; 2000DK-0001558.
 XX
 XX (MAXY-) MAXYGEN APS.
 PA
 XX
 XX Andersen KV, Pedersen AH, Bornaes C;
 XX WPI: 2001-581807/65.
 XX
 XX New conjugate, useful for treating Factor VIIa related diseases or
 PT disorders such as haemophilia, liver disease, myocardial infarction and
 PT deep-vein thrombosis, comprises non-polypeptide group covalently
 PT attached to polypeptide group -
 XX
 PS Example 3; Page -: 89pp; English.
 XX
 CC The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
 CC polypeptide conjugates, comprising at least one non-polypeptide group
 CC covalently attached to a polypeptide, where the amino acid sequence of
 CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
 CC least one amino acid residue containing an attachment group for the
 CC non-polypeptide group has been introduced or removed. The FVIIa
 CC conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and
 CC cerebroprotective activity and are useful for treating FVIIa/TF-related
 CC diseases or disorders such as haemophilia, liver disease, myocardial
 CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
 CC have increased functional in vivo half life and/or increased plasma half
 CC life, increased bioavailability and/or reduced sensitivity to proteolytic
 CC degradation. Consequently medical treatment using the conjugates has a
 CC number of advantages over currently available such as longer duration
 CC between injections. The present sequence is that of a human FVII mutant,

XX Factor VII: FVII; Factor VIIa: FVIIa; haemostatic; thrombolytic;
 KW cardiatic; hepatotropic; cerebroprotective; haemophilia; liver disease;
 KW myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;
 KM mutain.
 XX Homo sapiens.
 OS Synthetic.
 XX Key Location/Qualifiers
 FT Misc-difference 6 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxylutamic acid"
 FT Misc-difference 7 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxylutamic acid"
 FT Misc-difference 14 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxylutamic acid"
 FT Misc-difference 16 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxylutamic acid"
 FT Misc-difference 19 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxylutamic acid"
 FT Misc-difference 20 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxylutamic acid"
 FT Misc-difference 25 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxylutamic acid"
 FT Misc-difference 26 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxylutamic acid"
 FT Misc-difference 29 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxylutamic acid"
 FT Misc-difference 35 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxylutamic acid"
 FT Modified-site 52 /note= "O-glycosylated"
 FT Modified-site 60 /note= "O-glycosylated"
 FT Modified-site 145 /note= "N-glycosylated"
 FT Cleavage-site 152..153 /note= "proteolytic cleavage site converting FVII zymogen to an activated form, comprising two chains linked by a single disulphide bridge"
 FT Misc-difference 290 /note= "Wild-type Arg substituted by Asn"
 FT Misc-difference 292 /note= "Wild-type Ala substituted by Thr"
 FT Modified-site 322 /note= "N-glycosylated"
 XX WO200158935-A2.
 XX 16-AUG-2001.
 XX 12-FEB-2001; 2001WO-DK00094.
 XX 11-FEB-2000; 2000DK-0000218.
 XX 18-OCT-2000; 2000DK-0001558.
 XX (MAXY-) MAXGEN APS.
 XX Andersen KV, Pedersen AH, Bornaes C;
 DR WPI: 2001-581807/65.
 XX New conjugate, useful for treating Factor VIIa related diseases or

PT disorders such as haemophilia, liver disease, myocardial infarction and
 PT deep-vein thrombosis, comprises non-polypeptide group covalently
 PT attached to polypeptide group -
 XX Example 3; Page -: 89pp; English.
 PS
 CC The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
 CC polypeptide conjugates, comprising at least one non-polypeptide group
 CC covalently attached to a polypeptide, where the amino acid sequence of
 CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
 CC least one amino acid residue containing an attachment group for the
 CC non-polypeptide group has been introduced or removed. The FVIIa
 CC conjugates have haemostatic, thrombolytic, cardiatic, hepatotropic and
 CC cerebroprotective activity and are useful for treating FVIIa/TF-related
 CC diseases or disorders such as haemophilia, liver disease, myocardial
 CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
 CC have increased functional in vivo half life and/or increased plasma half
 CC life, increased bioavailability and/or reduced sensitivity to proteolytic
 CC degradation. Consequently medical treatment using the conjugates has a
 CC number of advantages over currently available such as longer duration
 CC between injections. The present sequence is that of a human FVII mutant,
 CC having an addition in vivo glycosylation site and tested for its
 CC amidolytic activity.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from the human wild-type FVII sequence shown in SEQ ID NO 1
 CC (AAM52171).
 XX Sequence 406 AA;
 SQ
 Query Match 86.3%; Score 157; DB 22; Length 406;
 Best Local Similarity 95.5%; Pred. No. 4,7e-19;
 Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ANAFLXXLRXGSLRXKXXQCSFXXAXYIFDAXRTKLFWISY 44
 DB 1 anaflxxlrpsglrxrckxxgcsfxxarxlfidaxrtklfwisy 44
 ID AAM52185
 XX AAM52185 standard; Protein; 406 AA.
 AC AAM52185;
 XX 07-FEB-2002 (first entry)
 DT
 XX Human FVII mutant G291N.
 DE
 KW Factor VII: FVII; Factor VIIa: FVIIa; haemostatic; thrombolytic;
 KW cardiatic; hepatotropic; cerebroprotective; haemophilia; liver disease;
 KW myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;
 KM mutain.
 XX Homo sapiens.
 OS Synthetic.
 XX Key Location/Qualifiers
 FT Misc-difference 6 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxylutamic acid"
 FT Misc-difference 7 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxylutamic acid"
 FT Misc-difference 14 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxylutamic acid"
 FT Misc-difference 16 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxylutamic acid"
 FT Misc-difference 19 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxylutamic acid"
 FT Misc-difference 19 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxylutamic acid"

FT Misc-difference 20 /label= GIU, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT Misc-difference 25 /label= GIU, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT Misc-difference 26 /label= GIU, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT Misc-difference 29 /note= "OTHER = gamma carboxyglutamic acid"
 FT /label= GIU, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT Misc-difference 35 /label= GIU, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT Modified-site 52 /note= "OTHER = gamma carboxyglutamic acid"
 FT Modified-site 60 /note= "O-glycosylated"
 FT Modified-site 145 /note= "O-glycosylated"
 FT Modified-site 152..153 /note= "N-glycosylated"
 FT Cleavage-site /note= "proteolytic cleavage site converting FVII zymogen to an activated form, comprising two chains linked by a single disulphide bridge"
 FT Misc-difference 291 /note= "Wild-type Gly substituted by Asn"
 FT Modified-site 322 /note= "N-glycosylated"
 FT /note= "N-glycosylated"
 PN W0200158935-A2.
 XX 16-AUG-2001.
 PD 12-FEB-2001; 2001WO-DK00094.
 PE 11-FEB-2000; 2000DK-0000218.
 PR 18-OCT-2000; 2000DK-0001558.
 XX (MAXY-) MAXGEN APS.
 PA Andersen KV, Pedersen AH, Bornaes C;
 PI WPI; 2001-581807/65.
 DR
 XX New conjugate, useful for treating Factor VIIa related diseases or
 PT disorders such as haemophilia, liver disease, myocardial infarction and
 PT deep-vein thrombosis, comprises non-polypeptide group covalently
 PT attached to polypeptide group -
 PT
 XX Example 3; Page -: 89pp; English.
 PS
 XX The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
 CC polypeptide conjugates, comprising at least one non-polypeptide group
 CC covalently attached to a polypeptide, where the amino acid sequence of
 CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
 CC least one amino acid residue containing an attachment group for the
 CC non-polypeptide group has been introduced or removed. The FVIIa
 CC conjugates have haemostatic, thrombolytic, cardiant, hepatotropic and
 CC cerebroprotective activity and are useful for treating FVIIa/FI-related
 CC diseases or disorders such as haemophilia, liver disease, myocardial
 CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
 CC have increased functional in vivo half life and/or increased plasma half
 CC life, increased bioavailability and or reduced sensitivity to proteolytic
 CC degradation. Consequently medical treatment using the conjugates has a
 CC number of advantages over currently available such as longer duration
 CC between injections. The present sequence is that of a human FVII mutant,
 CC having an addition in vivo glycosylation site and tested for its
 CC amidolytic activity.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from the human wild-type FVII sequence shown in SEQ ID NO 1
 CC (AAM52171).
 CC

SO Sequence 406 AA;
 Query Match 86.3%; Score 157; DB 22; Length 406;
 Best Local Similarity 95.5%; Pred. No. 4,7e-19;
 Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ANAFLLXLRXGSLRXKCKXQCSFXAXXIFPKAXRRLFWISY 44
 Db 1 anafllxlrpslxrxckxqcsfxaxrxlfkdxrcklfwlsy 44
 RESULT 18
 AAM52186
 ID AAM52186 standard; Protein: 406 AA.
 XX
 AC AAM52186;
 XX
 DT 07-FEB-2002 (first entry)
 XX
 DE Human FVII mutant R315N/V317F.
 XX
 KW Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
 KW cardiant; hepatotropic; cerebroprotective; haemophilia; liver disease;
 KW myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;
 KW muteln.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 6 /label= GIU, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT Misc-difference 7 /label= GIU, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT Misc-difference 14 /label= GIU, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT Misc-difference 16 /label= GIU, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT Misc-difference 19 /label= GIU, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT Misc-difference 20 /label= GIU, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT Misc-difference 25 /label= GIU, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT Misc-difference 26 /label= GIU, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT Misc-difference 29 /label= GIU, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT Misc-difference 35 /label= GIU, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT Modified-site 52 /note= "O-glycosylated"
 FT Modified-site 60 /note= "O-glycosylated"
 FT Modified-site 145 /note= "O-glycosylated"
 FT Modified-site 152..153 /note= "N-glycosylated"
 FT Cleavage-site /note= "proteolytic cleavage site converting FVII zymogen to an activated form, comprising two chains linked by a single disulphide bridge"
 FT Misc-difference 315 /note= "Wild-type Arg substituted by Asn"
 FT

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FT Misc-difference 317 /note= "Wild-type Val substituted by Thr"
FT Modified-site 322 /note= "N-glycosylated"
FT
XX WO200158935-A2.
XX
XX 16-AUG-2001.
XX
XX 12-FEB-2001; 2001WO-DK00094.
XX
XX 11-FEB-2000; 2000DK-0000218.
XX 18-OCT-2000; 2000DK-0001558.
XX
XX (MAXY-) MAXYGEN APS.
XX
XX Andersen KV, Pedersen AH, Bornaes C;
XX WPI; 2001-581807/65.
XX
XX New conjugate, useful for treating Factor VIIa related diseases or
XX disorders such as haemophilia, liver disease, myocardial infarction and
XX deep-vein thrombosis, comprises non-polypeptide group covalently
XX attached to polypeptide group -
XX
XX Example 3; Page -: 89pp; English.
XX
XX The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
XX polypeptide conjugates, comprising at least one non-polypeptide group
XX covalently attached to a polypeptide, where the amino acid sequence of
XX polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
XX least one amino acid residue containing an attachment group for the
XX non-polypeptide group has been introduced or removed. The FVIIa
XX conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and
XX cerebroprotective activity and are useful for treating FVIIa/TF-related
XX diseases or disorders such as haemophilia, liver disease, myocardial
XX infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
XX have increased functional in vivo half life and/or increased plasma half
XX life, increased bioavailability and or reduced sensitivity to proteolytic
XX degradation. Consequently medical treatment using the conjugates has a
XX number of advantages over currently available such as longer duration
XX between injections. The present sequence is that of a human FVII mutant,
XX having an addition in vivo glycosylation site and tested for its
XX amidolytic activity.
XX Note: The present sequence is not shown in the specification but is
XX derived from the human wild-type FVII sequence shown in SEQ ID NO 1
XX (AAM52171).
XX
XX Sequence 406 AA:
SQ

```

```

Query Match 86.3%; Score 157; DB 22; Length 406;
Best Local Similarity 95.5%; Pred. No. 4.7e-19;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 ANAFELXXLRGSLRXCKXXQCSFXXAXITFKAXRTKLFWISY 44
DB 1 anaflxxlrfpslrxckxxqcsfxxaxlfxkaxrtklfwisy 44

```

```

RESULT 19
AAM52187
ID AAM52187 standard; Protein; 406 AA.
XX
XX AAM52187;
XX
XX 07-FEB-2002 (first entry)
XX
XX Human FVII mutant K143N/M145T/R315N/V317T.
XX
XX Factor VII; FVII; Factor VIIa; haemostatic; thrombolytic;
XX cardiant; hepatotrophic; cerebroprotective; haemophilia; liver disease;
XX myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;

```

```

KW mutain.
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Misc-difference 6 /label= Glu, OTHER
XX /note= "OTHER = gamma carboxylutamic acid"
XX
XX Misc-difference 7 /label= Glu, OTHER
XX /note= "OTHER = gamma carboxylutamic acid"
XX
XX Misc-difference 14 /label= Glu, OTHER
XX /note= "OTHER = gamma carboxylutamic acid"
XX
XX Misc-difference 16 /label= Glu, OTHER
XX /note= "OTHER = gamma carboxylutamic acid"
XX
XX Misc-difference 19 /label= Glu, OTHER
XX /note= "OTHER = gamma carboxylutamic acid"
XX
XX Misc-difference 20 /label= Glu, OTHER
XX /note= "OTHER = gamma carboxylutamic acid"
XX
XX Misc-difference 25 /label= Glu, OTHER
XX /note= "OTHER = gamma carboxylutamic acid"
XX
XX Misc-difference 26 /label= Glu, OTHER
XX /note= "OTHER = gamma carboxylutamic acid"
XX
XX Misc-difference 29 /label= Glu, OTHER
XX /note= "OTHER = gamma carboxylutamic acid"
XX
XX Misc-difference 35 /label= Glu, OTHER
XX /note= "OTHER = gamma carboxylutamic acid"
XX
XX Modified-site 52 /note= "O-glycosylated"
XX /note= "O-glycosylated"
XX
XX Misc-difference 143 /note= "O-glycosylated"
XX
XX Misc-difference 145 /note= "Wild-type Lys substituted by Asn"
XX /note= "Wild-type Asn substituted by Thr"
XX
XX Cleavage-site 152..153 /note= "proteolytic cleavage site converting FVII zymogen
XX to an activated form, comprising two chains
XX linked by a single disulphide bridge"
XX
XX Misc-difference 315 /note= "Wild-type Arg substituted by Asn"
XX
XX Misc-difference 317 /note= "Wild-type Val substituted by Thr"
XX
XX Modified-site 322 /note= "N-glycosylated"
XX
XX WO200158935-A2.
XX
XX 16-AUG-2001.
XX
XX 12-FEB-2001; 2001WO-DK00094.
XX
XX 11-FEB-2000; 2000DK-0000218.
XX 18-OCT-2000; 2000DK-0001558.
XX
XX (MAXY-) MAXYGEN APS.
XX
XX Andersen KV, Pedersen AH, Bornaes C;
XX WPI; 2001-581807/65.
XX
XX New conjugate, useful for treating Factor VIIa related diseases or
XX disorders such as haemophilia, liver disease, myocardial infarction and
XX deep-vein thrombosis, comprises non-polypeptide group covalently

```


Db 1 anafleelrpslerekcegcscfeareifkdaertklfwisy 44

RESULT 22

AA84868 standard; Protein: 406 AA.

AA84868;

31-JUL-2001 (first entry)

DE Mutant blood coagulant factor VII (FVII-6).

KW Human: haemostatic; blood coagulant factor VII; FVII; haemophilia;

KW mutant; mutlein.

XX Homo sapiens.

OS Synthetic.

Key Location/Qualifiers

FT Misc-difference 164 /note= "Wild-type Cys substituted by Ala"

FT Misc-difference 299 /note= "Wild-type Val substituted by Cys"

FT JP2001061479-A.

XX 13-MAR-2001.

XX 24-AUG-1999; 99JP-0237610.

XX 24-AUG-1999; 99JP-0237610.

XX (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.

XX WPI; 2001-310677/33.

XX N-PSDB; AAH19461.

PT Mutant of blood coagulant factor VII, used for substitution therapy in

PT the treatment of hemophilia -

XX Claim 5; Page 14-15; 29pp; Japanese.

CC The present invention relates to mutants of blood coagulant factor VII

CC (FVII) or activated blood coagulant factor VII (FVIIa). The present

CC sequence is one such mutant FVII: VII-6. In the wild-type protein

CC (AA84868), there is a disulphide bond (159Cys-164Cys). In the present

CC protein, the disulphide bond is disrupted. The mutants can be used as an

CC agent for the substitution therapy of haemophilia inhibitor patients.

XX Sequence 406 AA;

Query Match 86.3%; Score 157; DB 22; Length 406;

Best Local Similarity 72.7%; Pred. No. 4.7e-19;

Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 1 ANAFLEXLRXGSLRXRCXKXOCSPFXAXXIFPDARTKLFWISY 44

Db 1 anafleelrpslerekcegcscfeareifkdaertklfwisy 44

RESULT 23

AA84869 standard; Protein: 406 AA.

AA84869;

31-JUL-2001 (first entry)

DE Mutant blood coagulant factor VII (FVII-30).

KW Human: haemostatic; blood coagulant factor VII; FVII; haemophilia;

KW mutant; mutlein.

XX Homo sapiens.

OS Synthetic.

Key Location/Qualifiers

FT Misc-difference 235..239 /note= "Wild-type Val-Pro-Gly-Thr-Thr substituted by

FT Asp-Arg-Lys-Thr-Leu"

XX JP2001061479-A.

XX 13-MAR-2001.

XX 24-AUG-1999; 99JP-0237610.

XX 24-AUG-1999; 99JP-0237610.

XX (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.

XX WPI; 2001-310677/33.

XX N-PSDB; AAH19462.

XX Mutant of blood coagulant factor VII, used for substitution therapy in

XX the treatment of hemophilia -

XX Claim 9; Page 17-18; 29pp; Japanese.

XX The present invention relates to mutants of blood coagulant factor VII

XX (FVII) or activated blood coagulant factor VII (FVIIa). The present

XX sequence is one such mutant FVII: VII-30. The mutants can be used as an

XX agent for the substitution therapy of haemophilia inhibitor patients.

XX Sequence 406 AA;

Query Match 86.3%; Score 157; DB 22; Length 406;

Best Local Similarity 72.7%; Pred. No. 4.7e-19;

Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 1 ANAFLEXLRXGSLRXRCXKXOCSPFXAXXIFPDARTKLFWISY 44

Db 1 anafleelrpslerekcegcscfeareifkdaertklfwisy 44

RESULT 24

AA64205 standard; Protein: 444 AA.

AA64205;

18-JUL-1995 (first entry)

DE Factor VII - modified forms of this act as an anticoagulant.

KW Factor VII: plasma glycoprotein; derivative: tissue factor; TF;

KW inhibition; vascular stenosis; platelet deposition; catalytic centre;

XX factor IX; factor X; inactivation; thrombosis; embolism; stroke; ss.

XX Homo sapiens.

XX Key

XX Active-site

XX Active-site

XX Active-site

XX Cleavage-site

XX Location/Qualifiers

XX 193

XX /note= "forms a catalytic triad with Ser344 and Asp242"

XX 242

XX /note= "forms catalytic triad with Ser344 and His193"

XX 344

XX /note= "forms catalytic triad with Asp242 and His193"

XX 152..153

XX /note= "internal cleavage site - cleavage activates

XX the zymogen into active 2-chain Factor VIIa"

PN W09427631-A.
 XX
 PD 08-DEC-1994.
 XX
 PF 23-MAY-1994: 94WO-US05779.
 XX
 PR 21-MAY-1993: 93US-0065725.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Berkner KL, Hart CE, Petersen LC;
 XX
 DR WPI: 1995-022464/03.
 DR N-PSDB; AAQ80296.
 XX
 PT Inhibition of tissue factor, vascular restenosis and platelet
 PT deposition - using modifier factor VII unable to activate
 PT factors IX and X, e.g. for treating thrombosis, embolism, stroke
 PT etc..
 PS Disclosure: Page 39-40; 51pp: English.
 XX
 CC AAR64205 shows the amino acid sequence of human Factor VII, encoded
 CC by AAQ80296. Factor VII is a trace plasma glycoprotein that circulates
 CC in blood as a single-chain zymogen. The zymogen is catalytically
 CC inactive, and is converted into a two-chain active mol. by cleavage of an
 CC internal peptide bond located approx. in the middle of the mol. Factor
 CC VIIa rapidly activates Factor X or Factor IX by limited proteolysis.
 CC Modified Factor VII, partic. where the Ser344 in the catalytic triad is
 CC substituted with alanine, has anticoagulant properties, for preventing
 CC the coagulation cascade. The modified Factor VII has an active site
 CC modified by at least one amino acid substitution, and in its modified
 CC form is capable of binding tissue factor and inhibiting its action.
 XX
 SQ Sequence 444 AA:
 QY 1 ANAFLLXLRKSLRCKXXQCSFXXXXIFKDAARFKLFWISY 44
 Db 39 anafllelrpgslereckeqcsfeearelfkdaerklfwisy 82
 RESULT 25
 AAW31687 standard; Protein: 444 AA.
 ID AAW31687;
 AC AAW31687;
 XX
 DT 08-JUN-1998 (first entry)
 XX
 DE Homo sapiens Ser344Ala modified factor VII.
 XX
 KW Factor VII: modified; Ser344Ala mutant; vascular patency;
 KW prevention; myocardial injury; blood flow; angioplasty; trauma;
 KW intimal hyperplasia; restenosis; deep vein thrombosis; treatment;
 KW pulmonary embolism; stroke; disseminated intravascular coagulation;
 KW fibrin deposition; endotoxaemia; myocardial infarction;
 KW anticoagulant.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 344
 XX /note= "Ser344Ala mutated"
 XX
 PN W09747651-A1.
 XX
 PD 18-DEC-1997.

XX
 PF 06-JUN-1997: 97WO-DK00251.
 XX
 PR 07-JUN-1996: 96US-0660289.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 PA (ZYMO) ZYMOGENETICS.
 XX
 PI Hart CE, Hedner U, Petersen LC, Rasmussen ME;
 XX
 DR WPI: 1998-052245/05.
 DR N-PSDB; AAV02230.
 XX
 PT Inhibiting thrombus formation by topical administration of modified
 PT factor VII - also used to maintain vascular patency, prevent
 PT myocardial injury and improve regional myocardial blood flow
 XX
 PS Example 1: Pages 74-76; 97pp: English.
 XX
 CC The sequence is that of a Ser344Ala modified factor VII which
 CC can be used as part of a method for inhibiting thrombus formation.
 CC The method is used to maintain or improve vascular patency,
 CC to prevent or minimise myocardial injury associated with
 CC post-ischaemic reperfusion and to improve regional myocardial blood
 CC flow during post-ischaemic reperfusion. The method is particularly
 CC used where the site of thrombus or reduced patency is associated with
 CC (micro)surgery, angioplasty or trauma or where the myocardial injury
 CC is myocardial necrosis. Particular applications are in treatment or
 CC prevention of intimal hyperplasia or restenosis caused by acute (e.g.
 CC mechanical) injury; deep vein thrombosis; pulmonary embolism; stroke;
 CC disseminated intravascular coagulation; fibrin deposition associated
 CC with endotoxaemia and myocardial infarction. When used in conjunction
 CC with tissue plasminogen activator or streptokinase, it can also be
 CC used to treat acute closure of a coronary artery. It effectively
 CC interrupts the coagulation cascade: is active at relatively low doses
 CC and lacks the side effects of known anticoagulants (particularly it
 CC is more selective than heparin, does not destroy other coagulation
 CC proteins and is less likely to cause bleeding complications). It
 CC acts specifically at the site of injury and binds to tissue factor,
 CC preventing coagulation induced by this. It may also have a
 CC longer plasma half-life than other anticoagulants.
 XX
 SQ Sequence 444 AA:
 QY 1 ANAFLLXLRKSLRCKXXQCSFXXXXIFKDAARFKLFWISY 44
 Db 39 anafllelrpgslereckeqcsfeearelfkdaerklfwisy 82
 RESULT 26
 AAV67967 standard; Protein: 444 AA.
 ID AAV67967;
 AC AAV67967;
 XX
 DT 05-APR-2000 (first entry)
 XX
 DE Factor VII SEQ ID NO:2.
 XX
 KW Factor VII: catalytic active site; blood coagulation; plasma;
 KW Factor X; Factor IX; vasotropic; antithrombotic; anticoagulant;
 KW myocardial injury; post-ischaemic reperfusion; platelet deposition;
 KW thrombus formation; vascular patency.
 XX
 OS Unidentified.
 XX
 PN US5997864-A.
 XX


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PD 07-DEC-1999.
XX
XX 06-JUN-1997; 97US-0871003.
XX
PR 28-FEB-1991; 91US-0662920.
PR 21-MAY-1993; 93US-0065725.
PR 23-MAY-1994; 94WO-US05779.
PR 24-OCT-1994; 94US-0327690.
PR 07-JUN-1995; 95US-0475845.
PR 07-JUN-1996; 96US-0660289.
XX
PA (NOVO ) NOVO-NORDISK AS.
PA (ZYMO ) ZYMOGENETICS INC.
XX
PI Hart CE, Petersen LC, Hedner U, Rasmussen ME;
XX
DR WPI: 2000-104599/09.
DR N-PSDB; AA257385.
XX
PT Inhibition or minimization of myocardial injury associated with
PT post-ischemic reperfusion -
XX
PS Disclosure: Column 47-50; 34pp; English.
XX
CC The present invention describes a method for the inhibition or
CC minimization of myocardial injury associated with post-ischemic
CC reperfusion by administering factor VII, which has at least 1
CC modification in its catalytic tried (therefore inhibiting the ability
CC of factor VII to activate plasma factor X or IX). The method can be
CC used for inhibiting or minimizing myocardial injury and for imparting
CC regional myocardial blood flow associated with post-ischaemic
CC reperfusion. It can also be used for inhibiting blood coagulation,
CC platelet deposition, thrombus formation and maintaining or improving
CC vascular potency. Factor VII can be administered at relatively low
CC doses and does not produce undesirable side effects. Further it acts
CC specifically at sites of injury. The present sequence represents
CC Factor VII.
XX
SQ Sequence 444 AA:

Query Match 86.3%; Score 157; DB 21; Length 444;
Best Local Similarity 72.7%; Pred. No. 5,1e-19;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLXLRXGSLRXRCXXOCSEFXAXXIFDAXRTKLFWSY 44
Db 39 anaflleirpyslereckeeqcsfeearelfkdaertklfwisy 82

RESULT 27
AAB61992
ID AAB61992 standard; Protein; 444 AA.
XX
AC AAB61992;
XX
DT 14-MAY-2001 (first entry)
XX
DE Human Factor VII polypeptide.
XX
KW Factor VIIa; thrombus; vascular patency; blood coagulation; Factor X;
KW plasma factor; Factor IX; myocardial injury; human; Factor VII.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH Peptide 1..38
FT /note= "signal peptide"
FT Protein 39..444
FT /note= "mature peptide"
FT Misc-difference 10
FT /note= "indicated incorrectly as Trp under sequence
FT listing ID 2"

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XX
XX US6183743-B1.
PN
XX
PD 06-FEB-2001.
XX
PF 20-AUG-1999; 99US-0378907.
XX
PR 06-JUN-1997; 97US-0871003.
PR 28-FEB-1991; 91US-0662920.
PR 28-FEB-1992; 92WO-US01636.
PR 21-MAY-1993; 93US-0065725.
PR 23-MAY-1994; 94WO-US05779.
PR 24-OCT-1994; 94US-0327690.
PR 07-JUN-1995; 95US-0475845.
PR 07-JUN-1996; 96US-0660289.
XX
PA (ZYMO ) ZYMOGENETICS INC.
PA (NOVO ) NOVO NORDISK AS.
XX
PI Hart CE, Petersen LC, Hedner U, Rasmussen ME;
XX
DR WPI: 2001-201993/20.
DR N-PSDB; AAF57099.
XX
PT Use of modified human factor VIIa with a covalent modification in its
PT catalytic center, to inhibit thrombus formation or to maintain vascular
PT patency -
XX
PS Example: Columns 43-48; 34pp; English.
XX
CC The invention relates to the use of modified human Factor VIIa for
CC inhibiting thrombus formation, or maintaining or improving vascular
CC patency in a patient. The modified factor VIIa comprises a covalent
CC modification in its catalytic center which effectively interrupts the
CC blood coagulation cascade. The modifications render Factor VIIa
CC substantially unable to activate plasma factor IX or X. The modified
CC Factor VIIa can be used for preventing or treating myocardial injury
CC associated with post-ischemic reperfusion, for improving regional
CC myocardial blood flow during reperfusion and maintaining or improving
CC vascular patency in a patient. The present sequence represents the
CC human Factor VII polypeptide.
XX
SQ Sequence 444 AA:

Query Match 86.3%; Score 157; DB 22; Length 444;
Best Local Similarity 72.7%; Pred. No. 5,1e-19;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLXLRXGSLRXRCXXOCSEFXAXXIFDAXRTKLFWSY 44
Db 39 anaflleirpyslereckeeqcsfeearelfkdaertklfwisy 82

RESULT 28
AAP60056
ID AAP60056 standard; Protein; 466 AA.
XX
AC AAP60056;
XX
DT 23-MAY-1991 (first entry)
XX
DE Factor VII peptide encoded by cDNA clone lambda VIT2463.
XX
KW Factor VII; Factor VIIa; DNA construct;
XX
KW Factor VII; Factor VIIa; DNA construct;
XX
PN EP200421-A.
XX
PD 10-DEC-1986.
XX
PF 16-APR-1986; 86EP-0302855.
XX
PR 16-DEC-1985; 85US-0810002.

```

PR 17-APR-1985; 85US-0724311.
 PA (ZYMO-) ZYMOGENETICS INC.
 XX
 PI Hagen FS, Murry MJ, Berkner KL, Insley MY, Woodbury RG;
 PI Gray CL;
 XX WPI; 1986-326899/50.
 DR N-PSDB; AAN60064.
 XX
 PT DNA construct used to transfect hosts - to produce protein which
 PT activates to give factor VIIa
 XX
 PS Disclosure; Fig. 1B; 55pp; English.
 XX
 CC The partial factor VII cDNA sequence encoding the peptide is from
 CC cDNA clone lambda VII2463. It is used in a DNA construct which contains
 CC a nucleotide sequence encoding a protein which, on activation, has the
 CC same biological activity for blood coagulation as Factor VIIa. The
 CC nucleotide codes at least partially for factor VII and comprises a
 CC sequence encoding a calcium binding domain joined to a second sequence
 CC downstream of this encoding a catalytic domain for the serine protease
 CC activity of Factor VIIa. The calcium binding domain comprises a gene
 CC encoding Factor VII, IX, X, Protein C, prothrombin or Protein S. The
 CC construct is used to transfect host cells to produce the protein which,
 CC on activation, yields Factor VIIa.
 XX
 SQ Sequence 466 AA;

Query Match 86.3%; Score 157; DB 7; Length 466;
 Best Local Similarity 72.7%; Pred. No. 5.4e-19;
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 1 ANAFLLXLRKGSIXKXKXQCSFXXXXIFKDXARKFLWISY 44
 ||||| || ||| | || |||| | ||||| ||||| |||||
 Db 61 anafllelrpslereckeegcsfeearelfkdaerklfwisy 104

RESULT 29
 AAR52562
 ID AAR52562 standard; Protein: 466 AA.
 XX
 AC AAR52562;
 XX
 DT 27-MAY-1994 (first entry)
 XX
 DE Factor VIII.
 XX
 KW Truncated tissue factor; tTF; factor VIIa; FVIIa; activator;
 KW bleeding disorder; haemophilia; liver cirrhosis; coagulation;
 KW transmembrane domain; extracellular domain; soluble.
 XX
 OS Homo sapiens.
 XX
 PN W09323074-A.
 PD 25-NOV-1993.
 XX
 PF 12-MAY-1993; 93WO-US04493.
 XX
 PR 13-MAY-1992; 92US-0882202.
 PR 19-FEB-1993; 93US-0021615.
 XX
 PA (OKLA-) OKLAHOMA MED RES FOUND.
 XX
 PI Comp PC, Morrissey JH;
 XX
 DR WPI; 1993-386218/48.
 DR N-PSDB; AAO62299.
 XX
 PT Compn. of truncated tissue factor and factor-VIIa or activator
 PT of VII - useful for treating bleeding disorders, e.g. haemophilia

PT or liver cirrhosis
 XX
 PS Disclosure; Page 26-28; 43pp; English.
 XX
 CC A compsn. for treatment of patients with prolonged or excessive
 CC bleeding disorders comprises truncated tissue factor (tTF) (AAQ52439)
 CC and a substance effective to produce a plasma level of factor VIIa
 CC which in combination with tTF will control or stop the excessive
 CC bleeding. The substance may be factor VIIa itself or an activator
 CC which promotes the conversion of endogenous factor VII to factor VIIa.
 XX
 SQ Sequence 466 AA;

Query Match 86.3%; Score 157; DB 14; Length 466;
 Best Local Similarity 72.7%; Pred. No. 5.4e-19;
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 1 ANAFLLXLRKGSIXKXKXQCSFXXXXIFKDXARKFLWISY 44
 ||||| || ||| | || |||| | ||||| ||||| |||||
 Db 61 anafllelrpslereckeegcsfeearelfkdaerklfwisy 104

RESULT 30
 AAW69606
 ID AAW69606 standard; Protein: 466 AA.
 XX
 AC AAW69606;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Human Factor VIIa.
 XX

KW Human; truncated; tissue factor; tTF; TF; tumour; coagulation;
 KW blood vessel; Factor VIIa; FVIIa; benign growth; vascularised;
 KW benign prostatic hypertrophy; malignant; necrosis; angiodenesis;
 KW diabetic retinopathy; restenosis; neovascular glaucoma; psoriasis;
 KW rheumatoid arthritis.
 KW
 XX
 OS Homo sapiens.
 XX

PN W09831394-A2.
 PD 23-JUL-1998.
 XX
 PF 20-JAN-1998; 98WO-US01012.
 XX
 PR 27-MAR-1997; 97US-0042427.
 PR 22-JAN-1997; 97US-0035920.
 PR 27-JAN-1997; 97US-0036205.
 XX

PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Gao B, King SW, Thorpe PE;
 XX
 DR WPI; 1998-413821/35.
 DR N-PSDB; AAV40389.
 XX
 PT Composition containing coagulation-defective tissue factor for
 PT treating, e.g. tumours - useful for, e.g. promoting coagulation in
 PT pro-thrombotic and tumour-associated vasculature, used with, e.g.
 PT factor 7 or anti-cancer agent
 XX
 PS Claim 35; Page 196-197; 225pp; English.

CC A composition has been developed which comprises at least 1 coagulation-
 CC deficient tissue factor (TF) compound that is modified to increase its
 CC biological half-life, but excluding modification that involves attachment
 CC to an antibody (or its antigen-binding region) that binds to a component
 CC (cells, vasculature or stroma) of tumours. Also described in the present
 CC invention are compositions containing any coagulation-deficient TF for
 CC promoting coagulation. The coagulation-deficient TFs are used to promote
 CC coagulation preferentially in prothrombotic vessels, particularly those


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FT      Disulfide-bond /note= "proteolytic site"
FT      Disulfide-bond 50..61
FT      Disulfide-bond 55..70
FT      Modified-site 63
FT      /label= OTHER
FT      Disulfide-bond /note= "beta-hydroxy-aspartic acid"
FT      Disulfide-bond 72..81
FT      Disulfide-bond 91..102
FT      Disulfide-bond 98..112
FT      Disulfide-bond 114..127
FT      Disulfide-bond 135..162
FT      Cleavage-site 143..144
FT      /note= "proteolytic site"
FT      Modified-site 145
FT      /note= "glycosylation site"
FT      Disulfide-bond 159..164
FT      Disulfide-bond 178..194
FT      Active-site 193
FT      Active-site 242
FT      Active-site 344
FT      Cleavage-site 290..291
FT      /note= "proteolytic site"
FT      Disulfide-bond 310..329
FT      Cleavage-site 315..316
FT      Modified-site 322
FT      /note= "proteolytic site"
FT      Disulfide-bond /note= "glycosylation site"
FT      Disulfide-bond 340..368
FT      Cleavage-site 341..342
FT      Cleavage-site /note= "proteolytic site"
FT      Cleavage-site 392..393
FT      /note= "proteolytic site"
FT      Cleavage-site 396..397
FT      /note= "proteolytic site"
FT      Cleavage-site 402..403
FT      /note= "proteolytic site"
XX      US580560-A.
XX      03-DEC-1996.
XX      13-NOV-1989; 89US-0434149.
XX      09-AUG-1993; 93US-0104509.
XX      13-NOV-1989; 89US-0434149.
XX      12-JUN-1992; 92US-0898248.
XX      22-AUG-1994; 94US-0293778.
XX      (NOVO ) NOVO-NORDISK AS.
XX      Bjorn SE, Nicolaisen EM, Wiberg FC, Woodbury R;
XX      WPI; 1997-033523/03.
XX      Mutated human factor VII or VIIa proteins - with amino acid
XX      substitutions to improve proteolytic stability
XX      Claim 3; Page -: 28pp; English.
XX      Modified human factor VII or VIIa proteins are stabilised against
XX      proteolytic cleavage by substitution of one of the residues Lys32,
XX      Lys38, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and
XX      Lys341 by an amino acid that provides a proteolytically more stable
XX      peptide bond, provided that Lys32 is replaced by Gln, Glu, His,
XX      Gly, Thr, Ala or Ser. The modified proteins are useful for treating
XX      bleeding disorders such as thrombocytopenia and von Willebrand's
XX      disease. They are also suitable for addition to plasma substitutes.
XX      The present sequence is a specific example of a modified factor VII
XX      protein.
XX      Sequence 406 AA;

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Query Match 84.1%; Score 153; DB 18; Length 406;
Best Local Similarity 70.3%; Pred. No. 2,3e-18;
Matches 31; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

Qy      1 ANAFLLXLRKGSIXRXXKXXQCSFXXAXXIFKDXRTRKLFWISY 44
      ||||| | | | | | | | | | | | | | | | | | | | | | |
Db      1 anafllelrpslserckeegsfearelfqdaertklfwisy 44

RESULT 33
AAV18313
ID AAV18313 standard; peptide; 44 AA.
AC AAV18313;
DT 17-AUG-1999 (first entry)
XX
DE Modified GLA domain of vitamin K-dependent protein.
XX
KW GLA domain; muten; vitamin K-dependent protein; clotting disorder;
KW therapy.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Msc-difference 1..44 /note= "Xaa-gamma-carboxyglutamic acid, or glutamic
FT FT acid"
XX
PN W09920767-A1.
XX
PD 29-APR-1999.
XX
PF 20-OCT-1998; 98WO-US22152.
XX
PR 23-OCT-1997; 97US-0955636.
XX
XX (MINU ) UNIV MINNESOTA.
XX
XX Nelsaestuen GL;
XX
PI
XX
DR WPI; 1999-288309/24.
XX
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
XX PT acid domain, useful for treating clotting disorders
XX
XX
XX Disclosure; Page 81; 86pp; English.
XX
XX This sequence represents a modified GLA (gamma-carboxyglutamic acid)
XX CC domain. The invention relates to a vitamin K-dependent polypeptide
XX CC comprising a modified GLA domain containing an amino acid substitution
XX CC which enhances membrane binding of the modified polypeptide as compared
XX CC to the native polypeptide. The polypeptide is used to treat a clotting
XX CC disorder by decreasing or increasing clot formation. Modification of the
XX CC GLA domain results in a protein which has enhanced membrane binding
XX CC affinity as compared to the native protein.
XX
XX
XX Sequence 44 AA;

Query Match 83.0%; Score 151; DB 20; Length 44;
Best Local Similarity 93.2%; Pred. No. 5,6e-19;
Matches 41; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 ANAFLLXLRKGSIXRXXKXXQCSFXXAXXIFKDXRTRKLFWISY 44
      ||||| | | | | | | | | | | | | | | | | | | | | | |
Db      1 anaflxxlrpslrxckxxqcsfxxaxxifddaxrtklfwisy 44

RESULT 34
AAW14508
ID AAW14508 standard; protein; 406 AA.

```


[illegible]

FT	Active-site	242
FT	Active-site	344
FT	Cleavage-site	290..291
FT	/note= "proteolytic site"	
FT	Disulfide-bond	310...329
FT	Cleavage-site	315...316
FT	/note= "proteolytic site"	
FT	Modified-site	322
FT	/note= "glycosylation site"	
FT	Disulfide-bond	340...368
FT	Cleavage-site	341...342
FT	/note= "proteolytic site"	
FT	Cleavage-site	392...393
FT	/note= "proteolytic site"	
FT	Cleavage-site	396...397
FT	/note= "proteolytic site"	
FT	Cleavage-site	402...403
FT	/note= "proteolytic site"	
PN	US5580560-A.	
XX		
PD	03-DEC-1996.	
XX		
PX	13-NOV-1989;	89US-0434149.
XX		
PR	09-AUG-1993;	93US-0104509.
PR	13-NOV-1989;	89US-0434149.
PR	12-JUN-1992;	92US-0898248.
PR	22-AUG-1994;	94US-0293778.
XX		
PA	(NOVO) NOVO-NORDISK AS.	
XX		
PI	Bjorn SE, Nicolaisen EM, Wlberg FC, Woodbury R;	
XX		
DR	WPI: 1997-033523/03.	
XX		
PT	Mutated human factor VII or VIIa proteins - with amino acid	
PT	substitutions to improve proteolytic stability	
XX		
PS	Claim 8; Page -: 28pp; English.	
XX		
CC	Modified human factor VII or VIIa proteins are stabilised against	
CC	proteolytic cleavage by substitution of one of the residues Lys32,	
CC	Lys38, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and	
CC	Lys441 by an amino acid that provides a proteolytically more stable	
CC	peptide bond, provided that Lys32 is replaced by Gln, Glu, His,	
CC	Gly, Thr, Ala or Ser. The modified proteins are useful for treating	
CC	bleeding disorders such as thrombocytopenia and von Willebrand's	
CC	disease. They are also suitable for addition to plasma substitutes.	
CC	The present sequence is a specific example of a modified factor VII	
CC	protein.	
XX		
SQ	Sequence	406 AA:
Query Match	80.8%; Score 147; DB 18; Length 406;	
Best Local Similarity	68.2%; Pred. No. 2.6e-17;	
Matches 30; Conservative 1; Mismatches 13; Indels 0; Gaps 0;		
Oy	1 ANAFLXLRXGSLXRKXXQCSEFXAXXIIFDAXRRLFWISY 44	
Db	1 anaflaelrpslerckeeqcsfeearelfgdaertllfwisy 44	
RESULT 36		
AAM11904		
ID AAM11904 standard; peptide: 41 AA.		
AC AAM11904;		
XX		
DT 01-APR-1997 (first entry)		
XX		
DE Factor VII Gla region.		

XX	Prothrombin; PIVKA; Gla region; vitamin K dependent plasma protein;
KW	Factor X; Factor IX; Factor VII; Protein C; Protein S; Protein Z;
KW	protein induced vitamin K absence; vitamin K deficiency; vitamin K;
KW	hepatocellular carcinoma; gamma-carboxylase; anti-PIVKA-II antibody.
XX	
OS	Homo sapiens.
XX	
FT	Key
FT	Modified-site
FT	6
FT	/label= OTHER
FT	/note= "gamma-carboxylglutamic acid"
FT	7
FT	/label= OTHER
FT	/note= "gamma-carboxylglutamic acid"
FT	14
FT	/label= OTHER
FT	/note= "gamma-carboxylglutamic acid"
FT	16
FT	/label= OTHER
FT	/note= "gamma-carboxylglutamic acid"
FT	19
FT	/label= OTHER
FT	/note= "gamma-carboxylglutamic acid"
FT	20
FT	/label= OTHER
FT	/note= "gamma-carboxylglutamic acid"
FT	25
FT	/label= OTHER
FT	/note= "gamma-carboxylglutamic acid"
FT	26
FT	/label= OTHER
FT	/note= "gamma-carboxylglutamic acid"
FT	29
FT	/label= OTHER
FT	/note= "gamma-carboxylglutamic acid"
FT	35
FT	/label= OTHER
FT	/note= "gamma-carboxylglutamic acid"
XX	
PN	CA2121927-A.
XX	
PD	08-NOV-1994.
XX	
PF	22-APR-1994; 94CA-2121927.
XX	
PR	07-MAY-1993; 93JP-0130015.
PR	10-FEB-1994; 94JP-0016348.
XX	
PA	(EISA) EISAI CO LTD.
XX	
PI	Iwasaki Y, Naraki T, Watanabe K;
XX	
DR	WPI: 1995-052669/08.
XX	
PT	Determination of protein induced by vitamin-K absence (PIVKA) - by
PT	using an anti-PIVKA antibody, useful as vitamin-K deficiency marker
XX	
PS	Disclosure: Page 10; 34pp; English.
XX	
CC	AAW11901-W11907 represent Gla regions of vitamin K dependent plasma
CC	proteins. This sequence is the Gla region of Factor VII. The Gla
CC	region is the N-terminal region of the protein, and contains 10 glutamic
CC	acid residues which are gamma-carboxylated. These 10 residues are
CC	carboxylated in the precursor form, and require the presence of
CC	vitamin K and a carboxylase to be converted into an active form. These
CC	proteins suffer incomplete carboxylation when a state of protein induced
CC	vitamin K absence (PIVKA) occurs. Various PIVKAs have been found to be
CC	produced in the blood as a result of hepatocellular carcinoma. These
CC	sequences are all epitopes for the anti-PIVKA-II monoclonal antibody.
CC	The anti-PIVKA-II antibody (such as MW-3) specifically recognises the
CC	prothrombin Gla region (see AAW11901), but has also been found to
CC	recognise the rest of these Gla regions. The antibody can be used in the

CC	method of the invention for the determination of PIVKA in a specimen.
CC	The determination of PIVKA is clinically useful, as PIVKA is produced in
CC	blood as a result of incomplete gamma-carboxylation in a state of
CC	vitamin K deficiency or suppression. The determination of PIVKA can
CC	therefore be used as a marker of the state of vitamin K deficiency or
CC	suppression.
XX	
SQ	Sequence 41 AA:
Oy	
Db	Query Match 78.0%; Score 142; DB 16; Length 41; Best Local Similarity 95.1%; Pred. No. 1.9e-17; Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
	1 ANAFPLXLRGSLRXRCXKXOCSEFXAXXIIFDAPXRKLFW 41 1 anaflxxlrpslrxrcxkxgcsefxaxrifdaxrklfw 41
RESULT	37
AAM14506	
ID	AAM14506 standard; protein; 406 AA.
XX	
AC	AAM14506;
XX	
DR	14-MAY-1997 (first entry)
XX	
DE	Modified blood coagulation Factor VII.
XX	
KW	Blood coagulation; factor 7; muteln; mutation; modification;
KW	thrombocytopenia; von Willebrand's disease; plasma substitute.
XX	
OS	Homo sapiens.
XX	
FH	
Key	Location/Qualifiers
FT	/label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	6
FT	7
FT	/label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	14
FT	/label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	16
FT	/label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	19
FT	/label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	20
FT	/label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	25
FT	/label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	26
FT	/label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	29
FT	/label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	32..33
FT	/note= "proteolytic site in unmodified factor VII"
FT	32
FT	/label= Lys, Gln, Glu, His, Gly, Thr, Ala, Ser
FT	/note= "if native Lys32 is substituted by an amino
FT	acid which provides a proteolytically more
FT	stable peptide bond, then it must be substituted
FT	by one of the amino acids Gln, Glu, His, Gly,
FT	Thr, Ala or Ser"
FT	35
FT	Modified-site

FT /label- OTHER
 FT /note- "gamma-carboxyglutamic acid"
 FT Cleavage-site 38..39 /note- "proteolytic site in unmodified factor VII"
 FT Misc-difference 38 /note- "if native lys38 is substituted by an amino acid which provides a proteolytically more stable peptide bond, then it is pref. substituted by one of the amino acids Thr, Asp, Leu, Gly, Ala, Ser, Asn or His"
 FT Cleavage-site 42..43 /note- "proteolytic site in unmodified factor VII"
 FT Misc-difference 42 /note- "native Ile42 may be substituted by an amino acid which provides a proteolytically more stable peptide bond"
 FT Cleavage-site 44..45 /note- "proteolytic site in unmodified factor VII"
 FT Misc-difference 44 /note- "native Tyr44 may be substituted by an amino acid which provides a proteolytically more stable peptide bond"
 FT Disulfide-bond 50..61 /note- "native Tyr44 may be substituted by an amino acid which provides a proteolytically more stable peptide bond"
 FT Disulfide-bond 55..70 /note- "native Tyr44 may be substituted by an amino acid which provides a proteolytically more stable peptide bond"
 FT Modified-site 63 /label- OTHER
 FT /note- "beta-hydroxy-aspartic acid"
 FT Disulfide-bond 72..81 /note- "beta-hydroxy-aspartic acid"
 FT Disulfide-bond 91..102 /note- "beta-hydroxy-aspartic acid"
 FT Disulfide-bond 98..112 /note- "beta-hydroxy-aspartic acid"
 FT Disulfide-bond 114..127 /note- "beta-hydroxy-aspartic acid"
 FT Disulfide-bond 135..162 /note- "beta-hydroxy-aspartic acid"
 FT Cleavage-site 143..144 /note- "proteolytic site"
 FT Modified-site 145 /note- "proteolytic site"
 FT Disulfide-bond 159..164 /note- "glycosylation site"
 FT Disulfide-bond 178..194 /note- "glycosylation site"
 FT Active-site 193 /note- "glycosylation site"
 FT Active-site 242 /note- "glycosylation site"
 FT Active-site 344 /note- "glycosylation site"
 FT Misc-difference 278 /note- "native Phe278 may be substituted by an amino acid which provides a proteolytically more stable peptide bond"
 FT Cleavage-site 290 /note- "proteolytic site in unmodified factor VII"
 FT Misc-difference 290 /note- "proteolytic site in unmodified factor VII"
 FT /note- "if native Arg290 is substituted by an amino acid which provides a proteolytically more stable peptide bond, then it is pref. substituted by one of the amino acids Gly, Thr, Ala, Ser or Lys"
 FT Misc-difference 304 /note- "if native Arg304 is substituted by an amino acid which provides a proteolytically more stable peptide bond, then it is pref. substituted by one of the amino acids Gly, Thr, Ala, Ser or Lys"
 FT Disulfide-bond 310..329 /note- "if native Arg304 is substituted by an amino acid which provides a proteolytically more stable peptide bond, then it is pref. substituted by one of the amino acids Gly, Thr, Ala, Ser or Lys"
 FT Cleavage-site 315..316 /note- "if native Arg304 is substituted by an amino acid which provides a proteolytically more stable peptide bond, then it is pref. substituted by one of the amino acids Gly, Thr, Ala, Ser or Lys"
 FT Misc-difference 315 /note- "proteolytic site in unmodified factor VII"
 FT /note- "if native Arg315 is substituted by an amino acid which provides a proteolytically more stable peptide bond, then it is pref. substituted by one of the amino acids Gly, Thr, Ala, Ser or Lys"
 FT Modified-site 322 /note- "glycosylation site"
 FT Misc-difference 332 /note- "native Tyr332 may be substituted by an amino acid which provides a proteolytically more stable peptide bond, then it is pref. substituted by one of the amino acids Gly, Thr, Ala, Ser or Lys"
 FT /note- "native Tyr332 may be substituted by an amino acid which provides a proteolytically more stable peptide bond, then it is pref. substituted by one of the amino acids Gly, Thr, Ala, Ser or Lys"

FT Disulfide-bond 340..368 /note- "stable peptide bond"
 FT Cleavage-site 341..342 /note- "proteolytic site in unmodified factor VII"
 FT Misc-difference 341 /note- "if native Lys341 is substituted by an amino acid which provides a proteolytically more stable peptide bond, then it is pref. substituted by one of the amino acids Gly, Gln, Gly, Thr Ala or Ser"
 FT Cleavage-site 392..393 /note- "proteolytic site"
 FT Cleavage-site 396..397 /note- "proteolytic site"
 FT Cleavage-site 402..403 /note- "proteolytic site"
 FT /note- "proteolytic site"
 FT US5580560-A.
 FT 03-DEC-1996.
 FT 13-NOV-1989; 89US-0434149.
 FT 09-AUG-1993; 93US-0104509.
 FT 13-NOV-1989; 89US-0434149.
 FT 12-JUN-1992; 92US-0898248.
 FT 22-AUG-1994; 94US-0293778.
 FT (NOVO) NOVO-NORDISK AS.
 FT Bjorn SE, Nicolaisen EM, Wiberg FC, Woodbury R;
 FT WPI; 1997-033523/03.
 FT Mutated human factor VII or VIIa proteins - with amino acid substitutions to improve proteolytic stability
 FT Claim 1; Page -: 28pp; English.
 FT Modified human factor VII or VIIa proteins are stabilised against proteolytic cleavage by substitution of one of the residues Lys32, Lys38, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and Lys341 by an amino acid that provides a proteolytically more stable peptide bond, provided that Lys32 is replaced by Gln, Glu, His, Gly, Thr, Ala or Ser. The modified proteins are useful for treating bleeding disorders such as thrombocytopenia and von Willebrand's disease. They are also suitable for addition to plasma substitutes.
 FT Sequence 406 AA:
 FT
 FT Query Match 73.1%; Score 133; DB 18; Length 406;
 FT Best Local Similarity 65.1%; Pred. No. 7.1e-15;
 FT Matches 28; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
 FT
 FT QY 1 ANAFLLXKRGSLRXCKXXQCSEFXAXXIIFKDXRFLKLEWIS 43
 FT Db 1 anafllelrpslserckecqcsfeearelffxdaerclfxfs 43
 FT
 FT RESULT 38
 FT AAY18306
 FT ID AAY18306 standard; peptide: 44 AA.
 FT XX
 FT AAY18306;
 FT AC AAY18306;
 FT XX
 FT 17-AUG-1999 (first entry)
 FT DT
 FT XX
 FT Bovine factor VII GLA domain.
 FT DE
 FT XX
 FT GLA domain; vitamin K-dependent protein; clotting disorder;
 FT KW therapy.
 FT XX


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OS Bos taurus.
XX
XX Key Location/Qualifiers
FH Misc-difference 1..44
FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
FT acid"
XX
XX WO9920767-A1.
XX
XX 29-APR-1999.
XX
XX 20-OCT-1998; 98WO-US22152.
XX
XX 23-OCT-1997; 97US-0955636.
XX
XX (MINU ) UNIV MINNESOTA.
XX
XX Nelstuen GL;
XX
XX WPI: 1999-288309/24.
XX
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
XX acid domain, useful for treating clotting disorders
XX
XX PS Disclosure: Page 15; 86pp; English.
XX
XX This sequence is the factor VII GLA (gamma-carboxyglutamic acid)
XX domain. The invention relates to a vitamin K-dependent polypeptide
XX comprising a modified GLA domain containing an amino acid substitution
XX which enhances membrane binding of the modified polypeptide as compared
XX to the native polypeptide. The polypeptide is used to treat a clotting
XX disorder by decreasing or increasing clot formation. Modification of the
XX GLA domain results in a protein which has enhanced membrane binding
XX affinity as compared to the native protein.
XX
XX SQ Sequence 44 AA;

Query Match 66.5%; Score 121; DB 20; Length 44;
Best Local Similarity 75.0%; Pred. No. 9.4e-14;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 1 ANAFLLXLRGSLRXCKXKXQCSFXXAXXIFKDXRTKLFMISY 44
   || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 angflxxlirpsslrxrcxxlcsfxxahxlfmxxrtirgtwvay 44

RESULT 39
AAB36396
ID AAB36396 standard; peptide; 44 AA.
XX
XX AAB36396;
XX
XX 27-FEB-2001 (first entry)
XX
XX Bovine factor VII gamma-carboxyglutamic acid domain SEQ ID NO.4.
XX
XX Vitamin K-dependent protein; factor VII; protein C; GLA domain;
XX gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
XX factor X; prothrombin; enhanced membrane binding affinity;
XX clot formation; thrombolytic; haemostatic; bleeding disorder;
XX thrombosis; clotting disorder; haemophilia A; haemophilia B;
XX liver disease.
XX
XX Bos taurus.
XX
XX WO200066753-A2.
XX
XX 09-NOV-2000.
XX
XX 28-APR-2000; 2000WO-US11416.
XX
XX 29-APR-1999; 99US-0302239.

```

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XX
XX (MINU ) UNIV MINNESOTA.
XX
XX Nelstuen GL;
XX
XX WPI: 2001-007226/01.
XX
XX Novel vitamin K-dependent polypeptide useful for treating clotting
XX disorders such as thrombosis and hemophilia, comprises modified
XX gamma-carboxy glutamic acid domain that enhances membrane binding
XX affinity
XX
XX PS Disclosure: Page 12; 81pp; English.
XX
XX The present invention describes a vitamin K-dependent polypeptide (I)
XX comprising a modified gamma-carboxy glutamic acid (GLA) domain having
XX at least one amino acid substitution, that enhances membrane binding
XX affinity and the activity of the polypeptide relative to a corresponding
XX native vitamin K-dependent polypeptide and inhibits clot formation.
XX (I) can have thrombolytic and haemostatic activities, and can be used
XX as an inhibitor of clot formation. (I) is useful for decreasing clot
XX formation in a mammal, a factor VII or factor IX containing a modified
XX GLA domain is useful for increasing clot formation and for treating a
XX bleeding disorder, including thrombosis and clotting disorders such as
XX haemophilia A, haemophilia B and liver disease. The present sequence
XX represents a wild type bovine factor VII GLA domain sequence, given in
XX the exemplification of the present invention.
XX
XX SQ Sequence 44 AA;

Query Match 66.5%; Score 121; DB 22; Length 44;
Best Local Similarity 75.0%; Pred. No. 9.4e-14;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 1 ANAFLLXLRGSLRXCKXKXQCSFXXAXXIFKDXRTKLFMISY 44
   || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 angflxxlirpsslrxrcxxlcsfxxahxlfmxxrtirgtwvay 44

RESULT 40
AAU02959
ID AAU02959 standard; protein; 345 AA.
XX
XX AAU02959;
XX
XX 12-SEP-2001 (first entry)
XX
XX Angiotensin converting enzyme (ACEV) splice variant protein #59.
XX
XX Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
XX granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
XX platelet-derived endothelial cell growth factor; cardiovascular disease;
XX cellular tumour antigen p53; cyclin-dependent kinase inhibitor 1C;
XX vasocactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
XX myocardial infarction; coronary arterial thrombosis; renal disease;
XX diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
XX multiple sclerosis; immune complex nephritis; deep vein thrombosis;
XX noncardiotoxic pulmonary granulomatous disease; endothelial abnormality;
XX vascular disorder; asbestosis.
XX
XX Mus sp..
XX
XX WO200136632-A2.
XX
XX 25-MAY-2001.
XX
XX 17-NOV-2000; 2000WO-IL00766.
XX
XX 17-NOV-1999; 99IL-0132978.
XX
XX 10-DEC-1999; 99IL-0133455.
XX
XX (COMP-) COMPUGEN LTD.

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[illegible]

PT	Disulfide-bond	96..109
FT	Disulfide-bond	111..124
FT	Disulfide-bond	132
FT	/note=	"disulfide bond to residue 160 of Factor X heavy chain (see AAM05820), or to residue 108 of Factor Xa heavy chain (see AAR95597 and AAR95598)."
XX		
PN	WO9613274-A1.	
PD	09-MAY-1996.	
XX		
PF	27-OCT-1995;	95WO-US13940.
XX		
PR	28-OCT-1994;	94US-0330978.
XX		
PA	(CORT-) COR THERAPEUTICS INC.	
XX		
P1	King RS;	
XX		
XX	WPI, 1996-239270/24.	
DR		
XX		
PT	Prepn. of an inhibited form of an activated blood factor, e.g.	
PT	factor X - by treating partially purified blood factor preps. with	
PT	an activating factor and an inhibiting factor	
XX		
P5	Disclosure; Fig 1; 45pp: English.	
XX		
CC	This sequence represents the light chain of human Factor X (the heavy	
CC	chain is represented by AAM05820). Factor X must be activated to Factor	
CC	Xa before the protease is incorporated into the prothrombinase complex.	
CC	In Factor Xa the light chain sequence is identical to the Factor X light	
CC	chain, and the heavy chain is a truncated version of the Factor X heavy	
CC	chain. An inhibited form of activated Factor X is prepared by the	
CC	method of the invention. In this method, a partially purified	
CC	preparation containing the blood factor is treated to convert the factor	
CC	into an activated form (using an immobilised activating enzyme). The	
CC	activated form is then converted into an inhibited form in a single step,	
CC	and the inhibited factor is recovered. The inhibited blood factor is	
CC	recovered by immunofinity chromatography using an antigen specific	
CC	monoclonal antibody coupled to an activated resin (such as agarose), or	
CC	an anion exchange column with an anion-exchange group linked to a	
CC	naturally derived polysaccharide or a synthetically derived polymeric	
CC	matrix. The activated resin used preferably uses activation chemistry	
CC	selected from tressyl, azactone, aldehyde, hydrazide, N-hydroxy	
CC	succinimide or triazine. This method produces a highly purified	
CC	preparation of an inhibited form (either permanently or transiently	
CC	inhibited) of an activated blood factor in high yield. The factors	
CC	produced can be used in the treatment of coagulation disorders, or	
CC	disorders of vasculature function.	
XX		
SQ	Sequence	139 AA;
OY	Query Match	57.7%; Score 105; DB 17; Length 139;
Dd	Best Local Similarity	38.6%; Pred. No. 1.8e-10;
Matches	17; Conservative	7; Mismatches 20; Indels 0; Gaps 0;
OY	1 ANAFLXLRGSLRXCKXXQCSEFXAXXIFKDAARTKLFWISY	44
:	:: : :	
Dd	1 ansfltmkghlrrtcmcttcscytartvtfdsdkntutfwmyk	44
RESULT	42	
AAP60057	AAP60057 standard; protein: 453 AA.	
AC	AAP60057;	
XX		
DT	23-MAY-1991 (first entry)	
XX		
DE	Factor IX/Factor VII fusion peptide.	
XX		

1. **Introduction**

2. **Background**

3. **Methods**

4. **Results**

5. **Conclusion**

6. **References**

7. **Appendix**

8. **Table 1**

9. **Table 2**

10. **Table 3**

11. **Table 4**

12. **Table 5**

13. **Table 6**

14. **Table 7**

15. **Table 8**

16. **Table 9**

17. **Table 10**

18. **Table 11**

19. **Table 12**

20. **Table 13**

21. **Table 14**

22. **Table 15**

23. **Table 16**

24. **Table 17**

25. **Table 18**

26. **Table 19**

27. **Table 20**

28. **Table 21**

29. **Table 22**

30. **Table 23**

31. **Table 24**

32. **Table 25**

33. **Table 26**

34. **Table 27**

35. **Table 28**

36. **Table 29**

37. **Table 30**

38. **Table 31**

39. **Table 32**

40. **Table 33**

41. **Table 34**

42. **Table 35**

43. **Table 36**

44. **Table 37**

45. **Table 38**

46. **Table 39**

47. **Table 40**

48. **Table 41**

49. **Table 42**

50. **Table 43**

51. **Table 44**

52. **Table 45**

53. **Table 46**

54. **Table 47**

55. **Table 48**

56. **Table 49**

57. **Table 50**

58. **Table 51**

59. **Table 52**

60. **Table 53**

61. **Table 54**

62. **Table 55**

63. **Table 56**

64. **Table 57**

65. **Table 58**

66. **Table 59**

67. **Table 60**

68. **Table 61**

69. **Table 62**

70. **Table 63**

71. **Table 64**

72. **Table 65**

73. **Table 66**

74. **Table 67**

75. **Table 68**

76. **Table 69**

77. **Table 70**

78. **Table 71**

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ID	AA	Residue	Score	Rank	Protein	Length
1	AA	1	1.00	1	AA	1
2	AA	2	1.00	1	AA	2
3	AA	3	1.00	1	AA	3
4	AA	4	1.00	1	AA	4
5	AA	5	1.00	1	AA	5
6	AA	6	1.00	1	AA	6
7	AA	7	1.00	1	AA	7
8	AA	8	1.00	1	AA	8
9	AA	9	1.00	1	AA	9
10	AA	10	1.00	1	AA	10
11	AA	11	1.00	1	AA	11
12	AA	12	1.00	1	AA	12
13	AA	13	1.00	1	AA	13
14	AA	14	1.00	1	AA	14
15	AA	15	1.00	1	AA	15
16	AA	16	1.00	1	AA	16
17	AA	17	1.00	1	AA	17
18	AA	18	1.00	1	AA	18
19	AA	19	1.00	1	AA	19
20	AA	20	1.00	1	AA	20
21	AA	21	1.00	1	AA	21
22	AA	22	1.00	1	AA	22
23	AA	23	1.00	1	AA	23
24	AA	24	1.00	1	AA	24
25	AA	25	1.00	1	AA	25
26	AA	26	1.00	1	AA	26
27	AA	27	1.00	1	AA	27
28	AA	28	1.00	1	AA	28
29	AA	29	1.00	1	AA	29
30	AA	30	1.00	1	AA	30
31	AA	31	1.00	1	AA	31
32	AA	32	1.00	1	AA	32
33	AA	33	1.00	1	AA	33
34	AA	34	1.00	1	AA	34
35	AA	35	1.00	1	AA	35
36	AA	36	1.00	1	AA	36
37	AA	37	1.00	1	AA	37
38	AA	38	1.00	1	AA	38
39	AA	39	1.00	1	AA	39
40	AA	40	1.00	1	AA	40
41	AA	41	1.00	1	AA	41
42	AA	42	1.00	1	AA	42
43	AA	43	1.00	1	AA	43
44	AA	44	1.00	1	AA	44
45	AA	45	1.00	1	AA	45
46	AA	46	1.00	1	AA	46
47	AA	47	1.00	1	AA	47
48	AA	48	1.00	1	AA	48
49	AA	49	1.00	1	AA	49
50	AA	50	1.00	1	AA	50
51	AA	51	1.00	1	AA	51
52	AA	52	1.00	1	AA	52
53	AA	53	1.00	1	AA	53
54	AA	54	1.00	1	AA	54
55	AA	55	1.00	1	AA	55
56	AA	56	1.00	1	AA	56
57	AA	57	1.00	1	AA	57
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59	AA	59	1.00	1	AA	59
60	AA	60	1.00	1	AA	60
61	AA	61	1.00	1	AA	61
62	AA	62	1.00	1	AA	62
63	AA	63	1.00	1	AA	63
64	AA	64	1.00	1	AA	64
65	AA	65	1.00	1	AA	65
66	AA					

DT 09-OCT-1991 (first entry)

XX
XX

XX

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FT      /label= xlc
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FT	Domain	55	64
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FT
/label= growth_factor_domains
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FT	Disulfide-bond	57..62
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[illegible]

PERCUT E 11

AC AAR22513;

XX

KW Mutant; prothrombinase complex; proteolytic; precursor; thrombosis;

OS Homo sapiens.

XX

PF 04-SEP-1991; 91WO-US063337.

XX
FN 07 SEP 1960, 2000 00/0040.
XX

PA	(CORT-) COR THERAPEUTICS IN.
XX	
PI	Wolf D:
XX	
DR	WPI: 1992-114303/14.
XX	
PT	New analogues of Factor Xa peptide - useful for treating
PT	haemophilia, thrombosis, inflammation and transplant
PT	complications, for in-vivo diagnosis
PS	Claim 7; Fig 1; 59pp: English.
XX	
CC	The full length cDNA of human factor X (Mp19X) was converted to
CC	encode a truncated form of human Factor X, designated 'rx', by deletion
CC	of the activation peptide by oligonucleotide site directed mutagenesis.
CC	An oligonucleotide was used to align Arg 142 following the
CC	C-terminus of the Factor X light chain with Ile 53 of the Factor X
CC	activation peptide (1st residue of the heavy chain). When expressed
CC	in CHO cells the truncated peptide was cleaved endogenously.
CC	Modified Factor Xa was further produced by acylation e.g. with the
CC	p-nitrophenyl ester of p-toluoylic acid. Factor 'rx' is used to
CC	treat or prevent thrombosis: inflammation; restenosis or complications
CC	of transplantation. It is also used in treatment of adult respiratory
CC	distress syndrome and haemophilia. The modified Factor X has no
CC	proteolytic activity and interferes with the ability of endogenous
CC	factor Xa to convert prothrombin to thrombin. Antibodies reactive
CC	with Factor 'rx' are passive therapeutic agents and used for diagnosis.
CC	See also AAR22512.
XX	
XX	Sequence 436 AA:
SQ	
	Query Match 52.7%; Score 96; DB 13; Length 436;
	Best Local Similarity 38.6%; Pred. NO. 2.1e-08;
	Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;
QY	1 ANAFLXLRLGSLRXRCXXQCSEFXAXXIFKDXARTRFLFWISY 44
	: : :
Db	41 ansfleemkghlhercemetscyeatzevfdsdktnfwmky 84
RESULT 45	
AAR35762	
ID	AAR35762 standard; protein: 448 AA.
XX	
AC	AAR35762;
XX	
DT	24-SEP-1993 (first entry)
XX	
DE	Factor X (X).
XX	
KW	PC; protein C; IX; Factor IX; X; Factor X; PT; prothrombin; VII;
KW	Factor VII; CT; chymotrypsinogen; SP; serine protease; binding;
XX	exosite; catalytic activity.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Region
FT	1..139 location/Qualifiers
FT	/note: "Factor X light chain"
FT	140..142
FT	/note: "Factor X activation"
FT	143..448
FT	/note: "Factor X heavy chain"
FT	409..423
FT	/note: "exosite 1"
FT	330..350
FT	/note: "exosite 2"
FT	330..344
FT	/note: "pref. PC polypeptide; claim 2, page 136"
FT	404..418
FT	/note: "pref. PC polypeptide; claim 2, page 136"
FT	415..429
FT	Peptide

FT		/note= "pref. PC polypeptide; clalm 2, page 136"
FT	Peptide	285..306
FT		/note= "clalm 7, page 138 describes an antibody
FT		that reacts with Factor X; fragments
FT		330-344, 404..418 and 415-429 but not
FT		with fragment 285-306"
XX		
PN	WO9309804-A.	
XX		
PD	27-MAY-1993.	
XX		
PF	18-NOV-1992;	92MO-US10242.
XX		
PR	18-NOV-1991;	91US-0793989.
XX		
PA	(SCRI) SCHRIPPS RES INST.	
XX		
PI	Griffin JH, Masters RM;	
XX		
DR	WPI: 1993-182244/22.	
XX		
PT	Serine protease derived-polypeptide(s) and anti-peptide	
PT	antibodies - For inhibiting coagulation and assaying for the	
PT	presence of serine protease in fluid samples	
XX		
PS	Disclosure; Page 128-130; 149pp; English.	
XX		
CC	The PC polypeptides indicated in the Features Table inhibit	
CC	coagulation (they prevent binding of serine protease to natural	
CC	substrates, esp. when admin. to give an intravascular blood	
CC	concn. of 0.1-100 (Pref. 0.5-10) microm.	
CC	NB: Sequences corresp. to SEQ ID NO 6, 7, 8 and 9 are described	
CC	in the specification but have not yet been added to the SEQUENCE	
CC	LISTING.	
XX		
SQ	Sequence	448 AA;
Query Match	52.7%;	Score 96; DB 14; Length 448;
Best Local Similarity	38.6%;	Pred. No. 2,2e+08;
Matches 17; Conservative	8; Mismatches 19; Indels	0; Gaps 0;
OY	1 ANAFLXLRXGSLXRCKXXOCSPFXAXXIIFDAXRTKLFWTSY 44	
	: :: : : : :	
DB	1 ansfileemkkghlerecmeetsyeaearevfedsdsktnefunky 44	
RESULT 46		
AAR37402		
ID	AAR37402 standard; protein; 448 AA.	
XX		
AC	AAR37402;	
XX		
DJ	15-SEP-1993 (first entry)	
DE		
XX		
Factor X.		
XX		
KM	Mac-1; macrophage-monocyte adhesive receptor; procoagulant;	
KW	Inflammation; thrombosis; atherosclerosis; septic shock;	
KW	diseminated vascular coagulation; delayed hypersensitivity;	
KW	haemostasis; angiogenesis; leucocyte recruitment; adhesion.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Region	1..139
FT		/note= "Factor X light chain"
FT	Region	140..142
FT		/note= "Factor X connecting tripeptide"
FT	Region	143..448
FT		/note= "Factor X heavy chain"
FT	Region	238..246
FT		/note= "recombination site for Mac-1 binding"

FT	Region	366..373
FT	"note= "recognition site for Mac-1 binding"	
FT	Region	423..430
XX	/note= "recognition site for Mac-1 binding"	
PX		
PN	MO9309803-A.	
XX		
PD	27-MAY-1993.	
XX		
PE	20-NOV-1992; 92WO-US10068.	
XX		
PR	22-NOV-1991; 91US-0798221.	
XX		
PA	(SCHA/) SCHAFER S C.	
PA	(SCRI) SCRIPPS RES INST.	
PX		
PI	Altieri DC, Edgington TS;	
DR	WPI: 1993-182243/22.	
XX		
PT	Factor X-derived polypeptide(s) inhibit binding of factor X to	
PT	Mac-1 - useful for treating thrombosis, atherosclerosis,	
PT	disseminated intravascular coagulation, septic shock etc.	
XX		
PS	Disclosure: Page 101-103; 122pp; English.	
XX		
CC	The sequence shown represents the complete amino acid sequence of	
CC	human Factor X. Fragments of this sequence corresp. to the Mac-1	
CC	(macrophage-monocyte adhesive receptor) recognition sites (see	
CC	features) of 10-25 amino acid residues may be used to inhibit Factor	
CC	Xa monocyte procoagulant activity, specifically inflammation. The	
CC	same effect may be achieved with antibodies raised to such fragments.	
CC	Typical applications include treatment of patients at risk of thrombosis	
CC	or atherosclerosis before surgery, disseminated intravascular	
CC	coagulation, septic shock, inflammation caused by infection (esp. by	
CC	herpes simplex) or autoimmune diseases, delayed hypersensitivity, etc.	
CC	The fragments also inhibit leucocyte/endothelial cell interaction and	
CC	thus regulate responses such as leucocyte recruitment, adhesion and	
CC	extravasation, haematopoiesis, antigen presentation, angiogenesis,	
CC	syncytial formation and haemostasis.	
CC	See also AAR37403-20.	
SQ		
Sequence	448 AA;	
Query Match	52.7%; Score 96; DB 14; Length 448;	
Best Local Similarity	38.6%; Pred. No. 2.2e+08;	
Matches 17; Conservative	8; Mismatches 19; Indels	0; Gaps
OY	1 ANAFLXLRLRGSLNRKCKXXQCSEFXAXXIIFKDAYRTKLFWISY 44	
	::: :: : :	
Dd	1 ansfleeemkghlerecmeetsyeearrevfedsktnefwnky 44	
RESULT 47		
AAM66092		
ID	AAM66092 standard; peptide: 448 AA.	
XX		
AC	AAM66092:	
XX		
DE	16-NOV-1998 (first entry)	
XX		
DE	Human factor X variant.	
XX		
KM	factor X variant; factor V; fVa; diagnostic assay; heparin; thrombin;	
RW	blood coagulation.	
XX		
OS	Homo sapiens.	
XX		
FN	W09839456-A1.	
XX		
DD	11-SEP-1998.	
XX		

[illegible]

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FT      Domain /label= EGF2 domain
FT      154..165
FT      /label= EGF2 domain
FT      Domain 166..216
FT      /label= Activating domain
FT      Domain 217..454
FT      /label= catalytic domain
XX      WO9747737-A1.
XX      18-DEC-1997.
XX      11-JUN-1997; 97WO-EP03027.
XX      06-JUL-1996; 96EP-0110959.
XX      11-JUN-1996; 96EP-0109288.
XX      22-JUN-1996; 96EP-0110109.
XX      (BOEF ) BOEHRINGER MANNHEIM GMBH.
XX      Hopfner K, Kopetzki E;
XX      WPI; 1998-052304/05.
XX      N-PSDB; AAV10462.
XX      Non-glycosylated, truncated forms of factor IX family protein with
XX      serine protease activity - used to screen for specific modulators
XX      and to assay factor IXa
XX      Disclosure; Fig 3; 49pp; German.
XX      This sequence represents a human factor X protease. This protein is used
XX      in the construction of a novel non-glycosylated protein and truncated
XX      and zymogen forms of this protein, which have serine protease activity.
XX      The protein is composed of various domains from a factor IX family
XX      protein, namely a catalytic domain (CD) N-terminally bound to a
XX      zymogen-activating domain (ZAD) N-terminally bound to an EGF1 and/or
XX      EGF2 domain (EGF - epidermal growth factor-like domain). Such proteins
XX      are used to identify activators/inhibitors of factor IX family proteins
XX      (potentially useful as regulators of coagulation, fibrinolysis and
XX      homeostasis). The protein in zymogen form is also useful in assays for
XX      detecting factor IXa activity in aqueous solution (specifically in body
XX      fluids). The protein can be used to produce co-crystals with protease
XX      variants or inhibitors for x-ray structural analysis and drug modelling
XX      and as restriction proteases in biotechnology. These truncated proteins
XX      have the same specificity as factor IX family proteases and can be
XX      produced in prokaryotes in a form that allows production of active enzyme
XX      by conversion to native form and enzymatic cleavage.
XX      Sequence 467 AA:
SO

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Query Match 52.7%; Score 96; DB 19; Length 467;
 Best local Similarity 38.6%; Pred. No. 2.3e-08;
 Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

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QY      1 ANAFLLXLRKXSLKXKCKXXKQCSFXXAXXIFKDXKRTKLEWISY 44
      |||:::| | | | | | | | | | | | | | | | | | | | | |
      23 ansfleemkkghlercemecscyeaarevfedsknefwky 66

```

RESULT 49
 AAR22512
 ID AAR22512 standard; Protein; 488 AA.
 AC AAR22512;
 XX
 DT 28-JUL-1992 (first entry)
 XX
 DE Mutated precursor of human Factor X analogue.
 XX
 KM Mutant; prothrombinase complex; proteolytic; precursor; thrombosis;
 KM Inflammation; restenosis; transplantation; haemophilia; antibodies.

```

XX      Homo sapiens.
XX      OS
XX      WO9204378-A.
XX      19-MAR-1992.
XX      04-SEP-1991; 91WO-US06337.
XX      04-SEP-1990; 90US-0578646.
XX      (CORT-) COR THERAPEUTICS IN.
XX      WOLF D;
XX      WPI; 1992-114303/14.
XX      New analogues of Factor Xa peptide - useful for treating
XX      haemophilia, thrombosis, inflammation and transplant
XX      complications, for in-vivo diagnosis
XX      Claim 3; Fig 1; 59pp; English.
XX      The full length cDNA of human factor X was obt'd. from Dr. W.R.
XX      Church, University of Vermont. This human factor X cDNA was cloned
XX      into the EcoRI site of vector pBSII (Stratagene) to obtain pBSX.
XX      The HindIII-XbaI fragment of pBSX comprising the entire factor X
XX      coding region was subcloned into the HindIII-XbaI site of vector
XX      M3mp19 (Mpi19X). Oligonucleotide site-directed mutagenesis was
XX      then performed using oligomers to convert serine 185 on the factor
XX      X heavy chain to alanine, and to convert aspartic acid 88 on the
XX      factor X heavy chain to asparagine. Modified factor Xa was further
XX      produced by acylation e.g. with the p-nitrophenyl ester of p-toluoylic
XX      acid. Modified factor X is used to treat or prevent thrombosis;
XX      inflammation; restenosis or complications of transplantation. It
XX      is also used in treatment of adult respiratory distress syndrome
XX      and haemophilia. The modified factor X has no proteolytic activity
XX      and interferes with the ability of endogenous factor Xa to convert
XX      prothrombin to thrombin. Antibodies reactive with modified factor X
XX      are passive therapeutic agents and used for diagnosis.
XX      See also AAR22513.
XX      Sequence 488 AA:
SO

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Query Match 52.7%; Score 96; DB 13; Length 488;
 Best local Similarity 38.6%; Pred. No. 2.4e-08;
 Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

```

QY      1 ANAFLLXLRKXSLKXKCKXXKQCSFXXAXXIFKDXKRTKLEWISY 44
      |||:::| | | | | | | | | | | | | | | | | | | | | |
      41 ansfleemkkghlercemecscyeaarevfedsknefwky 84

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RESULT 50
 AAR22511
 ID AAR22511 standard; Protein; 488 AA.
 AC AAR22511;
 XX
 DT 28-JUL-1992 (first entry)
 XX
 DE Human Factor Xa1.
 XX
 KM Mutant; prothrombinase complex; proteolytic; precursor; thrombosis;
 KM Inflammation; restenosis; transplantation; haemophilia; antibodies.
 XX
 OS Homo sapiens.
 XX
 PN WO9204378-A.
 XX
 PD 19-MAR-1992.

PF 04-SEP-1991; 91WO-US06337.
 XX
 PR 04-SEP-1990; 90US-0578646.
 XX
 PA (CORT-) COR THERAPEUTICS IN.
 XX
 PI Wolf D;
 XX
 DR WPI: 1992-114303/14.
 XX
 PT New analogues of Factor Xa peptide - useful for treating
 PT haemophilia, thrombosis, inflammation and transplant
 PT complications, for in-vivo diagnosis
 XX
 PS Claim 3: Fig 1: 59pp: English.
 XX
 CC The full length cDNA for factor X (see Leytus, S.P. et al., Proc.
 CC Natl. Acad. Sci. USA (1984) 81: 3699) was subcloned in M13mp19 and
 CC subjected to site specific mutagenesis to replace Ser 185 and Asp 88.
 CC In a typical case mutagenesis was first performed with an
 CC oligonucleotide extending Arg 142 of the light chain by Arg and Lys,
 CC then aligning with the 53 of the activation peptide. When expressed
 CC in CHO cells the truncated peptide was cleaved endogenously.
 CC Modified Factor Xa was further produced by acylation e.g. with the
 CC p-nitrophenyl ester of p-toluoylic acid. Factor Xai is used to
 CC treat or prevent thrombosis; inflammation; resenosis or complications
 CC of transplantation. It is also used in treatment of adult respiratory
 CC distress syndrome and haemophilia. The modified factor Xai has no
 CC proteolytic activity and interferes with the ability of endogenous
 CC factor Xa to convert prothrombin to thrombin. Antibodies reactive
 CC with Factor Xai are passive therapeutic agents and used for diagnosis.
 CC See also AAR22513.
 XX
 SQ Sequence 488 AA:

Query Match 52.7%; Score 96; DB 13; Length 488;
 Best Local Similarity 38.6%; Pred. No. 2.4e-08;
 Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

OY 1 ANAFELXLRXGSLRXKXKXCSFXAXXIFKDXRFXLFWISY 44
 ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
 Db 41 ansfleemkkghlrecmeetsyeaarevfedsdktnefmky 84

Search completed: September 3, 2002, 15:14:50
 Job time: 778 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 3, 2002, 15:05:07 ; Search time 20.6 Seconds
(without alignments)
52.171 Million cell updates/sec

Title: US-09-302-239-3-COPY

Perfect score: 182
Sequence: 1 ANAFLLXLRGSLRXCKXX.....XXAXIFKDXRTKLEWISY 44

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/laa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/laa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/laa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/laa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/laa/PCITUS.COMB.pep:*
6: /cgn2_6/ptodata/2/laa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	158	86.8	44	3	US-08-955-636-26 Sequence 26, Appl
2	158	86.8	44	3	US-08-955-636-27 Sequence 27, Appl
3	157	86.3	44	3	US-08-955-636-3 Sequence 3, Appl
4	157	86.3	44	3	US-08-955-636-28 Sequence 28, Appl
5	157	86.3	406	1	US-08-293-778-24 Sequence 24, Appl
6	157	86.3	406	1	US-08-293-411-5 Sequence 5, Appl
7	157	86.3	406	5	US-08-955-471-5 Sequence 5, Appl
8	157	86.3	406	5	PCIT-US92-10242-5 Sequence 5, Appl
9	157	86.3	444	1	US-08-475-845-2 Sequence 2, Appl
10	157	86.3	444	2	US-08-327-690-2 Sequence 2, Appl
11	157	86.3	444	2	US-08-660-289-2 Sequence 2, Appl
12	157	86.3	444	2	US-08-537-807-2 Sequence 2, Appl
13	157	86.3	444	2	US-08-871-003-2 Sequence 2, Appl
14	157	86.3	444	4	US-08-464-233-2 Sequence 2, Appl
15	157	86.3	444	4	US-09-189-607-2 Sequence 2, Appl
16	157	86.3	444	4	US-09-378-907-2 Sequence 2, Appl
17	157	86.3	444	5	PCIT-US94-05779-2 Sequence 2, Appl
18	157	86.3	466	1	US-07-882-202A-4 Sequence 4, Appl
19	157	86.3	466	1	US-08-021-615A-4 Sequence 4, Appl
20	157	86.3	466	1	US-08-321-777-4 Sequence 4, Appl
21	157	86.3	466	4	US-09-009-217-14 Sequence 14, Appl
22	157	86.3	466	4	US-09-009-656-14 Sequence 14, Appl
23	157	86.3	466	5	PCIT-US93-04493-4 Sequence 4, Appl
24	154	86.6	44	3	US-08-955-636-30 Sequence 30, Appl
25	151	83.0	44	3	US-08-955-636-29 Sequence 4, Appl
26	142	78.0	41	1	US-08-229-280-4 Sequence 4, Appl
27	121	66.5	44	3	US-08-955-636-4 Sequence 4, Appl

28	105	57.7	139	1	US-08-330-978-2 Sequence 2, Appl
29	105	57.7	139	1	US-08-474-042-2 Sequence 2, Appl
30	105	57.7	139	1	US-08-484-558-2 Sequence 2, Appl
31	105	57.7	139	1	US-08-774-592-2 Sequence 2, Appl
32	105	57.7	437	1	US-08-487-037-2 Sequence 2, Appl
33	105	57.7	437	1	US-08-487-037-3 Sequence 3, Appl
34	105	57.7	488	1	US-08-487-037-1 Sequence 1, Appl
35	96	52.7	448	1	US-08-295-411-3 Sequence 3, Appl
36	96	52.7	448	2	US-08-955-471-3 Sequence 3, Appl
37	96	52.7	448	5	PCIT-US92-10068-1 Sequence 1, Appl
38	96	52.7	448	5	PCIT-US92-10242-3 Sequence 3, Appl
39	95	52.2	44	3	US-08-955-636-18 Sequence 18, Appl
40	95	52.2	487	1	US-08-469-486-53 Sequence 53, Appl
41	95	52.2	487	2	US-08-469-658-53 Sequence 53, Appl
42	95	52.2	492	1	US-08-469-486-2 Sequence 2, Appl
43	95	52.2	492	2	US-08-469-486-2 Sequence 2, Appl
44	93	51.1	44	3	US-08-955-636-24 Sequence 24, Appl
45	93	51.1	44	3	US-08-955-636-35 Sequence 35, Appl
46	92	50.5	41	1	US-08-229-280-2 Sequence 2, Appl
47	90	49.5	44	3	US-08-955-636-23 Sequence 23, Appl
48	89	48.9	44	3	US-08-955-636-2 Sequence 2, Appl
49	87	47.8	44	3	US-08-955-636-19 Sequence 19, Appl
50	87	47.8	44	3	US-08-955-636-20 Sequence 20, Appl

ALIGNMENTS

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RESULT 1
US-08-955-636-26
; Sequence 26, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelstuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-26

Query Match      86.8%; Score 158; DB 3; Length 44;
Best local Similarity 95.5%; Pred. No. 7.2e-21;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 ANAFLLXLRGSLRXCKXQCSFXAXXIFKDXRTKLEWISY 44
      ||||||| ||||||| ||||||| ||||||| |||||||
Db      1 ANAFLLXLRGSLRXCKXQCSFXAXXIFKDXRTKLEWISY 44

RESULT 2
US-08-955-636-27
; Sequence 27, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelstuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)..(0)
; OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid
US-08-955-636-27

Query Match          86.3%; Score 157; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 7.2e-21;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ANAFLXLRXGSLXRXCKXKXCSFXAXXIFKDXARTKLFWISY 44
Db 1 ANAFLXLRDQSLXRXCKXKXCSFXAXXIFKDXARTKLFWISY 44

RESULT 3
US-08-955-636-3
; Sequence 3, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelissestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ. ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)..(0)
; OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid
US-08-955-636-3

Query Match          86.3%; Score 157; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 1.1e-20;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ANAFLXLRXGSLXRXCKXKXCSFXAXXIFKDXARTKLFWISY 44
Db 1 ANAFLXLRPGSLXRXCKXKXCSFXAXXIFKDXARTKLFWISY 44

RESULT 4
US-08-955-636-28
; Sequence 28, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelissestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ. ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
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; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid
US-08-955-636-28

Query Match          86.3%; Score 157; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 1.1e-20;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ANAFLXLRXGSLXRXCKXKXCSFXAXXIFKDXARTKLFWISY 44
Db 1 ANAFLXLRPGSLXRXCKXKXCSFXAXXIFKDXARTKLFWISY 44

RESULT 5
US-08-293-778-24
; Sequence 24, Application US/08293778
; Patent No. 5580560
; GENERAL INFORMATION:
; APPLICANT: Nicolaisen, Else M.
; APPLICANT: Bjorn, Soren E.
; APPLICANT: Wiberger, Finn C.
; APPLICANT: Woodbury, Richard
; TITLE OF INVENTION: MODIFIED FACTOR VII/VIII
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5580560o No. 5580560disk of No. 5580560th America, Inc.
; STREET: 405 Lexington Avenue, 62nd Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,778
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/104,509
; FILING DATE:
; APPLICATION NUMBER: DK 3235/87
; FILING DATE: 25-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/434,149
; FILING DATE: 13-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK88/00103
; FILING DATE: 24-JUN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,248
; FILING DATE: 12-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Agilis, Cheryl H.
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 3129,224-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-867-0298
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-293-778-24

Query Match          86.3%; Score 157; DB 1; Length 406;
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APPLICANT: Griffin, John H.
APPLICANT: Westers, Rolf
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESSEE: Research Institute
STREET: 10666 North Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10242
FILING DATE: 19921118
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Filling, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRO472P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..152
OTHER INFORMATION: /note= "Factor VII light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
PCT-US92-10242-5
Query Match 86.3%; Score 157; DB 5; Length 406;
Best Local Similarity 72.7%; Pred. No. 1.1e-19;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
OY 1 ANAFLXLRXGSLXRXCKXXQCSEFXAXXIFKDXARTKLFWISY 44
Db 1 ANAFLLELRPGSLERCKEEOCSFEAREIFKDAERTKLFWISY 44
RESULT 9
US-08-475-845-2
Sequence 2, Application US/08475845
Patent No. 5788965
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Brenggaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,845
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/327,690
FILING DATE: 24-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-475-845-2
Query Match 86.3%; Score 157; DB 1; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.2e-19;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
OY 1 ANAFLXLRXGSLXRXCKXXQCSEFXAXXIFKDXARTKLFWISY 44
Db 39 ANAFLLELRPGSLERCKEEOCSFEAREIFKDAERTKLFWISY 82
RESULT 10
US-08-327-690-2
Sequence 2, Application US/08327690
Patent No. 5817788
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Brenggaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:


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: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.24
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/189,607
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/660,289
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/327,690
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/065,725
: FILING DATE: 21-MAY-1993
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/662,920
: FILING DATE: 28-FEB-1991
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Parmelee, Steven W.
: REGISTRATION NUMBER: 31,990
: REFERENCE/DOCKET NUMBER: 13952-8-4
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 206-467-9600
: TELEFAX: 415-543-5043
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 444 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-09-189-607-2

Query Match      86.3%; Score 157; DB 4; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.2e-19;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLRXCKXQCSFXXAXXIFKDXRTKLFWISY 44
Db 39 ANAFLELRGSLRECKEKCSEFARLIFKDAERTKLFWISY 82

RESULT 16
US-09-378-907-2
: Sequence 2, Application US/09378907
: Patent No. 6183743
: GENERAL INFORMATION:
: APPLICANT: Hart, Charles E.
: APPLICANT: Petersen, Lars C.
: APPLICANT: Hedner, Ulla
: APPLICANT: Rasmussen, Mirella E.
: TITLE OF INVENTION: Modified Factor VII
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Zymogenetics, Inc.
: STREET: 1201 Eastlake Avenue East
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98102
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.24
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/378,907
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: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/871,003
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Sawislak, Deborah A
: REGISTRATION NUMBER: 37,438
: REFERENCE/DOCKET NUMBER: 90-07C7
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 444 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-09-378-907-2

Query Match      86.3%; Score 157; DB 4; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.2e-19;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLRXCKXQCSFXXAXXIFKDXRTKLFWISY 44
Db 39 ANAFLELRGSLRECKEKCSEFARLIFKDAERTKLFWISY 82

RESULT 17
PCT-US94-05779-2
: Sequence 2, Application PC/TUS9405779
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: Modified Factor VII
: NUMBER OF SEQUENCES: 4
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/05779
: FILING DATE: 23-MAY-1994
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/065,725
: FILING DATE: 21-MAY-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/662,920
: FILING DATE: 28-FEB-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Parmelee, Steven W.
: REGISTRATION NUMBER: 31,990
: REFERENCE/DOCKET NUMBER: 13952-8-1PC
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 206-467-9600
: TELEFAX: 415-543-5043
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 444 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: PCT-US94-05779-2

Query Match      86.3%; Score 157; DB 5; Length 444;
Best Local Similarity 72.7%; Pred. No. 1.2e-19;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLRXCKXQCSFXXAXXIFKDXRTKLFWISY 44
Db 39 ANAFLELRGSLRECKEKCSEFARLIFKDAERTKLFWISY 82
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RESULT 18
US-07-882-202A-4
Sequence 4, Application US/07882202A
Patent No. 5374617
GENERAL INFORMATION:
APPLICANT: Morrissey, James H.
APPLICANT: Comp, Philip C.
TITLE OF INVENTION: Treatment of Bleeding with Modified
TITLE OF INVENTION: Tissue Factor In Combination with FVIIa
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Richards, Medlock & Andrews
STREET: 1201 Elm Street, Suite 4500
CITY: Dallas
STATE: Texas
COUNTRY: US
ZIP: 75270-2197
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/882,202A
FILING DATE: 13-MAY-1992
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Hansen, Eugenia S.
REGISTRATION NUMBER: 31,966
REFERENCE/DOCKET NUMBER: OMRF B34290
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4500
TELEFAX: 214-939-4600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 466 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-882-202A-4

Query Match 86.3%; Score 157; DB 1; Length 466;
Best Local Similarity 72.7%; Pred. No. 1,2e-19;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFILXLRXGSLRXKXKXOCSEFXAXXIFKDAKRTKLFMISY 44
Db 61 ANAFLEELRPGSLERECKEEOCSFEAREIFKDAERTKLFMISY 104

RESULT 19
US-08-021-615A-4
Sequence 4, Application US/08021615A
Patent No. 5504064
GENERAL INFORMATION:
APPLICANT: Morrissey, James H.
APPLICANT: Comp, Philip C.
TITLE OF INVENTION: Treatment of Bleeding with Modified
TITLE OF INVENTION: Tissue Factor In Combination with an Activator of
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Richards, Medlock & Andrews
STREET: 1201 Elm Street, Suite 4500
CITY: Dallas
STATE: Texas
COUNTRY: US
ZIP: 75270-2197
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/021,615A
FILING DATE: 19-FEB-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/882,202
FILING DATE: 13-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hansen, Eugenia S.
REGISTRATION NUMBER: 31,966
REFERENCE/DOCKET NUMBER: OMRF B34290CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4500
TELEFAX: 214-939-4600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 466 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-021-615A-4

Query Match 86.3%; Score 157; DB 1; Length 466;
Best Local Similarity 72.7%; Pred. No. 1,2e-19;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFILXLRXGSLRXKXKXOCSEFXAXXIFKDAKRTKLFMISY 44
Db 61 ANAFLEELRPGSLERECKEEOCSFEAREIFKDAERTKLFMISY 104

RESULT 20
US-08-321-777-4
Sequence 4, Application US/08321777
Patent No. 5504067
GENERAL INFORMATION:
APPLICANT: Morrissey, James H.
APPLICANT: Comp, Philip C.
TITLE OF INVENTION: Treatment of Bleeding with Modified
TITLE OF INVENTION: Tissue Factor In Combination with FVIIa
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Richards, Medlock & Andrews
STREET: 1201 Elm Street, Suite 4500
CITY: Dallas
STATE: Texas
COUNTRY: US
ZIP: 75270-2197
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321,777
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/882202
FILING DATE: 13-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hansen, Eugenia S.
REGISTRATION NUMBER: 31,966
REFERENCE/DOCKET NUMBER: OMRF B34290C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4500
TELEFAX: 214-939-4600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

TITLE OF INVENTION: Truncated Tissue Factor and FvIIa or
TITLE OF INVENTION: FvIIa Activator for Blood Coagulation
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Richards, Medlock & Andrews
STREET: 1201 Elm Street, Suite 4500
CITY: Dallas
STATE: Texas
COUNTRY: US
ZIP: 75270-2197
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/04493
FILING DATE: 19930512
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/882202
FILING DATE: 13-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/021615
FILING DATE: 19-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Y.
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: OMRF B34290CIPC/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-639-4500
TELEFAX: 214-939-4600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 466 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-04493-4

Query Match 86.3%; Score 157; DB 5; Length 466;
Best Local Similarity 72.7%; Pred. No. 1.2e-19;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLXLRGSLXRXCKXCSFXXAXXIFKDAKRTKLFWISY 44
Db 61 ANAFLXLRPGSLERCKEKGCSFEARXEIFKDAKRTKLFWISY 104

RESULT 24
US-08-955-636-30
Sequence 30, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Nelsstuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 30
LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid
US-08-955-636-30

Query Match 84.6%; Score 154; DB 3; Length 44;
Best Local Similarity 93.2%; Pred. No. 3.6e-20;
Matches 41; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ANAFLXLRGSLXRXCKXCSFXXAXXIFKDAKRTKLFWISY 44
Db 1 ANAFLXLRGSLXRXCKXCSFXXARXIFKDAKRTKLFWISY 44

RESULT 25
US-08-955-636-29
Sequence 29, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Nelsstuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 29
LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid
US-08-955-636-29

Query Match 83.0%; Score 151; DB 3; Length 44;
Best Local Similarity 93.2%; Pred. No. 1.2e-19;
Matches 41; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ANAFLXLRGSLXRXCKXCSFXXAXXIFKDAKRTKLFWISY 44
Db 1 ANAFLXLRPGSLXRXCKXCSFXXARXIFKDAKRTKLFWISY 44

RESULT 26
US-08-229-280-4
Sequence 4, Application US/08229280
Patent No. 5516640
GENERAL INFORMATION:
APPLICANT: WATANABE, Keisuke
APPLICANT: : NAKAKI, Toru
APPLICANT: : IWASAKI, Yoshihiro
TITLE OF INVENTION: METHOD OF DETERMINATION OF
TITLE OF INVENTION: PIVKA OF EVERY KIND AND
TITLE OF INVENTION: REAGENT THEREFOR
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESSES:
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS, P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/229,280
FILING DATE:
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-130015

FILING DATE: MAY 7, 1993
APPLICATION NUMBER: JP 6-16348
FILING DATE: FEBRUARY 10, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Teriyence F. Chapman
REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Furuya Case 1312
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homosapiens
FEATURE:
OTHER INFORMATION: Xaa in the sequence is
US-08-229-280-4
OTHER INFORMATION: -carboxyglutamic acid

Query Match 78.0%; Score 142; DB 1; Length 41;
Best local Similarity 95.1%; Pred. No. 4.2e-18;
Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 ANAFLLXLRKGSLLRXCKXKXQCSFXXAXXIFKDXRTKLEW 41
1 ANAFLLXLRKGSLLRXCKXKXQCSFXXAXXIFKDXRTKLEW 41
Db

RESULT 27
US-08-955-636-4
Sequence 4, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Nelstuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 44
TYPE: PRT
ORGANISM: Bos taurus
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-4

Query Match 66.5%; Score 121; DB 3; Length 44;
Best local Similarity 75.0%; Pred. No. 2.1e-14;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
OY 1 ANFLXLLRKGSLRXCKXKXQCSFXXAXXIFKDXRTKLEWISY 44
1 ANFLXLLRKGSLRXCKXKXQCSFXXAXXIFRNXRTROPWVS 44
Db

RESULT 28
US-08-330-978-2
Sequence 2, Application US/08330978
Patent No. 5389571
GENERAL INFORMATION:
APPLICANT: King, Robert
TITLE OF INVENTION: PROCESS FOR PRODUCTION OF INHIBITED

TITLE OF INVENTION: FORMS OF ACTIVATED BLOOD FACTORS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,978
FILING DATE: 28-OCT-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,558
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2803-0007.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)887-1500
TELEFAX: (202)822-0168
TELEX: 90-4030 MRSNFORSMH
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 17..22
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 50..61
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 55..70
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 72..81
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 89..100
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 96..109
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 111..124
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 132
OTHER INFORMATION: /note= "Disulfide linkage with
OTHER INFORMATION: residue 160 of SEQ ID NO:1, residue 108 of SEQ ID NO:3 or
US-08-330-978-2

Query Match 57.7%; Score 105; DB 1; Length 139;
Best local Similarity 38.6%; Pred. No. 4.4e-11;
Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;
OY 1 ANAFLLXLRKGSLLRXCKXKXQCSFXXAXXIFKDXRTKLEWISY 44
1 ANFLTKMKKGHLRRTCMTTTCSTYRTARVFTDSDKNTFTWVK 44
Db


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? LOCATION: -17
? OTHER INFORMATION: /note= "Location of Intron A"
?
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: (37^38)
? OTHER INFORMATION: /note= "Location of Intron B"
?
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: 46
? OTHER INFORMATION: /note= "Location of Intron C"
?
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: 63
? OTHER INFORMATION: /note= "An amino acid represented
? OTHER INFORMATION: by the greek letter Beta"
?
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: 84
? OTHER INFORMATION: /note= "Location of Intron D"
?
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: 128
? OTHER INFORMATION: /note= "Location of Intron E"
?
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: (158^159)
? OTHER INFORMATION: /note= "Location of Intron F"
?
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: 198
? OTHER INFORMATION: /note= "Location of Intron G"
?
? FEATURE:
? NAME/KEY: Disulfide-bond
? LOCATION: group(17..22, 50..61, 55..70, 72..81, 89..100, 96
? LOCATION: ..109, 111..124, 132..251, 150..155, 170..186,
? LOCATION: 299..313, 324..352)
?
US-08-487-037-2

Query Match 57.7%; Score 105; DB 1; Length 437;
Best Local Similarity 38.6%; Pred. No. 1.4e-10;
Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANAFLLXLRKGSLLRXCKXKXOCSEFXAXXIFKDAKRTLEWISY 44
Db 41 ANSFLTTMKKGHLTRCMTTCSYTTATVFTDSDKNTFNWNY 84

RESULT 33
US-08-487-037-3
? Sequence 3, Application US/08487037
? Patent No. 5795863
? GENERAL INFORMATION:
? APPLICANT: Wolf, David L.
? TITLE OF INVENTION: RECOMBINANT AGENTS AFFECTING THROMBOSIS
? NUMBER OF SEQUENCES: 11
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: MORRISON & FOERSTER
? STREET: 2000 Pennsylvania Avenue, NW
? CITY: Washington
? STATE: DC
? COUNTRY: USA
? ZIP: 20006-1812
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/487,037
? FILING DATE: 07-JUN-1995
? CLASSIFICATION: 514
? ATTORNEY/AGENT INFORMATION:

```

```

? NAME: Adler, Reid G.
? REGISTRATION NUMBER: 30,988
? REFERENCE/DOCKET NUMBER: 2803-0002.02
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (202) 887-1500
? TELEFAX: (202) 887-0763
? TELEX: 90-4030
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 437 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: both
?
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: -40..397
? OTHER INFORMATION: /note= "Same features apply from
? OTHER INFORMATION: SEQ ID NO:2"
?
? FEATURE:
? NAME/KEY: Protein
? LOCATION: 1..139
? OTHER INFORMATION: /note= "Factor Xa - Light Chain"
?
? FEATURE:
? NAME/KEY: Peptide
? LOCATION: -40..0
? OTHER INFORMATION: /note= "Pre-pro leader sequence"
?
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: -17
? OTHER INFORMATION: /note= "Location of Intron A"
?
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: (37^38)
? OTHER INFORMATION: /note= "Location of Intron B"
?
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: 46
? OTHER INFORMATION: /note= "Location of Intron C"
?
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: 63
? OTHER INFORMATION: /note= "An amino acid represented
? OTHER INFORMATION: by the greek letter Beta"
?
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: 84
? OTHER INFORMATION: /note= "Location of Intron D"
?
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: 198
? OTHER INFORMATION: /note= "Location of Intron G"
?
? FEATURE:
? NAME/KEY: Disulfide-bond
? LOCATION: group(17..22, 50..61, 55..70, 72..81, 89..100, 96
? LOCATION: ..109, 111..124, 132..251, 150..155, 170..186,
? LOCATION: 299..313, 324..352)
?
US-08-487-037-3

```

```

Query Match 57.7%; Score 105; DB 1; Length 437;
Best Local Similarity 38.6%; Pred. No. 1.4e-10;
Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANAFLLXLRKGSLLRXCKXKXOCSEFXAXXIFKDAKRTLEWISY 44
Db 41 ANSFLTTMKKGHLTRCMTTCSYTTATVFTDSDKNTFNWNY 84

RESULT 34

```

```

: Sequence 1, Application US/08487037
: Patent No. 5795863
: GENERAL INFORMATION:
: APPLICANT: Wolf, David L.
: TITLE OF INVENTION: RECOMBINANT AGENTS AFFECTING THROMBOSIS
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 2000 Pennsylvania Avenue, NW
: City: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20006-1812
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/487,037
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Adler, Reid G.
: REGISTRATION NUMBER: 30,988
: REFERENCE/DOCKET NUMBER: 2803-0002.02
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 887-1500
: TELEFAX: (202) 887-0763
: TELEX: 90-4030
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 488 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: both
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: -17
: OTHER INFORMATION: /note= "Location of Intron A"
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: (37~38)
: OTHER INFORMATION: /note= "Location of Intron B"
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 46
: OTHER INFORMATION: /note= "Location of Intron C"
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 63
: OTHER INFORMATION: /note= "Amino acid represented by
: OTHER INFORMATION: the greek letter Beta"
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 84
: OTHER INFORMATION: /note= "Location of Intron D"
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 128
: OTHER INFORMATION: /note= "Location of Intron E"
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: (209~210)
: OTHER INFORMATION: /note= "Location of Intron F"
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 249
: OTHER INFORMATION: /note= "Location of Intron G"
: FEATURE:
: NAME/KEY: Peptide
: LOCATION: -40..0

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```

OTHER INFORMATION: /note= "Pre-Pro leader sequence"
FEATURE:
NAME/KEY: Protein
LOCATION: 1..139
OTHER INFORMATION: /note= "Factor Xa- light chain"
FEATURE:
NAME/KEY: Peptide
LOCATION: 143..194
OTHER INFORMATION: /note= "Activation Peptide"
FEATURE:
NAME/KEY: Protein
LOCATION: 195..448
OTHER INFORMATION: /note= "Factor Xa-Heavy Chain"
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: group(17..22, 50..61, 55..70, 72..81, 89..100, 96
LOCATION: 109, 111..124, 132..302, 201..206, 221..237,
LOCATION: 350..364, 375..403)
US-08-487-037-1

Query Match          57.7%; Score 105; DB 1; Length 488;
Best Local Similarity 38.6%; Pred. No. 1.6e-10;
Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

QY      1 ANAFPLXLRXGSLKXCKXQCSPFXAXXIFRKDAXRTLFWMISY 44
        |||||::| | | | | | | | | | | | | | | | | | | |
Db       41 ANSFLTTMKKGHLFRTCMTTSCSYTARTAVFTDSOKTNFMWKY 84

RESULT 35
US-08-295-411-3
Sequence 3, Application US/08295411
Patent No. 5679639
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Westers, Rolf M.
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESSEE: Research Institute
STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US//08/295,411
FILING DATE: 22-AUG-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI263_0CI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: amino acid

```

TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..139
OTHER INFORMATION: /note= "Factor X Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 140..142
OTHER INFORMATION: /note= "Factor X Connecting
OTHER INFORMATION: Tripeptide"
FEATURE:
NAME/KEY: Region
LOCATION: 143..448
OTHER INFORMATION: /note= "Factor X Heavy Chain"
US-08-295-411-3

Query Match 52.7%; Score 96; DB 1; Length 448;
Best Local Similarity 38.6%; Pred. No. 5.5e-09;
Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

OY 1 ANAFLXLRKXSLRXCKXXOCSEFXAXXIFKDXAKTKLEWISY 44
DB 1 ANSFLBEMKKGHLRECMEEETCSYEAREVEFEDSDKTNEFWNKY 44

RESULT 36
US-08-955-471-3
Sequence 3, Application US/08955471
Patent No. 5968751
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESSEE: Research Institute
STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955,471
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/295,411
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI263.0C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..139
OTHER INFORMATION: /note= "Factor X Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 140..142
OTHER INFORMATION: /note= "Factor X Connecting
OTHER INFORMATION: Tripeptide"
FEATURE:
NAME/KEY: Region
LOCATION: 143..448
OTHER INFORMATION: /note= "Factor X Heavy Chain"
US-08-955-471-3

Query Match 52.7%; Score 96; DB 2; Length 448;
Best Local Similarity 38.6%; Pred. No. 5.5e-09;
Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

OY 1 ANAFLXLRKXSLRXCKXXOCSEFXAXXIFKDXAKTKLEWISY 44
DB 1 ANSFLBEMKKGHLRECMEEETCSYEAREVEFEDSDKTNEFWNKY 44

RESULT 37
PCT-US92-10068-1
Sequence 1, Application PC/TUS9210068
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C
APPLICANT: Edgington, Thomas S
APPLICANT: Fair, Daryl S
TITLE OF INVENTION: Factor X-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Inflammation
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESSEE: Research Institute
STREET: 10666 North Torrey Pines Road
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10068
FILING DATE: 19921120
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/798,221
FILING DATE: 22-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: SCR1221P
REFERENCE/DOCKET NUMBER: 34,163
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO

ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version
SOFTWARE: #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,486
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06363/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070
TELEFAX: 617 542 8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-469-486-53

Query Match 52.2%; Score 95; DB 1; Length 487;
Best Local Similarity 40.9%; Pred. No. 9e-09;
Matches 18; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

OY 1 ANAPLXLRXGSLRXCKXKXOCSPFXAXXIRKDAKRTLFWISY 44
DB 41 ANSFLVEVKGNLERECLEACSLSEAREVFEADAQDTDFWSKY 84

RESULT 41
US-08-469-658-53
Sequence 53, Application US/08469658
Patent No. 5917018
GENERAL INFORMATION:
APPLICANT: Th egeresen, Hans Christian
APPLICANT: Holzet, Thor Las
APPLICANT: Elzerodt, Michael
TITLE OF INVENTION: IMPROVED METHOD FOR THE REFOOLDING OF
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRES:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version
SOFTWARE: #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,658
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06363/002002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070
TELEFAX: 617 542 8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-469-658-53

Query Match 52.2%; Score 95; DB 2; Length 487;
Best Local Similarity 40.9%; Pred. No. 9e-09;
Matches 18; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

OY 1 ANAPLXLRXGSLRXCKXKXOCSPFXAXXIRKDAKRTLFWISY 44
DB 41 ANSFLVEVKGNLERECLEACSLSEAREVFEADAQDTDFWSKY 84

RESULT 42
US-08-469-486-2
Sequence 2, Application US/08469486
Patent No. 5739281
GENERAL INFORMATION:
APPLICANT: Hoegersen, Hans Christian
APPLICANT: Holzet, Thor Las
APPLICANT: Elzerodt, Michael
TITLE OF INVENTION: Improved method for the refolding of
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRES:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version
SOFTWARE: #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,486
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06363/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070
TELEFAX: 617 542 8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-469-486-2

Query Match 52.2%; Score 95; DB 1; Length 492;
Best Local Similarity 40.9%; Pred. No. 9.1e-09;
Matches 18; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXCKXXQCSFXXAXXIFDAXRTKLFWISY 44
DB 41 ANSFLEEVKQGNLERECLEACSLLEBARVFEADQTDFFWSKY 84

RESULT 43

US-08-469-658-2
; Sequence 2, Application US/08469658
; Patent No. 5917018
; GENERAL INFORMATION:
; APPLICANT: Th egeresen, Hans Christian
; APPLICANT: Holteit, Thor Ias
; APPLICANT: Etzerodt, Michael
; TITLE OF INVENTION: IMPROVED METHOD FOR THE REFOOLDING OF
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version
; SOFTWARE: #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,658
; FILING DATE: June 5, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/192,060
; FILING DATE: February 4, 1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06363/002002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 542 5070
; TELEFAX: 617 542 8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 492 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-469-658-2

Query Match 52.2%; Score 95; DB 2; Length 492;
Best Local Similarity 40.9%; Pred. No. 9.1e-09;
Matches 18; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXCKXXQCSFXXAXXIFDAXRTKLFWISY 44
DB 41 ANSFLEEVKQGNLERECLEACSLLEBARVFEADQTDFFWSKY 84

RESULT 44
US-08-955-636-24

; Sequence 24, Application US/08955636A

; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Neilsenstuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 44
; TYPE: PPT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-24

Query Match 51.1%; Score 93; DB 3; Length 44;
Best Local Similarity 70.7%; Pred. No. 1.7e-09;
Matches 29; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXCKXXQCSFXXAXXIFDAXRTKLFW 41
DB 1 ANSFLLXLRGSLRXCKXXQCSFXXAXXIFDAXRTKLFW 41

RESULT 45

US-08-955-636-35
; Sequence 35, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Neilsenstuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 44
; TYPE: PPT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-35

Query Match 51.1%; Score 93; DB 3; Length 44;
Best Local Similarity 70.7%; Pred. No. 1.7e-09;
Matches 29; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXCKXXQCSFXXAXXIFDAXRTKLFW 41
DB 1 ANSFLLXLRGSLRXCKXXQCSFXXAXXIFDAXRTKLFW 41

RESULT 46

US-08-229-280-2
; Sequence 2, Application US/08229280
; Patent No. 551640
; GENERAL INFORMATION:
; APPLICANT: WATANABE, Keisuke
; APPLICANT: NARAKI, Toru
; APPLICANT: IMASAKI, Yoshihiro
; TITLE OF INVENTION: METHOD OF DETERMINATION OF

```
; TITLE OF INVENTION: PLVRA OF EVERY KIND AND
; OTHER INFORMATION: REAGENT THEREFOR
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS, P.C.
; STREET: 2026 Rambling Road
; CITY: Kalamazoo
; STATE: Michigan
; COUNTRY: USA
; ZIP: 49008-1699
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
; COMPUTER: IBM PC/XT/AT Compatible
; OPERATING SYSTEM: MS-DOS 5.0
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/229,280
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-130015
; FILING DATE: MAY 7, 1993
; APPLICATION NUMBER: JP 6-16348
; FILING DATE: FEBRUARY 10, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Terrylene F. Chapman
; REGISTRATION NUMBER: 32 549
; REFERENCE/DOCKET NUMBER: Furuya Case 1312
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (616) 381-1156
; TELEFAX: (616) 381-5465
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORGANISM SOURCE:
; ORGANISM: Homosapiens
; FEATURE:
; OTHER INFORMATION: Xaa in the sequence is
; OTHER INFORMATION: -carboxyglutamic acid
;
; US-08-229-280-2
;
Query Match 50.5%; Score 92; DB 1; Length 41;
Best Local Similarity 61.0%; Pred. No. 2.3e-09;
Matches 25; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 ANAFLXXLRKXSLKRXCKXXQCSFXXAXXIFKDXARTKLFWISY 41
Db 1 ANSFLXXKRGHXLKRXCMXXTCYSXXARXVFXSDKTNXEW 41

RESULT 47
; US-08-955-636-23
; Sequence 23, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelsstuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: MOD_RES
```

```
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
; US-08-955-636-23
;
Query Match 49.5%; Score 90; DB 3; Length 44;
Best Local Similarity 63.6%; Pred. No. 5.6e-09;
Matches 28; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANAFLXXLRKXSLKRXCKXXQCSFXXAXXIFKDXARTKLFWISY 44
Db 1 ANSFLXXLRHGNVXRKCSXXVCXFXXARXIFONTXDTMAFWSEY 44

RESULT 48
; US-08-955-636-2
; Sequence 2, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelsstuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
;
; US-08-955-636-2
;
Query Match 48.9%; Score 89; DB 3; Length 44;
Best Local Similarity 63.6%; Pred. No. 8.4e-09;
Matches 28; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANAFLXXLRKXSLKRXCKXXQCSFXXAXXIFKDXARTKLFWISY 44
Db 1 ANSFLXXLRPGNVXRKCSXXVCXFXXARXIFONTXDTMAFWSEY 44

RESULT 49
; US-08-955-636-19
; Sequence 19, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelsstuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
;
; US-08-955-636-19
;
Query Match 47.8%; Score 87; DB 3; Length 44;
Best Local Similarity 68.3%; Pred. No. 1.9e-08;
```

Matches 28; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

OY 1 ANAFXLRLKXGSLRXKCKXKXOCSEFYXXAXXIFKDAKRTKLEFW 41
||:||||| ||||| || ||||| ||:| | ||
Db 1 ANSFLXLRLHSSLXRXKCIXXICDFXXAKXIFEDVDTLAFW 41

RESULT 50
US-08-955-636-20
; Sequence 20, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelisestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-20

Query Match 47.8%; Score 87; DB 3; Length 44;
Best Local Similarity 68.3%; Pred. No. 1.9e-08;
Matches 28; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

OY 1 ANAFXLRLKXGSLRXKCKXKXOCSEFYXXAXXIFKDAKRTKLEFW 41
||:||||| ||||| || ||||| ||:| | ||
Db 1 ANSFLXLRLHSSLXRXKCIXXICDFXXAKXIFEDVDTLAFW 41

Search completed: September 3, 2002, 15:15:48
Job time: 641 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 3, 2002, 15:01:52 ; Search time 25.1 Seconds
(without alignments)
168.443 Million cell updates/sec

Title: US-09-302-239-3-COPY
Perfect score: 182
Sequence: 1 ANAFLLXLRGSLRXCKKX.....XXAXXIFKDXAKRTKLEWISY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : PIR.71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	157	86.3	466	1 KFHU7	coagulation factor
2	123	67.6	443	2 I46932	coagulation factor
3	113	62.1	407	1 KFE07	coagulation factor
4	99	54.4	461	1 S18994	protein C (activat
5	98	53.8	461	1 JX0210	protein C (activat
6	96	52.7	488	1 EXHU	coagulation factor
7	95	52.2	492	1 EXBO	coagulation factor
8	90	49.5	482	1 EXRT	coagulation factor
9	89	48.9	456	1 KXBO	protein C (activat
10	85	46.7	475	1 EXCH	coagulation factor
11	85	46.7	622	1 TBHU	coagulation factor
12	82	45.1	461	1 KXHU	thrombin (EC 3.4.2
13	81	44.5	617	2 S10511	protein C (activat
14	81	44.5	618	2 A35827	thrombin (EC 3.4.2
15	80	44.0	416	1 KFE0	coagulation factor
16	77	42.3	461	1 KFHU	coagulation factor
17	72	39.6	452	1 A30351	coagulation factor
18	72	39.6	459	2 J00419	coagulation factor
19	65	35.7	625	2 TBO	coagulation factor
20	63	34.6	642	1 S53433	thrombin (EC 3.4.2
21	60	33.0	675	1 KXBO	plasma protein S p
22	58	31.9	642	2 S53434	plasma protein S p
23	58	31.9	646	2 S38819	plasma protein S -
24	57	31.3	396	1 KXHU	plasma protein S p
25	57	31.3	396	1 KXBO	plasma protein S -
26	56.5	31.0	675	1 KXRTS	plasma protein S p
27	52	28.6	422	1 KXHU	probable MAP kinase
28	52	28.6	422	1 KXHU	plasma protein Z p
29	51.5	28.3	594	2 D84859	probable MAP kinase

30	51.5	28.3	603	2 C96575	probable MAP kinase
31	50	27.5	675	1 KXMS	plasma protein S p
32	49	26.9	673	2 A48089	growth arrest-spec
33	47	25.8	674	2 I55476	growth potentialin
34	47	25.8	678	2 B48089	growth arrest-spec
35	45	24.7	879	2 S55864	hypothetical prote
36	43	23.6	306	2 I49068	protein kinase SW
37	42.5	23.4	410	2 T25574	hypothetical prote
38	42	23.1	211	2 D9696	uncharacterized 10
39	42	23.1	255	2 JS0054	hypothetical 26.6k
40	41.5	22.8	322	2 T15792	hypothetical prote
41	41.5	22.8	322	2 T20272	hypothetical prote
42	41	22.5	219	2 AE2449	hypothetical prote
43	41	22.5	455	2 C83494	probable 2-isoprop
44	40	22.0	807	2 T28279	ORF MSV119 probabl
45	39.5	21.7	83	2 T17839	hypothetical prote
46	39.5	21.7	312	2 H90517	hypothetical prote
47	39.5	21.7	319	2 T15137	hypothetical prote
48	39.5	21.7	516	2 H84424	probable MAP kinase
49	39	21.4	271	2 S66691	probable membrane
50	39	21.4	281	2 AD3369	universal stress p

ALIGNMENTS

RESULT 1
KFHU7
coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human
C.Species: Homo sapiens (man)
C.Date: 19-May-1998 #sequence_revision 19-May-1994 #text_change 08-Dec-2000
C.Accession: A28322; A23819; A31186; B31186; S63524
R.O'Hara, P.J.; Grant, F.J.; Haldeman, B.A.; Grant, C.L.; Insley, M.Y.; Hagen, F.S.; M
Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987
A.Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-dep
A.Reference number: A28322; MUID:87260948
A.Accession: A28322
A.Molecule type: DNA
A.Residues: 1-466 <OH>
A.Cross-references: GB:J02933; NID:9180333; PIDN:AAA51983.1; PID:9180334
R.Hagen, F.S.; Gray, C.L.; O'Hara, P.; Grant, F.J.; Saarl, G.C.; Woodbury, R.G.; Hart
Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986
A.Title: Characterization of a cDNA coding for human factor VII.
A.Reference number: A23819; MUID:86205965
A.Accession: A23819
A.Molecule type: mRNA
A.Residues: 1-466 <HAG>
A.Cross-references: GB:M1323; NID:9182799; PIDN:AAA88040.1; PID:9182801
R.Thim, L.; Bjorn, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen,
Biochemistry 27, 7785-7793, 1988
A.Title: Amino acid sequence and posttranslational modifications of human factor VII-
A.Reference number: A90539; MUID:89088153
A.Accession: A31186
A.Molecule type: protein
A.Residues: 61-212 <THR>
A.Accession: B31186
A.Molecule type: protein
A.Residues: 213-466 <THR>
R.Bjorn, S.; Foster, D.C.; Thim, L.; Wlberg, F.C.; Christensen, M.; Komiyama, Y.; Pe
J. Biol. Chem. 266, 11051-11057, 1991
A.Title: Human plasma and recombinant factor VII. Characterization of O-glycosylation
A.Contents: annotation; carbohydrate binding sites
R.Persson, E.; Petersen, L.C.
Eur. J. Biochem. 234, 293-300, 1995
A.Title: Structurally and functionally distinct Ca(2+) binding sites in the gamma-car
A.Reference number: S63524; MUID:96096752
A.Accession: S63524
A.Molecule type: protein
A.Residues: 61-65; 99-103; 105-109; 213-217; 308-312 <PER>
C.Genetics: 61-65; 99-103; 105-109; 213-217; 308-312 <PER>
A.Gene: GDB:F7
A.Cross-references: GDB:119897; OMIM:227500

A:Residues: 1-461 <OKA2>
A:Cross-references: EMBL:X64336; NID:g56962; PIDN:CAA5617.1; PID:g56963
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; glycoprotein; hydrolase; serine proteinase
F:1-32/Domain: signal sequence #status predicted <SIG>
F:27-85/Domain: Gla domain homology <Gla>
F:33-42/Domain: propeptide #status predicted <PRO>
F:43-461/Product: protein C #status predicted <PRC>
F:91-130/Domain: EGF homology <EG1>
F:139-174/Domain: EGF homology <EG2>
F:213-445/Domain: trypsin homology <TRY>
F:47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status
F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F:121-130,139-150,146-159,161-174,182-202,239-255,373-387,398-426/Disulfide bonds: #stat
F:215,291,355/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:254,300,402/Active site: His, Asp, Ser #status predicted

Query Match 54.4%; Score 99; DB 1; Length 461;
Best Local Similarity 45.5%; Pred. No. 1.2e-09;
Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

OY 1 ANAFLLXLRGSLKRXCKXXGCSFXAXXIFKDAKTKLFWISY 44
DB 42 ANSFLEEVNAGSLERECMEICDFEAOEIFQNVEDTLAFWIKY 85

RESULT 5

protein C (activated) (EC 3.4.21.69) precursor - mouse
N:Alternate names: vitamin K-dependent serine proteinase
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: JX0210
R:Tada, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.
J. Biochem. 111, 491-495, 1992
A:Title: Isolation and characterization of a mouse protein C cDNA.
A:Reference number: JX0210; MUID:92316897
A:Accession: JX0210
A:Molecule type: mRNA
A:Residues: 1-461 <TAD>
A:Cross-references: GB:D10445; NID:g220385; PIDN:BAA01235.1; PID:g220386
A:Experimental source: liver
C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re
s:
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
F:1-33/Domain: signal sequence #status predicted <SIG>
F:27-85/Domain: Gla domain homology <Gla>
F:34-41/Domain: propeptide #status predicted <PRO>
F:42-196,199-461/Product: protein C #status predicted <PRC>
F:42-196/Domain: light chain #status predicted <PCL>
F:91-130/Domain: EGF homology <EG1>
F:139-174/Domain: EGF homology <EG2>
F:199-461/Domain: heavy chain #status predicted <PCH>
F:199-211/Domain: activation peptide #status predicted <ACV>
F:212-461/Product: vitamin K-dependent serine proteinase #status predicted <VIT>
F:212-445/Domain: trypsin homology <TRY>
F:47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status
F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F:121-130,139-150,146-159,161-174,182-219,238-254,373-387,398-426/Disulfide bonds: #stat
F:214,290,355/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:253,299,402/Active site: His, Asp, Ser #status predicted

Query Match 53.8%; Score 98; DB 1; Length 461;
Best Local Similarity 45.5%; Pred. No. 1.7e-09;
Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

OY 1 ANAFLLXLRGSLKRXCKXXGCSFXAXXIFKDAKTKLFWISY 44
DB 42 ANSFLEEVNAGSLERECMEICDFEAOEIFQNVEDTLAFWIKY 85

RESULT 6

EXHU
coagulation factor Xa (EC 3.4.21.6) precursor [validated] - human
N:Alternate names: Stuart factor
C:Species: Homo sapiens (man)
C:Date: 15-Nov-1984 #sequence_revision 02-May-1994 #text_change 08-Dec-2000
C:Accession: A24478; J00917; A42485; A25853; A22208; A21284; A20362; S39415; I54051;
R:Levy, S.P.; Foster, D.C.; Kurachi, K.; Davie, E.W.
Biochemistry 25, 5098-5102, 1986
A:Title: Gene for human Factor X: a blood coagulation factor whose gene organization
A:Reference number: A24478; MUID:87026600
A:Accession: A24478
A:Molecule type: DNA
A:Residues: 1-488 <LEV>
A:Cross-references: GB:L29433; GB:M4327; NID:g459809; PIDN:AAA52764.1; PID:g182831
R:Messier, T.L.; Pittman, D.D.; Long, G.L.; Kaufman, R.J.; Church, W.R.
Gene 99, 291-294, 1991
A:Title: Cloning and expression in COS-1 cells of a full-length cDNA encoding human c
A:Reference number: J00917; MUID:91216473
A:Accession: J00917
A:Molecule type: mRNA
A:Residues: 1-488 <MES>
A:Cross-references: GB:M57285; NID:g182389; PIDN:AAA52421.1; PID:g182390
R:Miao, C.H.; Leytus, S.P.; Chung, D.W.; Davie, E.W.
J. Biol. Chem. 267, 7395-7401, 1992
A:Title: Liver-specific expression of the gene coding for human factor X, a blood coa
A:Reference number: A42485; MUID:92218390
A:Accession: A42485
A:Molecule type: DNA
A:Residues: 1-15 <MIA>
A:Experimental source: liver
A:Note: Sequence extracted from NCB1 backbone (NCBI:93780, NCBIP:93787)
R:Kaul, R.K.; Hildebrand, B.; Roberts, S.; Jagadeeswaran, P.
Gene 41, 311-314, 1986
A:Title: Isolation and characterization of human blood-coagulation factor X cDNA.
A:Reference number: A25853; MUID:86221713
A:Accession: A25853
A:Molecule type: mRNA
A:Residues: 19-284, 'E', 289-488 <KAU>
A:Cross-references: GB:M2613; NID:g180335; PIDN:AAA51984.1; PID:g180336
R:Fung, M.R.; Hay, C.W.; Macgillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985
A:Title: Characterization of an almost full-length cDNA coding for human blood coagul
A:Reference number: A22208; MUID:85216545
A:Accession: A22208
A:Molecule type: mRNA
A:Residues: 13-441, 'S', 443-488 <FUN>
A:Cross-references: GB:K03194; NID:g182840; PIDN:AAA52490.1; PID:g182841
R:Leytus, S.P.; Chung, D.W.; Kistell, W.; Kurachi, K.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 81, 3699-3702, 1984
A:Title: Characterization of a cDNA coding for human factor X.
A:Reference number: A21284; MUID:84222026
A:Accession: A21284
A:Molecule type: mRNA
A:Residues: 13-284, 'F', 289-488 <LE2>
A:Cross-references: GB:K01886
R:McMullen, B.A.; Fujikawa, K.; Kistell, W.; Sasagawa, T.; Howald, W.N.; Kwa, E.Y.; We
Biochemistry 22, 2875-2884, 1983
A:Title: Complete amino acid sequence of the light chain of human blood coagulation f
A:Reference number: A20362; MUID:83257207
A:Accession: A20362
A:Molecule type: protein
A:Residues: 41-179 <MCM>
R:Inoue, K.; Morita, T.
Eur. J. Biochem. 218, 153-163, 1993
A:Title: Identification of O-linked oligosaccharide chains in the activation peptides
A:Reference number: S39414; MUID:94062825
A:Accession: S39415
A:Molecule type: protein
A:Residues: 183-234 <INO>
A:Note: glycosylation sites
A:Note: identification and characterization of beta-hydroxyaspartic acid

R.Jagadeeswaran P.; Reddy, S.V.; Rao, K.J.; Hamsabhusanam, K.; Lyman, G.
Gene 84, 517-519, 1989

A>Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human
A/Reference number: I54051; MUID:90128299

A/Accession: 154051

A:Molecule type: DNA

C>Status: translation not shown; translated from GB/EMBL/DDBJ

A/Residues: 1-23 <RES>

A/Cross-references: GB:M33297; NID:g183860; PIDN:AAA52636.1; PID:g553330

R.Padmanabhan, K., Padmanabhan, K.P.; Tullinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Blat
J. Mol. Biol. 232, 947-966, 1993

A>Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.

A/Reference annotation: A49458; MUID:93360277

C/Contents: annotation: x-ray crystallography, 2.2 angstroms

C/Comment: The two chains held together by one disulfide bond are formed from a single-c
C/Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or
C/Genetics:

A/Gene: GDB:F10

A/Cross-references: GDB:119890; OMIM:227600

A/Map position: 13q34-13q34

A/Introns: 24/1: 77/3; 86/1: 124/1; 150/3: 249/3; 289/L.

A>Note: deficiency of this factor causes Stuart disease

C/Function:

A>Description: catalyzes the proteolytic activation of prothrombin to thrombin In the pr
A/Pathway: blood coagulation

C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamat
F.1-732/Domain: signal sequence #status predicted <SIG>

F.24-40/Domain: propenptide #status predicted <PRO>

E.25-84/Domain: Gla domain homology <GLA>

F.41-179/Product: coagulation factor X light chain #status experimental <LCH>

F.90-121/Domain: EGF homology <EGF>

F.129-164/Domain: EGF homology <EGG>

F.183-488/Product: coagulation peptide #status experimental <APR>

F.223-488/Product: coagulation factor Xa heavy chain #status experimental <ACT>

F.238-462/Domain: trypsin homology <TRY>

F.46/47_54_56_59_60_65_66_69_72_79/Modified site: gamma-carboxylglutamic acid (Glu) #stat
E.57-62/Disulfide bonds: #status predicted

F.90-101_95-110_112-121_129-140_136-149_151-164_172-342_241-246_261-277_390-404_415-443/F
F.103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

F.199_211/Binding site: carbohydrate (Thr) (covalent) #status experimental

F.221_231/Binding site: carbohydrate (Asn) (covalent) #status experimental

E.234-235/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #stat
F.276_322_419/Active site: His, Asp, Ser #status experimental

Query Match 52.7%; Score 96; DB 1; Length 488;
Best Local Similarity 38.6%; Pred. No. 4,2e-09;
Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

OY 1 ANAFLLXLRKSGSLRXCKXXQCSFYXAXIFKDAAFKTLFWISY 44
II::I::I::I::I::I::I::I::I::I::I::I::I::I::I::I
Db 41 ANSFLEMKKGHLERECEMEFTCSYEAREVEDEDSKTNEFMNKY 84

RESULT 7

XBO
coagulation factor Xa (EC 3.4.21.6) precursor - bovine
N/Alternate names: Stuart factor
C/Species: Bos primigenius taurus (cattle)
C/Date: 24-Apr-1984 #sequence revision 17-Mar-1987 #text change 16-Jul-1999
C/Accession: A22867; AL4997; AJ2030; A34412; S33414; A00925
R/Fung, M.R.; Campbell, R.M.; Macgillivray, T.A.
Nucleic Acids Res. 12, 4481-4492, 1984
A>Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a
A/Reference number: A22867; MUID:84247315
A/Accession: A22867
A:Molecule type: mRNA
A/Residues: 1-487 <FUN>
A/Cross-references: GB:XO0673; NID:g192; PIDN:CAA2286.1; PID:g193
A/Helfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K.
Biochemistry 19, 659-667, 1980

A:Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).
A:Reference number: A14997; MUID:80130563
A:Accession: A14997
A:Molecule type: protein
A:Residues: 41-102, 'N', 104-180 <ENF>
R:McMullen, B.A.; Fujikawa, K.; Kistiel, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood
A:Reference number: A20274; MUID:83308813
A:Contents: annotation; revision to residue 103
R:Tiliani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.
Proc. Natl. Acad. Sci. U.S.A. 72, 3083-3086, 1975
A:Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.
A:Reference number: A12030; MUID:76053069
A:Accession: A12030
A:Molecule type: protein
A:Residues: 183-292,294-295, 'GDE', 299-334,336-348, 'AE', 351-354,356-441, 'GKEG', 446-492
A:Note: carboxyhydrate binding sites and disulfide bonds were determined
R:Persson, E.; Selandner, M.; Linse, S.; Drakenberg, T.; Oehlin, A.K.; Stenflo, J.
J. Biol. Chem. 264, 16897-16904, 1989
A:Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epiderm
A:Reference number: A34412; MUID:89380326
A:Accession: A34412
A:Molecule type: protein
A:Residues: 85-126 <PER>
A:Note: beta-hydroxyaspartic acid site
R:Inoue, K.; Morita, T.
Eur. J. Biochem. 218, 153-163, 1993
A:Title: Identification of O-linked oligosaccharide chains in the activation peptides
A:Reference number: S39414; MUID:94062825
A:Accession: S39414
A:Molecule type: protein
A:Residues: 183-196;199-209;216-233 <INO>
A:Note: carboxyhydrate binding sites
R:Tiliani, K.; Hermanson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.
Biochemistry 11, 4899-4903, 1972
A:Title: Bovine factor X-1a (activated Stuart factor). Evidence of homology with mamm
A:Reference number: A12453; MUID:7305314
A:Contents: annotation; active site
R:Fujikawa, K.; Tiliani, K.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975
A:Title: Activation of bovine factor X (Stuart factor): conversion of factor Xaalpha
A:Reference number: A13504; MUID:76053121
A:Contents: annotation; activation
R:Sugo, T.; Bjork, I.; Holmgren, A.; Stenflo, J.
J. Biol. Chem. 259, 5705-5710, 1984
A:Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxyglu
A:Reference number: A38024; MUID:84185716
A:Contents: annotation; calcium binding
R:Morita, T.; Jackson, C.M.
J. Biol. Chem. 261, 4008-4014, 1986
A:Reference number: A38025; MUID:86140210
A:Contents: annotation; sulfate binding
C:Comment: Factor Xa converts prothrombin to thrombin during blood clotting.
C:Comment: The two chains are formed from a single-chain precursor for the excision of
C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway)
activation.
C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with s
C:Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vita
C:Genetics:
A:Gene: F10
A:Map position: 13q34
C:Function:
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the
A:Pathway: blood coagulation
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglu
F:1-15/Domain: signal sequence #status predicted <IG>
F:16-40/Domain: propeptide #status predicted <PRO>
F:25-84/Domain: Gla domain homology <GLA>
F:41-180/Product: coagulation factor X light chain #status experimental <LCH>
F:90-121/Domain: EGF homology <EG1>
F:129-164/Domain: EGF homology <EG2>

F:183-492/Product: coagulation factor X heavy chain #status experimental <HCH>
F:183-233/Domain: activation peptide #status experimental <APT>
F:233-492/Product: coagulation factor Xa heavy chain #status experimental <AHC>
F:233-461/Domain: trypsin homology <TRY>
F:46/47/54/56/59/60/65/66/69/72/75/79/Modified site: gamma-carboxyglutamic acid (Glu) #s
F:57-62/90-101/95-110/112-121/129-140/136-149/151-164/172-341/Disulfide bonds: #status F
F:103/Modified site: erythro-beta-hydroxypartitic acid (Asp) #status experimental
F:200/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental
F:208/485/Binding site: carbohydrate (Thr) (covalent) #status experimental
F:218/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:233-233/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #stat
F:240-245/260-276/389-403/414-442/Disulfide bonds: #status experimental
F:275/321/418/Active site: His, Asp, Ser #status predicted

Query Match 52.2% Score 95; DB 1; Length 492;
Best Local Similarity 40.9% Pred. No. 6.3e-09;
Matches 18; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

OY 1 ANAPFLXLRXGSLXRRCKXKXOCFFXXAXIFPDARTKLEFWISY 44
DB 41 ANSFLEEVKQGNLERECLEAEACLEAEVFEEDADQDTDEFMSKY 84

RESULT 8
EXRT
coagulation factor Xa (EC 3.4.21.6) precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Jan-1995 #sequence_revision 07-Feb-1997 #text_change 08-Dec-2000
C:Accession: S49075; J04670; PS0191; PS0190; I62745
R:Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R.
Thromb. Res. 80, 63-73, 1995
A:Title: Evidence for competition between vitamin K-dependent clotting factors for intra
A:Reference number: A8498; MUID:96093366
A:Accession: S49075
A:Molecule type: mRNA
A:Residues: 1-482 <STA1>
A:Cross-references: EMBL:X79807; NID:9506600; PIDN:CAAS6202.1; PID:9506601
A>Note: submitted to the EMBL Data Library, June 1994
A>Note: neither the complete nucleic acid sequence nor the complete translation are show
R:Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R.
Gene 169, 269-273, 1996
A:Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.
A:Reference number: J04670; MUID:96194815
A:Accession: J04670
A:Molecule type: mRNA
A:Residues: 1-482 <STA2>
A:Cross-references: EMBL:X79807; NID:9506600; PIDN:CAAS6202.1; PID:9506601
A:Experimental source: Cos-1 cell
R:Enjyoji, K.; Miyazaki, K.; Kato, H.
J. Biochem. 109, 890-898, 1991
A:Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat pla
A:Reference number: PS0191; MUID:92041742
A:Accession: PS0191
A:Molecule type: protein
A:Residues: 41-58, 'X', 60-65 <ENJ1>
A:Accession: PS0190
A:Molecule type: protein
A:Residues: 183-186, 'X', 188-207 <ENJ2>
R:Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.
Eur. J. Haematol. 52, 162-166, 1994
A:Title: Analysis of the partial nucleotide sequences and deduced primary structures of
A:Reference number: I46196; MUID:94222160
A:Accession: I46196
A:Molecule type: DNA
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 295-383, 'G', 385-455 <MUR>
A:Cross-references: GB:D21215; NID:9415309; PIDN:BA04756.1; PID:94553396
C:Function:
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
A:Pathway: blood coagulation
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxypartitic acid; blood coagulation; calcium binding; carboxyglutam

F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-40/Domain: propeptide #status predicted <PRO>
F:25-84/Domain: Gla domain homology <GLA>
F:41-179/Product: coagulation factor X light chain #status predicted <LCH>
F:90-121/Domain: EGF homology <EG1>
F:129-164/Domain: EGF homology <EG2>
F:183-482/Product: coagulation factor X heavy chain #status predicted <HCH>
F:183-231/Domain: activation peptide #status predicted <APT>
F:232-482/Product: coagulation factor Xa heavy chain #status predicted <ACT>
F:232-460/Domain: trypsin homology <TRY>
F:46/47/54/56/59/60/65/66/69/72/75/79/Modified site: gamma-carboxyglutamic acid (Glu) #s
F:57-62/90-101/95-110/112-121/129-140/136-149/151-164/172-340/238-243/259-275/388-402
F:103/Modified site: erythro-beta-hydroxypartitic acid (Asp) #status predicted
F:187/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:208/Binding site: carbohydrate (Thr) (covalent) #status predicted
F:218/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:231-232/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #s
F:274/320/417/Active site: His, Asp, Ser #status predicted

Query Match 49.5% Score 90; DB 1; Length 482;
Best Local Similarity 38.6% Pred. No. 4.9e-08;
Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

OY 1 ANAPFLXLRXGSLXRRCKXKXOCFFXXAXIFPDARTKLEFWISY 44
DB 41 ANSFEEIKKGNLERECVEICISFEAEVFEEDNKTTEFMNXY 84

RESULT 9
KXBO
protein C (activated) (EC 3.4.21.69) precursor - bovine (fragment)
N:Alternate names: autoprothrombin IIA; plasma protein C
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Nov-1980 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999
C:Accession: A26250; A18385; A18386; A00928
R:Long, G.L.; Balagaje, R.M.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 81, 5653-5656, 1984
A:Title: Cloning and sequence of liver cDNA coding for bovine protein C.
A:Reference number: A26250; MUID:85014826
A:Accession: A26250
A:Molecule type: mRNA
A:Residues: 1-456 <LON>
R:Fernlund, P.; Stenflo, J.
J. Biol. Chem. 257, 12170-12179, 1982
A:Title: Amino acid sequence of the light chain of bovine protein C.
A:Reference number: A18385; MUID:83007325
A:Accession: A18385
A:Molecule type: protein
A:Residues: 40-194 <FER>
A>Note: 82-Lys was also found
R:Drakenberg, T.; Fernlund, P.; Roepstorff, P.; Stenflo, J.
Proc. Natl. Acad. Sci. U.S.A. 80, 1802-1806, 1983
A:Title: beta-Hydroxypartitic acid in vitamin K-dependent protein C.
A:Reference number: A19316; MUID:83169769
A:Contents: annotation; revision to residue 110
R:Stenflo, J.; Fernlund, P.
J. Biol. Chem. 257, 12180-12190, 1982
A:Title: Amino acid sequence of the heavy chain of bovine protein C.
A:Reference number: A18386; MUID:83007326
A:Accession: A18386
A:Molecule type: protein
A:Residues: 197-454, 'PV' <STE>
R:Esmon, N.L.; DeBaault, L.E.; Esmon, C.T.
J. Biol. Chem. 258, 5548-5553, 1983
A:Title: Proteolytic formation and properties of gamma-carboxyglutamic acid-domains
A:Reference number: A37541; MUID:83213513
A:Contents: annotation; activation; calcium binding
R:Johnson, A.E.; Esmon, N.L.; Lane, T.M.; Esmon, C.T.
J. Biol. Chem. 258, 5554-5560, 1983
A:Title: Structural changes required for activation of protein C are induced by Ca2+
A:Reference number: A37542; MUID:83213514
A:Contents: annotation; activation; calcium binding

5. C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that reacts with fibrinogen to form the enzyme thrombin.
C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is cleaved by a trypsin-like enzyme to form two chains, A and B. Chain A is the heavy chain, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reaction is irreversible. Chain B is the light chain, which remains bound to chain A. The gamma-carboxyglutamic acid (Gla) residues and, with stromelysin, the collagen of the thrombin-thrombomodulin complex.
C:Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin K-dependent modification of the propeptide.
C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding
F:1-29/Domain: signal sequence (fragment) #status predicted <Sig>
F:24-83/Domain: Gla domain homology <Gla>
F:30-39/Domain: propeptide #status predicted <Pro>
F:40-194/Product: protein C light chain #status experimental <LCH>
F:98-128/Domain: EGF homology <EG1>
F:137-172/Domain: EGF homology <EG2>
F:197-456/Product: protein C heavy chain #status experimental <HCH>
F:197-210/Domain: activation peptide #status experimental <AP>
F:211-440/Domain: trypsin homology <TRY>
F:445-464,53,55,58,59,62,64,65,68,74/Modified site: gamma-carboxyglutamic acid (Glu) #status experimental
F:110/Modified site: erythro-beta-hydroxyaspartic acid (ASP) #status experimental
F:119-128,137-148,144-151,159-172,180-318,237-253,368-382,393-421/Dsulfide bonds: #status experimental
F:136,289,350/Binding site: carboxylate (Asn) (covalent) #status predicted
F:252,298,397/Active site: His, Asp, Ser #status predicted
F:366/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match	48.9%	Score 89	DB 1	Length 455
Best Local Similarity	40.9%	Pred	No. 7e-08	21
Matches 18	Conservative	5	Mismatches	Indels 0
			Gaps	0

Oy	1	ANAF	LX	LR	GS	SL	NR	CK	XX	OC	SF	XX	XX	IF	DA	RT	KL	EW	TS	44
db	40	AN	SF	LE	LR	AP	GV	NR	EC	SE	VE	CF	FE	AR	DI	NT	DT	MA	FW	83

```

RESULT      10
EXCH
coagulation factor Xa (EC 3.4.21.6) precursor - chicken
N:Alternate names: virus-activating proteinase
C:Species: Gallus gallus (chicken)
C:Date: 12-Feb-1993 #sequence_revision 07-Feb-1997 #text-change 16-Jul-1999
C:Accession: S15838; S20380; S20381
R:Stuuk, H.; Harada, A.; Hayashi, Y.; Wada, K.; Asaka, J.; Gotoh, B.; Ogasawara, T.; Nishida, T.
FEBS Lett. 283, 261-265, 1991
A:Title: Primary structure of the virus activating protease from chick embryo. Its identification and characterization.
A:Reference number: S15838; MUID:91257322
A:Accession: S15838
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-475 <SUZ>
A:Cross-references: DDBJ:D00844; NID:9222869; PIDN:BAA00724.1; PID:9222870
R:Gotoh, B.; Yamauchi, F.; Ogasawara, T.; Nagai, Y.
FEBS Lett. 296, 274-278, 1992
A:Title: Isolation of factor Xa from chick embryo as the amniotic endoprotease responsible for the activation of prothrombin.
A:Reference number: S20380; MUID:92164779
A:Accession: S20380
A:Molecule type: protein
A:Residues: 41-55 <GO2>
A:Accession: S20381
A:Molecule type: protein
A:Residues: 241-246, 'X', 248-251, 'X', 253-261 <GOR>
C:Function:
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of calcium ions.
A:Pathway: blood coagulation
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid, blood coagulation; calcium binding; carboxylated
E:1-20/Domain: signal sequence #status predicted <IG>
E:21-40/Domain: propeptide #status predicted <PRO>
E:25-84/Domain: Gla domain homology <GLA>
F:41-185/Product: coagulation factor X light chain #status experimental <LCH>
F:90-121/Domain: EGF homology <EG1>
E:129-167/Domain: EGF homology <EG2>
F:166-475/Product: coagulation factor X heavy chain #status predicted <HCH>

```

F:186-240/Domain: activation peptide #status predicted <APT>
F:241-475/Product: coagulation Factor Xa heavy chain #status experimental <AHC>
F:241-468/Domain: trypsin homology <TRY>
F:457-62, 54-56, 59, 65, 69, 72, 75, 79/Modified site: gamma-carboxyglutamic acid (Glu) #status predicted
F:56-62, 90-101, 95-110, 112-121, 129-140, 136-152, 154-167, 175-340, 247-252, 267-283, 396-410
F:103/Modified site: eurythro-beta-hydroxyaspartic acid (Asp) #status predicted
F:196, 207, 228, 285/Binding site: carboxylate (asn) (covalent) #status predicted
F:282, 328, 425/Active site: His, Asp, Ser #status predicted

Query Match	46.7%	Score 85;	DB 1;	Length 475;
Best Local Similarity	36.4%	Pred. No. 3.8e-07;		
Matches 16; Conservative	9;	Mismatches 19;	Indels 0;	Gaps

Oy 1 ANAFLLXLRxGSLXRXCkXXOCSEFXAXXI FKDAXRTKLFWISY 44
 ||:|| ::||| :|| |::| :|||
Db 41 ANSFLLEMKOGNIERECNEERCskEAREAFEDNEKTEEFWNII 84

RESULT 11
TBHU

C:Date: 30-Nov-1980 #sequence_revision 22-Jul-1994 #text_change 08-Dec-2000
C:Accession: A29351; A00914; B00914; A37549; A37550; I51952
R:Degen, S.J.F.; Davis, E.W.
Biochemistry 26, 6165-6177, 1987
A:Title: Nucleotide sequence of the gene for human prothrombin.

A;Reference number: A29351; MUID:88077877

A;Accession: A29351
A;Molecule type: DNA

A;Molecule type: DNA
A;Residues: 1-622 <DEG>

A;CROSS-references: GB:MI/262; GB:M33691; NID:g558069; PIDN:AAC63054.1; PID:g3339641
R;Degen, S.J.F.; MacGillivray, R.T.A.; Davle, E.W.

R;Degen, S.J.F.; MacGillivray, R.T.A.; Davle, E.W.

Biochemistry 22, 2087-2097, 1983

A;Title: Characterization of the complete
A;Reference number: A00914; MUID:832314659

A;Accession: A00914
A;Molecule type: mRNA

A;Molecule type: mRNA
A;Residues: 8-163, 'N'

A;Cross-references: GB:V
A;Accession: B00914

A: Molecule type: DNA
A: Residues: 188-311 <DEF3>

R;Walz, D.A.; Hewett-Emmett, D.; Seegers, W.H.
Proc Natl Acad Sci USA 74 1969-1973 1977

A; Reference number: 337540

A;Accession: A37549

A:Residues: 44-118, 'N', 120, 'S', 122-163, 'I', 165-175, 'A', 177-182, 'T', 184-193, 'MV', 196-3

R; Butkowski, R.J.; Ellison, J.; Downing, M.R.; Mann, K.G.
 1981 Chem Soc 4043-4057 1977

A; Title: Primary structure of human prethrombin 2 and alpha-thrombin.
Reference number: A37550. WUID: 77027113

A;Reference number: A37550; MUID:77207112

A;Molecule type: proc

A:Residues: 315-334, 'N', 336-348, 'N', 350-368, 'N', 370-397, 'N', 399-413, 'N', 415-484, 'N', 4

R;Rabiet, M.J.; Blas

A; Reference number: A37551; MUID: 87008532

A;Contents: annotation; activation cle

Ann. N. Y. Acad. Sci. 485, 73-79, 1986

A/Title: Recombinant genetic approaches to functional mapping of thrombin.

A;Reference number: I51952; MUID:87182874

A;Status: translated from GB/EMBL/DBJ

A: molecule type: mRNA

A/Residues: 1-2, R1, 5-100 <RES>
A/Cross-references: GB:M3031; NID:q190723; PIDN:AAA60220.1; PID:q190724

C:Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to f1

C.Comment: Prothrombin is activated on the surface of a phospholipid membrane that binds) can be removed either by factor Xa or thrombin; the cleavage into light and heavy chain ter 314-Arg, are released in natural blood clotting.
 C.Comment: The cleavage after Arg-198, observed in vitro, does not occur in plasma.
 C.Comment: The gamma-carboxyglutamyl residues bind calcium ions, result from the carboxy ent interaction with the negatively charged phospholipid membrane surface.
 C.Comment: The prothrombin precursor is synthesized in the liver.
 C.Genetics:
 A.Gene: GDB:F2
 A.Cross-references: GDB:119894; OMIM:176930
 A.Map position: 11p11-11q12
 A.Introns: 27/1; 80/3; 89/1; 106/1; 141/2; 187/1; 292/1; 335/1; 377/2; 433/2; 491/2; 552
 C.Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
 C.Keywords: acute phase; blood coagulation; calcium binding; carboxyglutamic acid; dupli
 F.1-24/Domain: signal sequence #status predicted <SIG>
 F.25-33/Domain: propeptide #status predicted <PRO>
 F.28-87/Domain: Gla domain homology <GLA>
 F.44-622/Product: prothrombin #status experimental <MAT>
 F.44-327/Domain: activation peptide #status experimental <APT>
 F.108-186/Domain: kringle homology <KR1>
 F.213-291/Domain: thrombin light chain #status experimental <KR2>
 F.328-363/Product: thrombin light chain #status experimental <LCH>
 F.364-622/Product: thrombin heavy chain #status experimental <HCH>
 F.364-613/Domain: trypsin homology <TRY>
 F.49-50,57,59,62,63,68,69,72,75/Modified site: gamma-carboxyglutamic acid (Glu) #status
 F.60-65,90-103,108-186,129-169,157-181,213-291,234-274,262-286/Disulfide bonds: #status
 F.121,147/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F.336-482,536-550,564-594/Disulfide bonds: #status predicted
 F.391-407/Disulfide bonds: #status experimental
 F.406,462/Active site: His, Asp #status predicted
 F.416/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F.568/Active site: Ser #status experimental

Query Match 46.7%; Score 85; DB 1; Length 622;
 Best Local Similarity 36.4%; Pred. No. 4,8e-07;
 Matches 16; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

QY 1 ANAFLLXLRKGSIXRCKXXKCSFFXXAXIIFDKAXRTKLEFWISY 44
 DB 44 ANFLEEVKRGKGLERCEVETGSEYEPALLESSTATDVFMARY 87

RESULT 12
 KXHU
 protein C (activated) (EC 3.4.21.69) precursor - human
 M.Alternate names: autoprothrombin IIA; plasma protein C
 C.Species: Homo sapiens (man)
 C.Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999
 C.Accession: A22331; A25426; A21781; A23789; A00927
 R.Foster, D.C.; Yoshitake, S.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985
 A.Title: The nucleotide sequence of the gene for human protein C.
 A.Reference number: A22331; MUID:85270390
 A.Accession: A22331
 A.Molecule type: DNA
 A.Residues: 1-461 <FOS1>
 A.Cross-references: GB:M1128; NID:9190333; PIDN:AAA60166.1; PID:9190334
 R.Plutsky, J.; Hoskins, J.A.; Long, G.L.; Crabtree, G.R.
 Proc. Natl. Acad. Sci. U.S.A. 83, 546-550, 1986
 A.Title: Evolution and organization of the human protein C gene.
 A.Reference number: A25426; MUID:86120978
 A.Accession: A25426
 A.Molecule type: DNA
 A.Residues: 1-445, 'L', 446-461 <PLU>
 A.Cross-references: GB:M12712; NID:9190330; PIDN:AAA60165.1; PID:9190332
 R.Foster, D.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 81, 4766-4770, 1984
 A.Title: Characterization of a cDNA coding for human protein C.
 A.Reference number: A21781; MUID:84272714
 A.Accession: A21781
 A.Molecule type: mRNA
 A.Residues: 'Q', 107-461 <FOS2>

A.Cross-references: GB:K02059; NID:9190322; PIDN:AAA60164.1; PID:9190323
 R.Beckmann, R.J.; Schmidt, R.J.; Santerre, R.F.; Plutsky, J.; Crabtree, G.R.; Long, G
 Nucleic Acids Res. 13, 5233-5247, 1985
 A.Title: The structure and evolution of a 461 amino acid human protein C precursor an
 A.Reference number: A23789; MUID:85269639
 A.Accession: A23789
 A.Molecule type: mRNA
 A.Residues: 1-461 <BEC>
 A.Cross-references: GB:X02750; NID:935689; PIDN:CAA26528.1; PID:9763120
 R.Mileich, J.P.; Broze Jr., G.J.
 J. Biol. Chem. 265, 11397-11404, 1990
 A.Title: Beta protein C is not glycosylated at asparagine 329. The rate of translatio
 A.Reference number: A44605; MUID:90293094
 A.Contents: annotation; carbohydrate binding sites; activation peptide
 A.Note: the alpha form of protein C is glycosylated at Asn-329, and the beta form is
 R.Harris, R.J.; Ling, V.T.; Spellman, M.W.
 J. Biol. Chem. 267, 5102-5107, 1992
 A.Title: O-linked fucose is present in the first epidermal growth factor domain of fa
 A.Contents: annotation; beta-hydroxyaspartic acid
 C.Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that
 ivation of factor Va is strongly enhanced by complexing with protein S. Protein C als
 C.Comment: Protein C is synthesized in the liver as a single chain precursor, which i
 bin, which cleaves a dodecapeptide from the amino end of the heavy chain; this reacti
 C.Genetics:
 A.Gene: GDB:PROC
 A.Cross-references: GDB:120317; OMIM:176860
 A.Map position: 2q13-2q21
 A.Introns: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1
 C.Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol
 C.Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium bind
 F.1-33/Domain: signal sequence #status predicted <SIG>
 F.27-86/Domain: Gla domain homology <GLA>
 F.33-42/Domain: propeptide #status predicted <PRO>
 F.43-197/Product: protein C light chain #status predicted <LCH>
 F.92-131/Domain: EGF homology <EG1>
 F.140-175/Domain: EGF homology <EG2>
 F.200-461/Product: protein C heavy chain #status predicted <HCH>
 F.200-211/Domain: activation peptide #status experimental <APT>
 F.212-445/Domain: trypsin homology <TRY>
 F.48,49,56,58,61,62,67,68,71/Modified site: gamma-carboxyglutamic acid (Glu) #status
 F.59-64,92-105,101-120,122-131,140-151,147-160,162-175,183-175,238-254,373-387,398-42
 F.106-111/Disulfide bonds: #status predicted
 F.110/Binding site: carbohydrate (Thr) (covalent) #status absent
 F.113/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F.139,290,335/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F.211-212/Cleavage site: Arg-Leu (thrombin) #status experimental
 F.253,299,402/Active site: His, Asp, Ser #status predicted
 F.371/Binding site: carbohydrate (Asn) (covalent) (partial) #status atypical

Query Match 45.1%; Score 82; DB 1; Length 461;
 Best Local Similarity 43.9%; Pred. No. 1,3e-06;
 Matches 18; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANAFLLXLRKGSIXRCKXXKCSFFXXAXIIFDKAXRTKLEFW 41
 DB 43 ANFLEELRHSLERCIEICDPEAKELFQVNDTLAFW 83

RESULT 13
 S10511
 Thrombin (EC 3.4.21.5) B chain precursor - rat
 C.Species: Rattus norvegicus (Norway rat)
 C.Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 22-Jun-1999
 C.Accession: S10511; A60576; B42696
 R.Dihaneich, M.; Monard, D.
 Nucleic Acids Res. 18, 4251, 1990
 A.Title: cDNA sequence of rat prothrombin.
 A.Reference number: S10511; MUID:90332426
 A.Accession: S10511
 A.Molecule type: mRNA
 A.Residues: 1-617 <DIH>

```

A:Cross-references: EMBL:X52835, NID:956969, PIDN:CA37017.1, PID:956970
R:Henrikson, K.P., Jazlin, E.E., Greenwood, J.A., Dickerman, H.W.
Endocrinology 126, 167-175, 1990
A:Title: Prothrombin levels are increased in the estrogen-treated immature rat uterus.
A:Reference number: A60576; MUID:90091942
A:Accession: A60576
A:Molecule type: protein
A:Residues: 44-58 <HEN>
A:Note: The authors purified the proenzyme from the estrogen-stimulated maturing rat ute
R:Banfield, D.K.; Macgillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A:Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq
A:Reference number: A42696; MUID:92212913
A:Accession: B42696
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 383-617, 'E' <BAN>
A:Cross-references: GB:M81397
C:Superfamily: thrombin; Gla domain homology; kringe homology; trypsin homology
C:Keywords: blood coagulation; calcium binding; carboxylutamic acid; glycoprotein; hyd
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-43/Domain: propeptide #status predicted <PRO>
F:28-88/Domain: Gla domain homology <GLA>
F:44-617/Product: prothrombin #status experimental <PMAT>
F:109-187/Domain: kringe homology <KR1>
F:215-282/Domain: kringe homology <KR2>
F:360-609/Domain: trypsin homology <TRY>
F:50,51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxylutamic acid (Glu) #status
F:61-66,91-104,109-187,130-170,158-182,215-292,236-276,264-287,332-478,387-403,532-546,5
F:402,458,564/Active site: His, Asp, Ser #status predicted

```

Query Match 44.5%; Score 81; DB 2; Length 617;
Best Local Similarity 37.2%; Pred. No. 2.5e-06;
Matches 16; Conservative 5; Mismatches 22; Indels 0; Gaps 0;

```

OY 2 NAFLLXLRKXSLRCKXKXOCSEFXAXXIFKDAKTKLFMTSY 44
Db 46 SGFLERKGNLRECVCEQSYEAEFALESPOOTDFVFWAKY 88

RESULT 14
A35827
thrombin (EC 3.4.21.5) B chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 22-Jun-1999
C:Accession: A35827; A42696; S12081
R:Degen, S.J.F.; Schaefer, L.A.; Jamison, C.S.; Grant, S.G.; Fitzgibbon, J.J.; Pal, J.A.
DNA Cell Biol. 9, 487-498, 1990
A:Title: Characterization of the cDNA coding for mouse prothrombin and localization of t
A:Reference number: A35827; MUID:91025551
A:Accession: A35827
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-618 <DEG>
A:Cross-references: GB:A52308, NID:953813; PIDN:CA36548.1; PID:953814
A:Experimental source: strain C57BL/6
A:Note: the data were obtained from females resulting from the cross of M. domesticus at
R:Banfield, D.K.; Macgillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A:Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq
A:Reference number: A42696; MUID:92212913
A:Accession: A42696
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 384-618, 'E' <BAN>
A:Cross-references: GB:M81394
C:Superfamily: thrombin; Gla domain homology; kringe homology; trypsin homology
C:Keywords: blood coagulation; calcium binding; carboxylutamic acid; glycoprotein; hyd
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-43/Domain: propeptide #status predicted <PRO>
F:28-88/Domain: Gla domain homology <GLA>
F:44-618/Product: prothrombin B #status predicted <MAT>

```

```

F:109-187/Domain: kringe homology <KR1>
F:215-293/Domain: kringe homology <KR2>
F:361-610/Domain: trypsin homology <TRY>
F:50,51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxylutamic acid (Glu) #stat
F:61-66,91-104,109-187,130-170,158-182,215-293,236-276,264-288,333-479,388-404,533-54
F:403,459,565/Active site: His, Asp, Ser #status predicted

```

Query Match 44.5%; Score 81; DB 2; Length 618;
Best Local Similarity 37.2%; Pred. No. 2.5e-06;
Matches 16; Conservative 5; Mismatches 22; Indels 0; Gaps 0;

```

OY 2 NAFLLXLRKXSLRCKXKXOCSEFXAXXIFKDAKTKLFMTSY 44
Db 46 SGFLERKGNLRECVCEQSYEAEFALESPOOTDFVFWAKY 88

RESULT 15
KFBO
coagulation factor IXa (EC 3.4.21.22) precursor - bovine
N:Alternate names: Christmas factor
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Nov-1980 #sequence_revision 03-Aug-1984 #text_change 16-Jul-1999
C:Accession: A14757; B20274; I45891; A00923
R:Karayama, K.; Ericsson, L.H.; Enfield, D.L.; Walsh, K.A.; Neutra, H.; Davie, E.W.;
Proc. Natl. Acad. Sci. U.S.A. 76, 4990-4994, 1979
A:Title: Comparison of amino acid sequence of bovine coagulation factor IX (Christmas
A:Reference number: A14757; MUID:80056619
A:Accession: A14757
A:Molecule type: protein
A:Residues: 1-63, 'T', '65-416 <KAT>
R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood
A:Reference number: A20274; MUID:83308813
A:Accession: B20274
A:Molecule type: protein
A:Residues: 59-63, 'X', '65-69 <MCW>
R:Choo, K.H.; Gould, K.G.; Brownlee, G.G.
Nature 299, 178-180, 1982
A:Title: Molecular cloning of the gene for human anti-haemophilic factor IX.
A:Reference number: I45891; MUID:82272386
A:Accession: I45891
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 52-139 <CHO>
A:Cross-references: GB:J00007; NID:9163053; PIDN:AAA30520.1; PID:9163054
R:Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwano
J. Biochem. 104, 867-868, 1988
A:Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood c
A:Reference number: A44556; MUID:89213999
A:Accession: A44556
A:Contents: annotation
A:Note: structure and location of a carbohydrate covalently bound to Ser
C:Comment: Factor IX is activated by factor XIIa, which excises the activation peptide
C:Comment: The gamma-carboxylutamic acid residues arise by posttranslational, vitam
C:Comment: Calcium binds to the gamma-carboxylutamic acid (Gla) residues and, with s
C:Function:
A:Description: catalyzes the proteolytic activation of coagulation factor X in the pr
A:Pathway: blood coagulation intrinsic pathway
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylu
F:1-146/Product: coagulation factor IXa light chain #status experimental <ALC>
F:1-82/Domain: EGF homology <EG1>
F:51-82/Domain: EGF homology <EG2>
F:88-124/Domain: EGF homology <EG3>
F:147-181/Domain: activation peptide #status experimental <APT>
F:182-416/Product: coagulation factor IXa heavy chain #status experimental <AHC>
F:182-409/Domain: trypsin homology <TRY>
F:7,8,15,17,20,21,26,27,30,33,36,40/Modified site: gamma-carboxylutamic acid (Glu) #
F:18-23,51-62,56-71,73-82,88-99,95-109,111-124,132-290,207-223,337-351,362-390/Dsulfi
F:53/Modified site: carbohydrate (Ser) (covalent) #status experimental
F:64/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F:158,168,173,261/Binding site: carbohydrate (Asn) (covalent) #status experimental

```

F:222,270,366/Active site: His, Asp, Ser #status predicted

Query Match 44.0%; Score 80; DB 1; Length 416;
Best Local Similarity 41.2%; Pred. No. 2,6e-06;
Matches 14; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

OY 11 GSLKRXCKXCCSFXXXXIFKDXRTKLFWISY 44
DB 12 GNLERCKEKKCSFEAREVFEVNTETTFMKOY 45

RESULT 16

KPFU

coagulation factor IXa (EC 3.4.21.22) precursor [validated] - human
M:Alternate names: antihemophilic factor B; Christmas factor
C:Species: Homo sapiens (man)
C:Date: 17-Dec-1982 #sequence revision 30-Jun-1987 #text change 15-Sep-2000
C:Accession: A00922; A37570; A30511; A32989; A22673; A21337; A37546; A30623; A60486; A20
R:Yoshitake, S.; Schach, B.G.; Foster, D.C.; Davie, E.W.; Kurechi, K.
Biochemistry 24, 3736-3750, 1985

A:Title: Nucleotide sequence of the gene for human factor IX (antihemophilic factor B).
A:Reference number: A00922; MUID:86000558
A:Accession: A00922

A:Molecule type: DNA
A:Residues: 1-461 <YOS>
A:Cross-references: GB:K02402; NID:9182612; PIDN:AA59620.1; PID:9182613
R:Anson, D.S.; Choo, K.H.; Rees, D.J.G.; Giannelli, F.; Gould, K.; Huddleston, J.A.; Bro
EMBO J. 3, 1053-1060, 1984

A:Title: The gene structure of human anti-haemophilic factor IX.
A:Reference number: A37570; MUID:84236100
A:Accession: A37570

A:Molecule type: DNA
A:Residues: 1-461 <ANS>
A:Cross-references: GB:K02048
R:Reitsma, P.H.; Bertina, R.M.; Ploos van Amstel, J.K.; Riemens, A.; Briet, E.
Blood 72, 1074-1076, 1988

A:Title: The putative factor IX gene promoter in hemophilia B Leyden.
A:Reference number: A30511; MUID:88327116
A:Accession: A30511

A:Molecule type: DNA
A:Residues: 8-24 <REI>
A:Cross-references: EMBL:X55008; NID:9311288; PIDN:CA838245.2; PID:94469253
R:Koeberl, D.D.; Bottma, C.D.K.; Buerstedde, J.M.; Sommer, S.S.
Am. J. Hum. Genet. 45, 448-457, 1989

A:Title: Functionally important regions of the factor IX gene have a low rate of polymor
A:Reference number: A32989; MUID:89371752
A:Accession: A32989

A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 30-92 <KOE>
R:McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Lundblad, R.L.; Roberts, H.R.; Graham, J.B.; S
Proc. Natl. Acad. Sci. U.S.A. 82, 2847-2851, 1985

A:Title: Evidence for a prevalent polymorphism in the activation peptide of human coagulat
A:Reference number: A22673; MUID:85190593
A:Accession: A22673

A:Molecule type: mRNA
A:Residues: 1-193, 'T', 195-461 <MCG>
A:Cross-references: GB:M1309; NID:9180552; PIDN:AA52023.1; PID:9180553
A:Note: the authors translated the codon ACA for residue 29 as Tyr
R:Jaye, M.; de la Salle, H.; Schamber, F.; Bolland, A.; Kohli, V.; Findel, A.; Tolstost
Nucleic Acids Res. 11, 2325-2335, 1983

A:Title: Isolation of a human anti-haemophilic factor IX cDNA clone using a unique 52-bp
A:Reference number: A21337; MUID:83220788
A:Accession: A21337

A:Molecule type: mRNA
A:Residues: 1-193, 'T', 195-461 <JAV>
A:Cross-references: GB:J00137; NID:9182610; PIDN:AA52763.1; PID:9182611
R:Jagdeeswaran, P.; Lavelle, D.E.; Kaul, R.; Mohandas, T.; Warren, S.T.
Somat. Cell Mol. Genet. 10, 465-473, 1984
A:Title: Isolation and characterization of human factor IX cDNA: identification of Tag I
A:Reference number: A37546; MUID:84300526
A:Accession: A37546

A:Molecule type: mRNA
A:Residues: 38-193, 'T', 195-326 <JAG>
A:Cross-references: GB:M35672

R:Kutach, K.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 79, 6461-6464, 1982
A:Title: Isolation and characterization of a cDNA coding for human factor IX.
A:Reference number: A30623; MUID:83065193
A:Accession: A30623

A:Molecule type: mRNA
A:Residues: 1-12, 'S', 14-73, 'P', 75-82, 'K', 84-203, 'P', 205-216, 'G', 218-298, 'A', 299-356, '
A:Cross-references: GB:J00136; NID:9182608; PIDN:AA98726.1; PID:9182609
A:Experimental source: liver
R:Tharakan, J.; Strickland, D.; Burgess, W.; Drohan, W.N.; Clark, D.B.
Vox Sang. 58, 21-29, 1990

A:Title: Development of an immunoaffinity process for factor IX purification.
A:Reference number: A60486; MUID:90194857
A:Accession: A60486

A:Molecule type: protein
A:Residues: 47-52, 'XX', 55-60, 'X', 62, 'XX', 65 <THA>
R:McMullen, B.A.; Fujikawa, K.; Kistiel, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983

A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood
A:Reference number: A20274; MUID:83308813
A:Accession: A20274

A:Molecule type: protein
A:Residues: 105-109, 'X', 111-115 <MCM>
R:Balland, A.; Faure, T.; Carvallo, D.; Cordier, P.; Ulrich, P.; Fournet, B.; de la S
Eur. J. Biochem. 172, 565-572, 1988

A:Title: Characterisation of two differently processed forms of human recombinant fac
A:Reference number: S02527; MUID:88166735
A:Accession: S02527

A:Molecule type: protein
A:Residues: 29-63 <BAL>
A:Note: processed forms expressed in recombinant system
R:Jallat, S.; Perraud, F.; Dalemans, W.; Balland, A.; Dieterle, A.; Faure, T.; Meulie
EMBO J. 9, 3295-3301, 1990

A:Title: Characterization of recombinant human Factor IX expressed in transgenic mice
A:Reference number: S12058; MUID:91006024
A:Accession: S12058

A:Molecule type: protein
A:Residues: 1-68 <JAL>
A:Note: processed forms expressed in recombinant system
R:Handford, P.A.; Baron, M.; Mayhew, M.; Willis, A.; Beesley, T.; Brownlee, G.G.; Cam
EMBO J. 9, 475-480, 1990

A:Title: The first EGF-like domain from human factor IX contains a high-affinity calc
A:Reference number: S12377; MUID:90151623
A:Accession: S12377

A:Molecule type: protein
A:Residues: 92-130 <HAN>
A:Note: NMR detection of calcium binding by domain expressed in recombinant system
R:de la Salle, C.; Charmanlier, J.L.; Baas, M.C.; Schwartz, A.; Wiesel, M.L.; Gruneba
Thromb. Haemost. 70, 370-371, 1993

A:Title: A deletion located in the 3' non translated part of the factor IX gene respo
A:Reference number: I59612; MUID:94054330
A:Accession: I59612

A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 444-461 <RES>
A:Cross-references: GB:S66752; NID:9439773; PIDN:AA828588.1; PID:9439774
R:Stoflet, E.S.; Koeberl, D.D.; Sarkar, G.; Sommer, S.S.
Science 239, 491-494, 1988

A:Title: Genomic amplification with transcript sequencing.
A:Reference number: I59529; MUID:88127096
A:Accession: I59529

A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 290-359 <RB2>
A:Cross-references: GB:M10063; NID:9182622; PIDN:AA52456.1; PID:9182623
R:Agarwala, K.L.; Kawabata, S.; Takao, T.; Murata, H.; Shimomishu, Y.; Nishimura, H.;
Biochemistry 33, 5167-5171, 1994
A:Title: Activation peptide of human factor IX has oligosaccharides O-glycosidically
A:Reference number: A54255; MUID:94227047
A:Accession: A54255

A:Molecule type: protein
A:Residues: 'D', 204, 'X', 206-211, 212, 'D', 214, 'X', 216-221, 'D', <AGA>
A:Note: The residues designated 'X' were determined to be threonine bound to carboxylate
R:Di Scipio, R.G.; Kurachi, K.; Davie, E.W.
J. Clin. Invest. 61, 1528-1538, 1978
A>Title: Activation of human factor IX (Christmas factor).
A:Reference number: A18493; MUID:78194509
A:Contents: annotation; activation; active site; carboxylate binding
R:McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Graham, J.B.; Roberts, H.R.; Stafford, D.W.
Am. Soc. Hematol. Abstr. 64(Suppl.1), 262a, 1984
A:Reference number: A37569
A:Contents: annotation
A:Note: 194-Tf was also found
R:Morita, T.; Isaacs, B.S.; Esmen, C.T.; Johnson, A.E.
J. Biol. Chem. 259, 5698-5704, 1984
A>Title: Derivatives of blood coagulation factor IX contain a high affinity Ca2+-binding
A:Reference number: A37543; MUID:84185715
A:Contents: annotation; calcium binding
R:Morita, T.; Isaacs, B.S.; Esmen, C.T.; Johnson, A.E.
J. Biol. Chem. 260, 2583, 1985
A:Reference number: A37544
A:Contents: annotation; calcium binding; correction
R:Bentley, A.K.; Rees, D.J.G.; Rizza, C.; Brownlee, G.G.
Cell 45, 343-348, 1986
A>Title: Defective propeptide processing of blood clotting factor IX caused by mutation
A:Reference number: A37545; MUID:86189947
A:Contents: annotation; signal sequence; cleavage site
R:Shultz, K.; Kawabata, S.I.; Miyata, T.; Takeya, H.; Takamatsu, J.; Ogata, K.; Kamiya, J.
J. Biol. Chem. 264, 21257-21265, 1989
A>Title: Blood clotting factor IX B(M) Nagoya: substitution of arginine 180 by tryptophan
A:Reference number: A30622; MUID:90078229
A:Contents: annotation; sequence of mutant B(M) Nagoya
A:Note: recombinant form expressed in yeast
A:Contents: annotation; conformation by (1)H-NMR, residues 92-130
R:Baron, M.; Norman, D.G.; Harvey, T.S.; Hanford, P.A.; Mayhew, M.; Tse, A.G.D.; Brownlee, D.
submitted to the Brookhaven Protein Data Bank, November 1991
A:Reference number: A51252; PDB:1IXA
A:Contents: annotation; conformation by (1)H-NMR, residues 92-130
A:Note: recombinant form expressed in yeast
C:Comment: Factor IX is activated by factor XIIa, which excises the activation peptide propeptide
C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K
C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with strong
C:Genetics:
A:Gene: GDB:F9
A:Cross-references: GDB:119900; OMIM:306900
A:Map position: Xq27.1-Xq27.2
A:Intons: 30/1, 84/2, 93/1, 131/1, 174/1, 241/3, 280/1
C:Function:
A:Description: catalyzes the proteolytic activation of coagulation factor X in the presence
A:Pathway: blood coagulation intrinsic pathway
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamate
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-46/Domain: propeptide #status experimental <PP>
F:47-91/Domain: Gla domain homology <Gla>
F:47-191/Product: coagulation factor IXa light chain #status experimental <ALC>
F:97-128/Domain: EGF homology <EGF>
F:134-170/Domain: EGF homology <EG2>
F:193-226/Domain: activation peptide #status experimental <ACT>
F:227-461/Product: coagulation factor IXa heavy chain #status experimental <AHC>
F:227-454/Domain: trypsin homology <TRY>
F:53,54,61,63,66,67,72,73,76,77,78,79,82,86/Modified site: gamma-carboxyglutamic acid (Glu) #status
F:64-69,97-108,102-117,119-128,134-145,141-155,157-170,178-335,252-268,382-396,407-435/CD
F:99/Binding site: carboxylate (Ser) (covalent) #status experimental
F:191-192/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F:191-192/Cleavage site: Arg-Ala (coagulation factor Xla) #status experimental
F:203,213/Binding site: carboxylate (Asn) (covalent) #status experimental
F:205,215/Binding site: carboxylate (Thr) (covalent) #status experimental
F:226-227/Cleavage site: Arg-Val (coagulation factor Xla) #status experimental

```

QY      11 GSLARXCKXXQCSEFXAXXIIFRDAARTKLFMTISY 44
          1:-||| | :||| | ||| |
Db       58 GNLERECMEKCSEFEAREVEFENETERTTEPFMKOY 91

RESULT 17
A03051
coagulation factor IXa (EC 3.4.21.22) precursor - dog
C:Species: Canis lupus familiaris (dog)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A03051; I46201
R:Evans, J.P.; Watke, H.H.; Ware, J.L.; Stafford, D.W.; High, K.A.
Blood 74, 207-212, 1999
A>Title: Molecular cloning of a cDNA encoding canine factor IX.
A:Reference number: A03051; MUID:8932338
A:Accession: A03051
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-452 <EVA>
A:Cross-references: GB:M21757; NID:g972719; PIDN:AAA75006.1; PID:g163948
R:Axelrod, J.H.; Read, M.S.; Brinkhaus, K.M.; Vergara, I.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 5173-5177, 1990
A>Title: Phenotypic correction of factor IX deficiency in skin fibroblasts of hemophilic mice.
A:Reference number: I46201; MUID:90311364
A:Accession: I46201
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-452 <AXE>
A:Cross-references: GB:M3826; NID:g163949; PIDN:AAA30844.1; PID:g163950
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homolog; beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylate-binding site
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-40/Domain: propeptide #status predicted <PRO>
F:24-84/Domain: Gla domain homology <GLA>
F:41-452/Product: coagulation factor IX #status predicted <MAT>
F:90-121/Domain: EGF homology <EG1>
F:127-163/Domain: EGF homology <EG2>
F:164-445/Domain: trypsin homology <TRY>
F:46,47,54,56,59,60,65,66,72,75,79/Mutated site: gamma-carboxyglutamic acid (Glu)
F:57-62,90-101,95-110,112-121,127-138,134-148,150-163,171-326,243-259,373-387,398-426/Mutated site: His, Asp, Ser #status predicted
F:258,306,402/Active site: His, Asp, Ser #status predicted

Query Match           39.6%; Score 72; DB 1; Length 452;
Best Local Similarity 38.2%; Pred. No. 7,66-05;
Matches 13; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY      11 GSLRXCKXXQCSEFXAXXIIFRDAARTKLFMTISY 44
          1:-||| | :||| | ||| |
Db       51 GNLERECIEKCSEFEAREVEFENETERTTEPFMKOY 84

RESULT 18
A00419
coagulation factor IXa (EC 3.4.21.22) precursor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Jul-1999
C:Accession: J00419; I49667
R:Nw, S.M.; Stafford, D.W.; Ware, J.
Gene 86, 275-278, 1990
A>Title: Deduced amino acid sequence of mouse blood-coagulation factor IX.
A:Reference number: J00419; MUID:90215309
A:Accession: J00419
A:Molecule type: mRNA
A:Residues: 1-459 <WUS>
A:Cross-references: GB:M23109; NID:g193317; PIDN:AAA37629.1; PID:g387158
A:Experimental source: liver
R:Sarkar, G.; Koerber, D.D.; Sommer, S.S.
Genomics 6, 133-143, 1990
A>Title: Direct sequencing of the activation peptide and the catalytic domain of the proenzyme of tissue-type plasminogen activator from rat liver.
A:Reference number: I49667; MUID:90152675
A:Accession: I49667
A>Status: preliminary; translated from GB/EMBL/DBJ

```


RESULT 26

KXRTS

Plasma protein S precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 04-Oct-1995 #sequence_revision 26-Jan-1996 #text_change 16-Jul-1999

C:Accession: J04180

R:Yasuda, F.; Hayashi, T.; Tanitame, K.; Nishioka, J.; Suzuki, K.

J. Biochem. 117, 374-383, 1995

A:Title: Molecular cloning and functional characterization of rat plasma protein S.

A:Reference number: J04180; MUID:9533263

A:Accession: J04180

A:Molecule type: mRNA

A:Residues: 1-675 <YAS>

A:Cross-references: GB:S78744; NID:g1041903; PIDN:AAC60704.1; PID:g1041904

C:Comment: This protein is a vitamin K-dependent plasma glycoprotein that has an antitox

activation of coagulation factors Va and VIIa. This protein also binds to factor Va and

C:Superfamily: plasma protein S: EGF homology: gla domain homology: laminin G repeat hom

C:Keywords: beta-hydroxyasparagine, beta-hydroxyaspartic acid, blood coagulation; carbox

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-41/Domain: propeptide #status predicted <PRO>

F:26-85/Domain: gla domain homology <GLA>

F:42-675/Product: plasma protein S #status predicted <MAT>

F:88-116/Domain: thrombin-sensitive #status predicted <THS>

F:121-154/Domain: EGF homology <EG1>

F:161-199/Domain: EGF homology <EG2>

F:205-241/Domain: EGF homology <EG3>

F:247-282/Domain: EGF homology <EG4>

F:315-666/Domain: sex hormone-binding globulin homology <SHB>

F:325-478/Domain: laminin G repeat homology <LGR>

F:47-48,55-57,66,67,70,73,77/Modified site: gamma-carboxyglutamic acid (Glu) #stat

F:58-63,88-113,121-134,126-143,145-154,161-175,171-184,186-199,205-217,212-226,228-241,2

F:111-112/Cleavage site: Arg-Ser (thrombin) #status predicted

F:136/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted

F:177,219,258/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

F:499,509/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 31.3%; Score 57; DB 1; Length 675;

Best Local Similarity 29.5%; Pred. No. 0.052;

Matches 13; Conservative 7; Mismatches 24; Indels 0; Gaps 0;

OY 1 ANAFLLXRLKRGSLKRXKXKXCSFXKXAXIRKDXKRRKLFWISY 44

Db 42 ANLLEETKGNLEKECEIEELCNKEAREVEFNPEIDYFPHYKY 85

RESULT 27

G96763

Probable MAP kinase F25P22.9 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: G96763

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

Nansen, N.E.; Hughes, B.; Huizart, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

A.A.; Li, J.H.; Lin, Y.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sekano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: G96763

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-576 <STO>

A:Cross-references: GB:AE005173; NID:g6692731; PIDN:AAF24837.1; GSPDB:GN00141

A:Gene: F25P22.9

A:Map position: 1

Query Match

Best Local Similarity 31.0%; Score 56.5; DB 2; Length 576;

Matches 16; Conservative 4; Mismatches 23; Indels 3; Gaps 2;

OY 1 ANAFLLXRLKRGSL--XRXCKXKXCSFXKXAXIRKDXKRRKLFWISY 44

Db 210 ANFHRDLKPRNLIANADCKLKICDFGLARVSFNDA-PTAIFWTDY 254

RESULT 28

KXHUZ

Plasma protein Z precursor [validated] - human

N:Alternate names: vitamin K-dependent glycoprotein Z

C:Species: Homo sapiens (man)

C:Date: 18-Jan-1991 #sequence_revision 05-Jan-1996 #text_change 08-Dec-2000

C:Accession: A36244; A35893; B35893

R:Richman, A.; Tkeya, H.; Espilng, E.; Iwanaga, S.; Kistel, W.; Davle, E.W.

Biochem. Biophys. Res. Commun. 172, 1139-1144, 1990

A:Title: Amino acid sequence of human protein Z, a vitamin K-dependent plasma glycop

A:Reference number: A36244; MUID:91058548

A:Accession: A36244

A:Molecule type: mRNA

A:Residues: 1-422 <TCH>

A:Cross-references: GB:M55671; NID:g190465; PIDN:AAA36501.1; PID:g190466

A:Note: parts of this sequence, including the amino end of the mature protein, were d

R:Sejima, H.; Hayashi, T.; Deyashiki, Y.; Nishioka, J.; Suzuki, K.

Biochem. Biophys. Res. Commun. 171, 661-668, 1990

A:Title: Primary structure of vitamin K-dependent human protein Z.

A:Reference number: A35893; MUID:90386637

A:Accession: A35893

A:Molecule type: protein

A:Residues: 63-68, 'XX', '71-72, 'X', '74-76, 'X', '78, 'XX', '81, 'XX', '84, 'X', '86-87, 'XX', '90, 'XX',

A:Accession: B35893

A:Molecule type: mRNA

A:Residues: 103-422 <SE2>

A:Cross-references: GB:M59303; NID:g190461; PIDN:AAA36499.1; PID:g190462

A:Gene: GDB:PROZ

A:Cross-references: GDB:9957440; OMIM:176895

A:Map position: 13q34-13q34

C:Superfamily: coagulation factor X; EGF homology: gla domain homology: trypsin homol

C:Keywords: beta-hydroxyaspartic acid; calcium binding; carboxyglutamic acid; glycop

F:1-10/Domain: signal sequence #status predicted <SIG>

F:11-62/Domain: propeptide #status predicted <PRO>

F:47-107/Domain: gla domain homology <GLA>

F:63-422/Product: protein Z #status experimental <MAT>

F:113-144/Domain: EGF homology <EG1>

F:151-187/Domain: EGF homology <EG2>

F:199-417/Domain: trypsin homology <TRY>

F:69,70,73,77,79,82,83,88,89,92,95,97,102/Modified site: gamma-carboxyglutamic acid (

F:115/Binding site: carboxylate (Ser) (covalent) #status experimental

F:121,247,255,328,354/Binding site: carboxylate (Asn) (covalent) #status predicted

F:126/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted

F:134,137/Binding site: carboxylate (Thr) (covalent) #status predicted

F:225-241,349-363/Disulfide bonds: #status predicted

F:258/Binding site: carboxylate (Ser) (covalent) #status predicted

Query Match 28.6%; Score 52; DB 1; Length 422;

Best Local Similarity 30.0%; Pred. No. 0.27;

Matches 12; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

OY 5 LXXLRGSLKRXKXKXCSFXKXAXIRKDXKRRKLFWISY 44

Db 68 LEELEBGNLEKECEIEETCYEAAREVEFNPEIDYFPHYKY 107

RESULT 29

D84859

Probable MAP kinase [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C:Accession: D84859

Query Match 26.9%; Score 49; DB 2; Length 673;
Best Local Similarity 30.6%; Pred. No. 1.4;
Matches 11; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy 9 RXGLRXCKXXQCSFYXAXXIFKDXRTKLFWISY 44
Db 54 KQGLHRECVCEVCSKEAREVFENDETFYFPRY 89

RESULT 33
155476
growth potentiating factor - rat
C:Species: Rattus sp. (rat)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Apr-2001
C:Accession: I55476
R:Nakano, T.; Higashino, K.; Kikuchi, N.; Kishino, J.; Nomura, K.; Fujita, H.; Ohara, O.
J. Biol. Chem. 270, 5702-5705, 1995
A:Title: Vascular smooth muscle cell-derived, G1a-containing growth-potentiating factor
A:Reference number: I55476; MUID:95197586
A:Accession: I55476
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-674 <RFS>
A:Cross-references: GB:D42148; NID:g1526567; PIDN:BA07719.1; PID:9893402
C:Superfamily: plasma protein S; EGF homology; G1a domain homology; laminin G repeat hom
F:117-150/Domain: G1a domain homology <G1a>
F:157-192/Domain: EGF homology <EG1>
F:198-233/Domain: EGF homology <EG2>
F:239-274/Domain: EGF homology <EG3>
F:308-667/Domain: sex hormone-binding globulin homology <SHB>
F:318-470/Domain: laminin G repeat homology <LGR>

Query Match 25.8%; Score 47; DB 2; Length 674;
Best Local Similarity 30.6%; Pred. No. 3.2;
Matches 11; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

Qy 9 RXGLRXCKXXQCSFYXAXXIFKDXRTKLFWISY 44
Db 54 KQGLHRECVCEVCSKEAREVFENDETFYFPRY 89

RESULT 34
B48089
growth arrest-specific protein gas6 - human
C:Species: Homo sapiens (man)
C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 05-Nov-1999
C:Accession: B48089
R:Manfioletti, G.; Brancolini, C.; Avanzl, G.; Schneider, C.
Mol. Cell. Biol. 13, 4976-4985, 1993
A:Title: The protein encoded by a growth arrest-specific gene (gas6) is a new member of
A:Reference number: A48089; MUID:93330291
A:Accession: B48089
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-678 <MAN>
A:Cross-references: GB:L13720; NID:g401766; PIDN:AAA58494.1; PID:g401767
C:Superfamily: plasma protein S; EGF homology; G1a domain homology; laminin G repeat hom
F:120-153/Domain: G1a domain homology #status atypical <G1a>
F:160-195/Domain: EGF homology <EG1>
F:201-236/Domain: EGF homology <EG2>
F:242-277/Domain: EGF homology <EG3>
F:311-671/Domain: sex hormone-binding globulin homology <SHB>
F:321-473/Domain: laminin G repeat homology <LGR>

Query Match 25.8%; Score 47; DB 2; Length 678;
Best Local Similarity 30.6%; Pred. No. 3.2;
Matches 11; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

Qy 9 RXGLRXCKXXQCSFYXAXXIFKDXRTKLFWISY 44
Db 57 KQGLHRECVCEVCSKEAREVFENDETFYFPRY 92

RESULT 35
S55864
hypothetical protein YNL325c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein N0330
C:Species: Saccharomyces cerevisiae
C:Date: 27-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 23-Mar-2001
C:Accession: S55864; S51290; S63306
R:Kraft, M.; Nicaud, J.M.; Levesque, H.; Gallardin, C.
Yeast 11, 567-572, 1995
A:Title: Sequencing analysis of a 15.4 kb fragment of yeast chromosome XIV identifies
A:Reference number: S55859; MUID:95373280
A:Accession: S55864
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-879 <MAF>
A:Cross-references: EMBL:246259; NID:g633655; PIDN:CAAB6373.1; PID:g633661
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
R:Nicaud, J.J.
submitted to the EMBL Data Library, January 1995
A:Description: Sequence analysis of a 13.9 kb fragment of yeast chromosome XIV identifi
A:Reference number: S51285
A:Accession: S51290
A:Molecule type: DNA
A:Residues: 1-879 <NIC>
A:Cross-references: EMBL:246259; NID:g633655; PID:g633661
R:Kraft, M.; Nicaud, J.M.; Levesque, H.; Gallardin, C.
submitted to the Protein Sequence Database, April 1996
A:Reference number: S63287
A:Accession: S63306
A:Molecule type: DNA
A:Residues: 1-879 <MAN>
A:Cross-references: EMBL:271601; NID:g1302439; PID:e239571; PID:g1302440; MIPS:YNL325
A:Experimental source: strain S286C
C:Genetics:
A:Gene: SCD:FIG4
A:Cross-references: SCD:S0005269; MIPS:YNL325c
A:Map position: 14L

Query Match 24.7%; Score 45; DB 2; Length 879;
Best Local Similarity 60.0%; Pred. No. 9.3;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 30 IFKDXRTKLFWISY 44
Db 165 IFKDLDTKTFYFPRY 179

RESULT 36
I49068
protein kinase STY (EC 2.7.1.-) [imported] - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Jun-2000
C:Accession: I49068
R:Duncan, P.I.; Howell, B.W.; Marius, R.M.; Drmanic, S.; Douville, E.M.; Bell, J.C.
J. Biol. Chem. 270, 21524-21531, 1995
A:Title: Alternative splicing of STY, a nuclear dual specificity kinase.
A:Reference number: I49068; MUID:95394904
A:Accession: I49068
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-306 <RFS>
A:Cross-references: EMBL:U01054; NID:g507917; PIDN:AAA82185.1; PID:g507918
C:Genetics:
A:Introns: 129/3; 160/1; 221/2
C:Keywords: phosphotransferase

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Query Match      23.6%; Score 43; DB 2; Length 306;
Best Local Similarity 30.8%; Pred. No. 8;
Matches 8; Conservative 2; Mismatches 16; Indels 0; Gaps 0;

OY 17 CKXXQCSEFXAXXIFKDXARTKLFWI 42
||| | | | : |||
Db 272 CKSVMCKRLIFLVKFEFTNRLIMI 297

RESULT 37
T25574
hypothetical protein C30H7.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T25574
R:Goela, D.
submitted to the EMBL Data Library, April 1997
A:Description: The sequence of C. elegans cosmid C30H7.
A:Reference number: Z20053
A:Accession: T25574
A>Status: preliminary; translated from GB/EMBL/DDBU
A:Molecule type: DNA
A:Residues: 1-410 <GOE>
A:Cross-references: EMBL:U97402; PIDN:AAB63409.1; GSPDB:GN00019; CESP:C30H7.2
A:Experimental source: strain Bristol N2; clone C30H7
C:Genetics:
A:Gene: CESP:C30H7.2
A:Map position: 1
A:Introns: 99/1; 127/2; 161/3; 244/2; 303/1; 349/2; 377/3

Query Match      23.4%; Score 42.5; DB 2; Length 410;
Best Local Similarity 36.7%; Pred. No. 13;
Matches 11; Conservative 2; Mismatches 14; Indels 3; Gaps 1;

OY 17 CKXXQC---SFXAXXIFKDXARTKLFWIS 43
||| | | | | ||| | | |
Db 63 CRFSOMLKPIFLVASEKFKDAPAKIMWAS 92

RESULT 38
D96996
uncharacterized low-complexity protein [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C:Accession: D96996
R:Nolling, J.; Breton, G.; Omeichenko, M.V.; Markarova, K.S.; zeng, Q.; Gibson, R.; Lee,
J.; Bacteriol. 183, 4823-4839, 2001
A>Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: D96996
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-211 <KUR>
A:Cross-references: GB:AE001437; PIDN:AAK78759.1; PID:G15023669; GSPDB:GN00168
C:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC0783-

Query Match      23.1%; Score 42; DB 2; Length 211;
Best Local Similarity 34.4%; Pred. No. 8.6;
Matches 11; Conservative 3; Mismatches 10; Indels 8; Gaps 1;

OY 11 GSIXRXCKXXQCSFXAXXI-----FKDA 34
| : | : | | | | | | | | | |
Db 46 GAHFECMLYKRCSEFKHAFFIGSNLKGSDFKDA 77

RESULT 39
JS0054
hypothetical 26.6k protein precursor - Mycobacterium fortuitum plasmid pAL5000
C:Species: Mycobacterium fortuitum
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 13-Nov-1998
C:Accession: JS0054
R:Rauzier, J.; Moniz-Pereira, J.; Glacquel-Sanzy, B.
Gene 71, 315-321, 1988
A>Title: Complete nucleotide sequence of pAL5000, a plasmid from Mycobacterium fortui
A:Reference number: JS0052; MUID:89138007
A:Accession: JS0054
A:Molecule type: DNA
A:Residues: 1-255 <RAU>
C:Genetics:
A:Genome: plasmid
F:1-29/Domain: signal sequence #status predicted <SIG>

Query Match      23.1%; Score 42; DB 2; Length 255;
Best Local Similarity 41.2%; Pred. No. 10;
Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 27 AXXIFKDXARTKLFWIS 43
| : | : | | | |
Db 223 ASSVNEDSRTRTKFFWIA 239

RESULT 40
T15792
hypothetical protein C42D8.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
C:Accession: T15792
R:Hallsworth, K.
submitted to the EMBL Data Library, April 1996
A:Description: The sequence of C. elegans cosmid C42D8.
A:Reference number: Z18405
A:Accession: T15792
A>Status: preliminary; translated from GB/EMBL/DDBU
A:Molecule type: DNA
A:Residues: 1-907 <HAL>
A:Cross-references: EMBL:U56966; NID:G1293844; PID:G1293847; PIDN:AAA98719.1; GSPDB:G
C:Experimental source: strain Bristol N2; clone C42D8
C:Genetics:
A:Gene: CESP:C42D8.5
A:Map position: X
A:Introns: 140/3; 170/3; 194/3; 300/2; 467/3; 551/2; 600/2; 697/3; 774/2; 851/3

Query Match      23.1%; Score 42; DB 2; Length 907;
Best Local Similarity 53.8%; Pred. No. 33;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 32 KDAXRTKLFWISY 44
||| | | : | | |
Db 312 KDSARLGHLWVSY 324

RESULT 41
T20272
hypothetical protein C56G7.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C:Accession: T20272
R:Percy, C.
submitted to the EMBL Data Library, November 1994
A:Reference number: Z19245
A:Accession: T20272
A>Status: preliminary; translated from GB/EMBL/DDBU
A:Molecule type: DNA
A:Residues: 1-322 <WIL>
A:Cross-references: EMBL:Z46793; PIDN:CAA86771.1; GSPDB:GN00021; CESP:C56G7.3
A:Experimental source: clone C56G7
C:Genetics:
A:Gene: CESP:C56G7.3
A:Map position: 3

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A:Introns: 26/3: 225/3: 251/2: 294/1
C:Superfamily: Caenorhabditis elegans hypothetical protein C5667.3

Query Match 22.8%; Score 41.5; DB 2; Length 322;
Best Local Similarity 25.0%; Pred. No. 16;
Matches 9; Conservative 5; Mismatches 19; Indels 3; Gaps 1;

Qy 4 FLXLRKXGSLKXKC--KXQCSFXXXKIFKDAKR 36
Db 262 FFSALHASMCRCFSIVKSQKCTLANQTIFSEIR 297

RESULT 42

AE2449
hypothetical protein alr5149 [imported] - Anabaena sp. (strain PCC 7120)
C:Species: Anabaena sp.
A:Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
C:Accession: AE2449
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kurlitz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AE2449
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-219 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA076848.1; PID:917134287; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr5149

Query Match 22.5%; Score 41; DB 2; Length 219;
Best Local Similarity 21.4%; Pred. No. 13;
Matches 9; Conservative 8; Mismatches 23; Indels 2; Gaps 1;

Qy 3 AFLXLRKXGSLKXKXQCSFXXXKIFKDAKRTKLFMISY 44
Db 179 ALFHHSLSLTDHLCQ--SCQFLTSAKCFYNTQGSRYVWYRF 218

RESULT 43

C83494
probable 2-Isopropylmalate synthase PA1217 [imported] - Pseudomonas aeruginosa (strain F)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: C83494
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A:Reference number: A82950; MUID:20437337
A:Accession: C83494
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-455 <STO>
A:Cross-references: GB:AE004551; GB:AE004091; NID:99947135; PIDN:AG04606.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA1217

Query Match 22.5%; Score 41; DB 2; Length 455;
Best Local Similarity 36.8%; Pred. No. 26;
Matches 7; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 12 SLXRXKXQCSFXXXKX 30
Db 8 TLREGCCQARQCSFDSAGSV 26

RESULT 44

T28279
ORF MSV119 probable RNA polymerase associated vaccinia RAP94 homolog (vaccinia H4L) -
C:Species: Melanoplus sanguinipes entomopoxvirus
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T28279
R:Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999
A:Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A:Reference number: Z20484; MUID:99102612
A:Accession: T28279
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-807 <APC>
A:Cross-references: EMBL:AF063866; NID:94049647; PIDN:AC97801.1; PID:94049841
C:Genetics:
A:Note: MSV119
C:Superfamily: vaccinia virus H4 protein

Query Match 22.0%; Score 40; DB 2; Length 807;
Best Local Similarity 53.3%; Pred. No. 67;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 30 IFKDAKRTKLFMISY 44
Db 148 ITKPVSRRTKIYISY 162

RESULT 45

T17839
hypothetical protein a340R - Chlorella virus PBCV-1
C:Species: Chlorella virus PBCV-1
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T17839
R:Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A:Reference number: Z18806
A:Accession: T17839
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-83 <GRA>
A:Cross-references: EMBL:U42580; NID:94028896; PIDN:AC96708.1
A:Experimental source: specific host Chlorella strain NC64A
C:Genetics:
A:Note: a340R

Query Match 21.7%; Score 39.5; DB 2; Length 83;
Best Local Similarity 31.6%; Pred. No. 10;
Matches 12; Conservative 5; Mismatches 20; Indels 1; Gaps 1;

Qy 4 FLXLRKXGSLKXKXQCS-FXXAXKIFKDAKRTKLF 40
Db 23 FLFLRLSLALRFLIASSECSIFLKSFLTFENIFRANVF 60

RESULT 46

H90517
hypothetical protein mypu_0480 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C:Accession: H90517
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barde, V.; Samson, D.; Gallison, F.; Moszer, J.
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma p
A:Reference number: A99512; MUID:21267165; PMID:11353084
A:Accession: H90517
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-312 <KUR>

A:Cross-references: GB:AL445566; PID:g14089461; PIDN:CAC13221.1; GSPDB:GN00153
 A:Experimental source: strain UAB CTIP
 C:Genetics:
 A:Gene: MYPU_0480
 A:Genetic code: SGC3

Query Match 21.7%: Score 39.5; DB 2; Length 312;
 Best Local Similarity 37.5%; Pred. No. 34;
 Matches 9; Conservative 3; Mismatches 7; Indels 5; Gaps 1;
 QY 21 QCSFXXAXXIFKDAKRTKLFWISY 44
 DB 11 QLSFEGASFI-----FNIFWWSF 29

RESULT 47
 T15137
 hypothetical protein T28F2.3 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C:Accession: T15137
 R:Madsen, C.; Fromick, B.
 Submitted to the EMBL Data Library, April 1997
 A:Description: The sequence of C. elegans cosmid T28F2.
 A:Reference number: Z18300
 A:Accession: T15137
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-319 <MAD>
 A:Cross-references: EMBL:AF000198; NID:g2047345; PID:g2047348; PIDN:AAB53054.1; GSPDB:GN00153
 A:Experimental source: strain Bristol N2; clone T28F2
 C:Genetics:
 A:Gene: CESP-T28F2.3
 A:Map position: 1
 A:Introns: 90/2; 189/3; 266/3; 295/3

Query Match 21.7%: Score 39.5; DB 2; Length 319;
 Best Local Similarity 42.3%; Pred. No. 35;
 Matches 11; Conservative 2; Mismatches 10; Indels 3; Gaps 2;
 QY 17 CKXXOCFFXXAXXIFKDAKRTKLFWI 42
 DB 215 CKL--CSFDF-QTFPPVAKETKEFWM 237

RESULT 48
 H84424
 probable MAP kinase [imported] - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: H84424
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Umayam, L.; Tallon, L.;
 euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, L.
 Nature 402, 761-768, 1999
 A>Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A:Reference number: AB4420; MUID:20083487
 A:Accession: H84424
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-516 <STO>
 A:Cross-references: GB:AE002093; NID:g3785991; PIDN:AAC67338.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: At2g01450
 A:Map position: 2

Query Match 21.7%: Score 39.5; DB 2; Length 516;
 Best Local Similarity 32.1%; Pred. No. 55;
 Matches 9; Conservative 3; Mismatches 15; Indels 1; Gaps 1;

QY 17 CKXXOCFFXXAXXIFKDAKRTKLFWISY 44
 DB 154 CKIKICDGLARVFTDS-PSAVFTDY 180

RESULT 49
 S66691
 probable membrane protein YOL009c - yeast (*Saccharomyces cerevisiae*)
 M:Alternate names: hypothetical protein O2365
 C:Species: *Saccharomyces cerevisiae*
 C>Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 20-Jun-2000
 C:Accession: S66691
 R:Hughes, B.; Pohl, T.M.
 Submitted to the Protein Sequence Database, July 1996
 A:Reference number: S66685
 A:Accession: S66691
 A:Molecule type: DNA
 A:Residues: 1-271 <HUG>
 A:Cross-references: EMBL:Z74751; NID:g1419776; PID:g1419777; MIPS:YOL009c
 A:Experimental source: strain S288C
 C:Genetics:
 A:Gene: SGD:MDM12
 A:Cross-references: SGD:S0005369; MIPS:YOL009c
 A:Map position: 15L
 C:Superfamily: *Saccharomyces cerevisiae* probable membrane protein YOL009c
 C:Keywords: transmembrane protein
 F:165-181/Domain: transmembrane #status predicted <TMM>

Query Match 21.4%: Score 39; DB 2; Length 271;
 Best Local Similarity 53.3%; Pred. No. 37;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 30 IFKDAKRTKLFWISY 44
 DB 247 IFKDFLRELAMPSPW 261

RESULT 50
 AD3369
 universal stress protein uspa and related nucleotide-binding proteins [imported] - *Brucella melitensis*
 C:Species: *Brucella melitensis*
 C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
 C:Accession: AD3369
 R:DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujar, C.; Los, T.; Ivanov,
 .; Mazur, M.; Goldsman, E.; Selkov, E.; Elizer, P.H.; Hagius, S.; O'Callaghan, D.; Let
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A>Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*
 A:Reference number: AD3252; PMID:11756688
 A:Accession: AD3369
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-281 <KUR>
 A:Cross-references: GB:AE008917; PIDN:AAL52119.1; PID:g17982893; GSPDB:GN00190
 A:Experimental source: strain 16M
 C:Genetics:
 A:Gene: BMEI0938
 A:Map position: 1

Query Match 21.4%: Score 39; DB 2; Length 281;
 Best Local Similarity 43.8%; Pred. No. 38;
 Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 QY 27 AXKIFKDAKRTKLFWI 42
 DB 176 ALPLIKQAGRTETIWI 191

Search completed: September 3, 2002, 15:15:22
 Job time: 810 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 3, 2002, 15:15:37 : Search time 15.9 Seconds

(without alignments)
107.148 Million cell updates/sec

Title: US-09-302-239-3-COPY

Perfect score: 182

Sequence: 1 ANAFLXXLRGSLRXCKXX.....XXAXXIFKDXRTLFWISY 44

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 50 summaries

Database : SWISSProt_40:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	157	86.3	466	FA7_HUMAN	P08709 homo sapien
2	123	67.6	444	FA7_RABIT	P98139 oryctolagus
3	113	62.1	407	FA7_BOVIN	P22457 bos taurus
4	112	61.5	446	FA7_MOUSE	P70375 mus musculus
5	99	54.4	459	PRTC_PIG	O99122 sus scrofa
6	99	54.4	461	PRTC_RAT	P31394 rattus norv
7	99	54.4	490	FA10_RABIT	O19045 oryctolagus
8	98	53.8	461	PRTC_MOUSE	P33587 mus musculus
9	96	52.7	488	FA10_HUMAN	P00742 homo sapien
10	95	52.2	492	FA10_BOVIN	P00734 homo sapien
11	93	51.1	218	TMG1_HUMAN	O14668 homo sapien
12	89	46.9	456	PRTC_BOVIN	P00745 bos taurus
13	85	46.7	473	TMG3_HUMAN	O99bd7 homo sapien
14	85	46.7	251	FA10_CHICK	P25155 gallus gall
15	85	46.7	622	THRB_HUMAN	O28661 oryctolagus
16	82	45.1	458	PRTC_RABIT	P04070 homo sapien
17	82	45.1	461	PRTC_HUMAN	P18292 rattus norv
18	81	44.5	617	THRB_RAT	P19540 canis fami
19	81	44.5	618	THRB_MOUSE	P19521 mus musculi
20	80	44.0	416	FA9_BOVIN	P00741 bos taurus
21	77	42.3	376	FA10_TROCA	P81128 tropidochis
22	77	42.3	461	FA9_HUMAN	P00734 homo sapien
23	74	40.7	202	TMG2_HUMAN	O14669 homo sapien
24	72	38.6	452	FA9_CANFA	P19540 canis fami
25	72	38.6	459	FA9_MOUSE	P19540 mus musculi
26	68	37.4	226	TMG4_HUMAN	O99bd6 homo sapien
27	65	35.7	625	THRB_BOVIN	P00735 bos taurus
28	60	33.0	675	PRTC_HUMAN	P98118 oryctolagus
29	58	31.9	646	PRTC_RABIT	O28520 macaca mula
30	58	31.9	649	PRTC_MACAU	O28520 macaca mula
31	58	31.9	676	PRTC_HUMAN	P00744 bos taurus
32	57	31.3	396	PRTC_BOVIN	P53813 rattus norv
33	57	31.3	675	PRTC_RAT	

ALIGNMENTS

34	52	28.6	400	1	PRTC_HUMAN	P22891 homo sapien
35	50	27.5	675	1	PRTC_MOUSE	O08761 mus musculus
36	45	24.7	879	1	YMG5_YEAST	P42837 saccharomyc
37	43	23.6	263	1	PFTA_STRMU	O68575 streptococc
38	41.5	22.8	322	1	YOL3_CAEEL	O09292 caenorhabd1
39	39	21.4	271	1	MD12_YEAST	O92328 saccharomyc
40	39	21.4	440	1	Y788_BORBU	O51728 borrelia bu
41	39	21.4	514	1	YJJI_HAEIN	P44744 haemophilus
42	39	21.4	604	1	VE1_BPV2	P11298 bovine papl
43	39	21.4	605	1	VE1_BPV1	P03116 bovine papl
44	39	21.4	814	1	IF39_HUMAN	P55884 homo sapien
45	39	21.4	1333	1	YMG9_YEAST	P53756 saccharomyc
46	39	21.4	2476	1	ZAN_PIG	O28983 sus scrofa
47	38	20.9	215	1	CLDX_BRARE	O99192 brachydanio
48	38	20.9	354	1	LXAL_PHOLE	P09140 photobacter
49	38	20.9	413	1	NCAP_IHNV	P19691 infectious
50	38	20.9	539	1	CH61_MYCTU	O59573 mycobacteri

RESULT 1	FA7_HUMAN	STANDARD:	PRTC:	466 AA.
ID	FA7_HUMAN			
AC	P08709; Q14339;			
DT	01-JAN-1988 (Rel. 06, Created)			
DT	01-JAN-1988 (Rel. 06, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin			
DE	conversion accelerator) (Eptacog alfa).			
GN	F7.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RX	MEDLINE=86205965; PubMed=3486420;			
RA	Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C.,			
RA	Woodbury R.G., Hart C.E., Insley M.Y., Kissel W., Kurachi K.,			
RA	Davie E.W.;			
RT	"Characterization of a cDNA coding for human factor VII.,"			
RL	Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87260948; PubMed=3037537;			
RA	O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y.,			
RA	Hagen F.S., Murray M.J.;			
RT	"Nucleotide sequence of the gene coding for human factor VII, a			
RL	vitamin K-dependent protein participating in blood coagulation.,"			
RL	Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).			
RN	[3]			
RP	SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.			
RX	MEDLINE=89088153; PubMed=3264725;			
RA	Thim L., Bjorn S., Christensen M., Nicolaisen E.M., Lund-Hansen T.,			
RA	Pedersen A.H., Hedner U.;			
RT	"Amino acid sequence and posttranslational modifications of human			
RL	factor VIIa from plasma and transfected baby hamster kidney cells.,"			
RL	Biochemistry 27:7785-7793(1988).			
RN	[4]			
RP	CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.			
RX	MEDLINE=91250411; PubMed=1904059;			
RA	Bjoern S., Foster D.C., Thim L., Wberg F.C., Christensen M.,			
RA	Komiyama Y., Pedersen A.H., Kissel W.;			
RT	"Human plasma and recombinant factor VII. Characterization of O-			
RT	glycosylations at serine residues 52 and 60 and effects of site-			
RT	directed mutagenesis of serine 52 to alanine.,"			
RL	J. Biol. Chem. 266:11051-11057(1991).			
RN	[5]			
RP	STRUCTURE OF CARBOHYDRATE ON SER-112.			
RX	MEDLINE=90062160; PubMed=2511201;			

RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T., Takao T.,
 RA Shimomura Y., Iwanaga S.: Identification of a disaccharide (Xyl-Glc) and a trisaccharide
 RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first
 RT epidermal growth factor-like domain of human factors VII and IX and
 RT protein Z and bovine protein Z.";
 RL J. Biol. Chem. 264:20320-20325(1989).
 RN [6]
 RP STRUCTURE OF CARBOHYDRATE ON SER-112.
 RX MEDLINE=91344709; Pubmed=2129367;
 RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;
 RT "A new trisaccharide sugar chain linked to a serine residue in the
 RT first EGF-like domain of clotting factors VII and IX and protein Z.";
 RL Adv. Exp. Med. Biol. 261:121-131(1990).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE=96175641; Pubmed=8598903;
 RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,
 RA Konigsberg W.H., Nemerson Y., Kirchhofer D.;
 RT "The crystal structure of the complex of blood coagulation factor
 RT VIIa with soluble tissue factor.";
 RL Nature 380:41-46(1996).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE=99126538; Pubmed=9925787;
 RA Zhang E., St. Charles R., Tulinsky A.;
 RT "Structure of extracellular tissue factor complexed with factor VIIa
 RT inhibited with a BPTI mutant.";
 RL J. Mol. Biol. 285:2089-2104(1999).
 RN [9]
 RP STRUCTURE BY NMR OF 105-145.
 RX MEDLINE=98367502; Pubmed=9692950;
 RA Muranyi A., Finn B.E., Gippert G.P., Forsen S., Steinflo J.,
 RA Drakeberg T.;
 RT "Solution structure of the N-terminal EGF-like domain from human
 RT factor VII.";
 RL Biochemistry 37:10605-10615(1998).
 RN [10]
 RP VARIANT GLN-364.
 RX MEDLINE=91300046; Pubmed=2070047;
 RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,
 RA Meade T.W., Tuddenham E.G.D.;
 RT "Purification and characterization of factor VII 304-Gln: a variant
 RT molecule with reduced activity isolated from a clinically unaffected
 RT male.";
 RL Blood 78:132-140(1991).
 RN [11]
 RP VARIANTS GLN-364 AND PHE-370.
 RX MEDLINE=92340074; Pubmed=1634227;
 RA Marchetti G., Patrascchini P., Gemmati D., Derosa V., Pinotti M.,
 RA Rodorigo G., Casonato A., Girolami A., Bernardi F.;
 RT "Detection of two missense mutations and characterization of a repeat
 RT polymorphism in the factor VII gene (F7).";
 RL Hum. Genet. 89:497-502(1992).
 RN [12]
 RP VARIANT TYR-238.
 RX MEDLINE=93372811; Pubmed=8364544;
 RA Marchetti G., Ferrati M., Patrascchini P., Redaelli R., Bernardi F.;
 RT "A missense mutation (178Cys-->Tyr) and two neutral dimorphisms
 RT (115His and 333Ser) in the human coagulation factor VII gene.";
 RL Hum. Mol. Genet. 2:1055-1056(1993).
 RN [13]
 RP VARIANTS.
 RX MEDLINE=94061028; Pubmed=8242057;
 RA Takamiya O., Kemball-Cook G., Martin D.M.A., Cooper D.N.,
 RA von Felten A., Mell E., Hahn I., Prangnell D.R., Lumley H.,
 RA Tuddenham E.G.D., McVey J.H.;
 RT "Detection of missense mutations by single-strand conformational
 RT polymorphism (SSCP) analysis in five dysfunctional variants of
 RT coagulation factor VII.";
 RL Hum. Mol. Genet. 2:1355-1359(1993).
 RN [14]
 RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.
 RX MEDLINE=94264305; Pubmed=8204879;
 RA Chahing S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W.,
 RA Roberts H.R., Blachman M., Monroe D.M., High K.A.;
 RT "Severe factor VII deficiency caused by mutations abolishing the
 RT cleavage site for activation and altering binding to tissue factor.";
 RL Blood 83:3524-3535(1994).
 RN [15]
 RP VARIANT VAL-354.
 RX MEDLINE=95072589; Pubmed=7981691;
 RA Bernardi F., Castaman G., Redaelli R., Pinotti M., Lunghi B.,
 RA Rodeghiero F., Marchetti G.;
 RT "Topologically equivalent mutations causing dysfunctional coagulation
 RT factors VII (294Ala-->Val) and X (334Ser-->Pro).";
 RL Hum. Mol. Genet. 3:1175-1177(1994).
 RN [16]
 RP VARIANT MIE HIS-307.
 RX MEDLINE=95064662; Pubmed=7974346;
 RA Ohlwa M., Hayashi T., Wada H., Minamikawa K., Shirakawa S.,
 RA Suzuki K.;
 RT "Factor VII Mle: homozygous asymptomatic type I deficiency caused by
 RT an amino acid substitution of His (CAC) for Arg(247) (CGC) in the
 RT catalytic domain.";
 RL Thromb. Haemost. 71:773-777(1994).
 RN [17]
 RP VARIANT MET-419.
 RX MEDLINE=96247510; Pubmed=8652821;
 RA Ardin A.A., Mannucci P.M., Bauer K.A.;
 RT "A Thr359Met mutation in factor VII of a patient with a hereditary
 RT deficiency causes defective secretion of the molecule.";
 RL Blood 87:5085-5094(1996).
 RN [18]
 RP VARIANTS W-283, K-325, V-358, Q-364, E-402 AND Q-413.
 RX MEDLINE=97001216; Pubmed=8844208;
 RA Bernardi F., Castaman G., Pinotti M., Ferraresi P., di Iasio M.G.,
 RA Lunghi B., Rodeghiero F., Marchetti G.;
 RT "Mutation pattern in clinically asymptomatic coagulation factor VIII
 RT deficiency.";
 RL Hum. Mutat. 8:108-115(1996).
 RN [19]
 RP VARIANT VAL-304.
 RX MEDLINE=97037613; Pubmed=8883260;
 RA Tanary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N.,
 RA Brenner B., Paz M., Luder A.S., Blau O., Korostilshvsky M.,
 RA Zaitov R., Seligsohn U.;
 RT "Ala244Val is a common, probably ancient mutation causing factor VII
 RT deficiency in Moroccan and Iranian Jews.";
 RL Thromb. Haemost. 76:283-291(1996).
 RN [20]
 RP VARIANTS MALTA THR-194 AND VAL-304.
 RX MEDLINE=98112461; Pubmed=9452082;
 RA Alshinawi G., Scerif C., Galdies R., Aguilina A., Felice A.E.;
 RT "Two new missense mutations (P134T and A244V) in the coagulation
 RT factor VII gene.";
 RL Hum. Mutat. Suppl. 1:S189-S191(1998).
 CC -I- FUNCTION: CIRCULATES IN THE BLOOD. IN A ZWOGEN FORM. FACTOR VII IS
 CC CONVERTED TO FACTOR VIIA BY FACTOR XIa, FACTOR XIIa, FACTOR IXa, OR
 CC THROMBIN BY MINOR PROTEOLYSES. IN THE PRESENCE OF TISSUE FACTOR
 CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
 CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
 CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.
 CC -I- CATALYTIC ACTIVITY: Hydrolyses one Arg-1-Ile bond in factor X to
 CC form factor Xa.
 CC -I- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
 CC BY A DISULFIDE BOND.
 CC -I- ALTERNATIVE PRODUCTS: 2 isoforms: A (shown here) and B; are
 CC produced by alternative splicing.
 CC -I- TISSUE SPECIFICITY: PLASMA.
 CC -I- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC -I- DISEASE: DEFECTS IN F7 CAN CAUSE COAGULOPATHY.
 CC -I- PHARMACEUTICAL: Available under the names Niasase or Novoseven
 CC (Novo Nordisk). Used for the treatment of bleeding episodes in

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CC hemophilia A or B patients with antibodies to coagulation factors
CC VITR or IX.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.

Query Match 86.3%: Score 157; DB 1; Length 466;
Best Local Similarity 72.7%: Pred. No. 8e-21;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 1 ANAFILXLRGSLXKXRCXKXOCSPFXAXXIFPDARKLTFMYST 44
DB 61 ANAFLEELRPGSLERECKECCSFEEANERFKDAERTKLFMYST 104

RESULT 2
FA7_RABIT
ID FA7_RABIT STANDARD; PRT: 444 AA.
AC P98139; P79224;
DT 01-FEB-1996 (Rel. 33, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator).
CN F7.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Liver;
RC MEDLINE=93190306; PubMed=8383365;
RA Brothers A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;
RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation
RT factor VII."
RL Thromb. Res. Suppl. 69:231-238(1993).
RN [2]
RP REVISION TO 395.
RC TISSUE=Liver;
RA Ruiz S.R., Blajchman M.A., Clarke B.J.;
RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR
CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
CC SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Hydrolyses one Arg-1-Ile bond in factor X to
CC form factor Xa.
CC -1- SUBUNIT: HEMERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
CC BY A DISULFIDE BOND (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- PM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
-----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: U77477; AAB37326.1; -.
CC HSSP: P08709; 1BP9.
CC MEROPS: S01.215; -.
CC InterPro: IPR002086; Aldehyde_dehydr.

```

	Query Match	Best Local Similarity	Score 123;	DB 1;	Length 444;
DR InterPro: IPR000152; Asx_hydroxyl.	67.6%;	54.5%;	Pred. No. 1.le-14;		
DR InterPro: IPR001314; Chymotrypsin.					
DR InterPro: IPR000561; EGF-like.					
DR InterPro: IPR000742; EGF_2.					
DR InterPro: IPR001881; EGF_Ca.					
DR InterPro: IPR002383; GLA_blood.					
DR InterPro: IPR001254; Trypsin.					
DR InterPro: IPR000294; Vitk_dep_GLA.					
DR Pfam: PF00508; EGF_2.					
DR Pfam: PF00594; gla_1.					
DR Pfam: PF00089; trypsin_1.					
DR PRINTS: PR00722; CHYMOTRYPSIN.					
DR PRINTS: PRO0001; GLABLOOD.					
DR SMART: SM00179; EGF_CA_1.					
DR SMART: SM00001; EGF_like_1.					
DR SMART: SM00069; GLA_1.					
DR SMART: SM00020; TRYD_SPC_1.					
DR PROSITE: PS00010; ASX_HYDROXYL_1.					
DR PROSITE: PS00022; EGF_1; 1.					
DR PROSITE: PS01186; EGF_2; 1.					
DR PROSITE: PS01187; EGF_CA_1.					
DR PROSITE: PS00011; GLU CARBOXYLATION; 1.					
DR PROSITE: PS50240; TRYP SIN_DOM; 1.					
DR PROSITE: PS00134; TRYP SIN_SER; 1.					
DR PROSITE: PS00135; TRYP SIN_HIS; 1.					
KM Hydrolyase: Serine protease; Blood coagulation; zymogen; glycoprotein; Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid; EGF-like domain; Repeat; signal; Hydroxylation.					
KW EGF-like domain; Repeat; signal; Hydroxylation.					
FT SIGNAL	1	21	POTENTIAL.		
FT PROPEP	22	39	POTENTIAL.		
FT CHAIN	40	191	FACTOR VII LIGHT CHAIN.		
FT CHAIN	192	444	FACTOR VII HEAVY CHAIN.		
FT DOMAIN	45	74	GPA-RICH.		
FT DOMAIN	85	121	EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).		
FT DOMAIN	126	167	EGF-LIKE 2.		
FT DOMAIN	192	444	SERINE PROTEASE.		
FT SITE	191	192	CLEAVAGE (BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR THROMBIN) (BY SIMILARITY), BY SIMILARITY.		
FT ACT_SITE	232	232	BY SIMILARITY.		
FT ACT_SITE	281	281	SUBSTRATE (BY SIMILARITY).		
FT BINDING	377	377	BY SIMILARITY.		
FT DISULFID	56	61	BY SIMILARITY.		
FT DISULFID	89	100	BY SIMILARITY.		
FT DISULFID	94	109	BY SIMILARITY.		
FT DISULFID	111	120	BY SIMILARITY.		
FT DISULFID	130	141	BY SIMILARITY.		
FT DISULFID	137	151	BY SIMILARITY.		
FT DISULFID	153	166	BY SIMILARITY.		
FT DISULFID	174	301	BY SIMILARITY.		
FT DISULFID	198	203	BY SIMILARITY.		
FT DISULFID	217	233	BY SIMILARITY.		
FT DISULFID	349	368	BY SIMILARITY.		
FT DISULFID	379	407	BY SIMILARITY.		
FT MOD_RES	45	45	GAMMA-CARBOXYGLUTAMIC ACID.		
FT MOD_RES	46	46	GAMMA-CARBOXYGLUTAMIC ACID.		
FT MOD_RES	53	53	GAMMA-CARBOXYGLUTAMIC ACID.		
FT MOD_RES	55	55	GAMMA-CARBOXYGLUTAMIC ACID.		
FT MOD_RES	58	58	GAMMA-CARBOXYGLUTAMIC ACID.		
FT MOD_RES	59	59	GAMMA-CARBOXYGLUTAMIC ACID.		
FT MOD_RES	64	64	GAMMA-CARBOXYGLUTAMIC ACID.		
FT MOD_RES	65	65	GAMMA-CARBOXYGLUTAMIC ACID.		
FT MOD_RES	68	68	GAMMA-CARBOXYGLUTAMIC ACID.		
FT MOD_RES	74	74	GAMMA-CARBOXYGLUTAMIC ACID.		
FT MOD_RES	102	102	HYDROXYLATION (BY SIMILARITY).		
FT CARBOHYD	211	211	N-LINKED (GLCNAC...) (POTENTIAL).		
FT CARBOHYD	242	242	N-LINKED (GLCNAC...) (POTENTIAL).		
FT CARBOHYD	306	306	N-LINKED (GLCNAC...) (POTENTIAL).		
SO SEQUENCE	444 AA;	49011 MP;	0481ABC4FE5427F8 CRC64;		

Matches 24; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRXGSLKRXKXCCSFXXAXIFKDAKRTLEWISY 44
Db 40 ANSFLLELRPGSLERCKEELCSFEAREVFQSTERTKQFWVSY 83

RESULT 3
ID FA7_BOVIN STANDARD; PRT; 407 AA.
AC P22457;
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Coagulation factor VII (EC 3.4.21.21) (Serum prothrombin conversion accelerator).
GN F7.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
OX NCBI_TaxID:9913;
RN [1]
RP MEDLINE=89008362; PubMed=3049594;
RX Takeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T., Iwanaga S.;
RA "Bovine factor VII. Its purification and complete amino acid sequence."
RT J. Biol. Chem. 263:14868-14877(1988).
RL [2]
RN STRUCTURE OF CARBOHYDRATE ON SER-52.
RX MEDLINE=8921399; PubMed=3149637;
RA Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T., Miyata T., Iwanaga S., Takao T., Shimomishi Y., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in bovine blood coagulation factors VII and IX."
RL J. Biochem. 104:867-868(1988).
RN [3]
RP STRUCTURE OF CARBOHYDRATE ON SER-52.
RX MEDLINE=91344709; PubMed=2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in the first EGF-like domain of clotting factors VII and IX and protein Z."
RL Adv. Exp. Med. Biol. 281:121-131(1990).
CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.
CC -1- CATALYTIC ACTIVITY: Hydrolyses one Arg-|-Ile bond in factor X to form factor Xa.
CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED BY A DISULFIDE BOND.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
DR PIR: A31979; A31979.
DR HSSP: P08709; 1BF9.
DR MEROPS: S01.215; -.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR0001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001438; EGF_II.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; trypsin.

DR InterPro: IPR000294; Vitk_dep_GLA.
DR Pfam: PF00008; EGF; 2.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; EGFBLD.
DR PRINTS: PR00019; GLABLOOD.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00001; EGF-like; 1.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; Tryp_spc; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS02400; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Serine protease; Blood coagulation; Zymogen; Glycoprotein; Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid; EGF-like domain; Repeat.
KW EGF-like domain; Repeat.
FT CHAIN 1 152
FT CHAIN 153 407
FT DOMAIN 6 35
FT DOMAIN 46 82
FT DOMAIN 87 128
FT DOMAIN 153 407
FT SITE 152 153
FT ACT_SITE 193 193
FT ACT_SITE 242 242
FT ACT_SITE 344 344
FT BINDING 338 338
FT DISULFID 17 22
FT DISULFID 50 61
FT DISULFID 55 70
FT DISULFID 72 81
FT DISULFID 91 102
FT DISULFID 98 112
FT DISULFID 114 127
FT DISULFID 135 262
FT DISULFID 159 164
FT DISULFID 178 194
FT DISULFID 310 329
FT DISULFID 340 368
FT MOD_RES 6 6
FT MOD_RES 7 7
FT MOD_RES 14 14
FT MOD_RES 16 16
FT MOD_RES 19 19
FT MOD_RES 20 20
FT MOD_RES 25 25
FT MOD_RES 26 26
FT MOD_RES 29 29
FT MOD_RES 35 35
FT CARBOHYD 52 52
FT CARBOHYD 145 145
FT CARBOHYD 203 203
SQ SEQUENCE 407 AA; 44431 MW; 703ELFE06367FF10 CRC64;

Query Match 62.1%; Score 113; DB 1; Length 407;
Best Local Similarity 50.0%; Pred. No. 6.8e-13;
Matches 22; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRXGSLKRXKXCCSFXXAXIFKDAKRTLEWISY 44
Db 1 ANSFLLELRPGSLERCKEELCSFEAREVFQSTERTKQFWVSY 44

RESULT 4
FA7_MOUSE

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ID FA7_MOUSE STANDARD: PRT; 446 AA.
AC P70375;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator).
GN F7 OR CF7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE-97127167; PubMed-8972017;
RA Idusogie E., Rosen E.D., Carmeliet P., Collen D., Castellino F.J.;
RT "Nucleotide structure and characterization of the murine blood
RT coagulation factor VII gene.";
RL Thromb. Haemost. 76:957-964(1996).
CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR
CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
CC SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Hydrolyses one Arg-1-Ile bond in factor X to
CC form factor Xa.
CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
CC BY A DISULFIDE BOND (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U66079; AAC33796.1; -.
DR HSSP: P08709; 1BF9.
DR MEROPS: S01.215; -.
DR MGD: MGI:109325; F7.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF-2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Trypsin.
DR InterPro: IPR000294; Vitk_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00001; EGF_Like; 1.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; TRYP_Spc; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; FALSE_NEG.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.

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DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Serine protease; Blood coagulation; zymogen; glycoprotein;
KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
KW EGF-like domain; Repeat; Signal; Hydroxylation.
FT SIGNAL 1 24
FT PROPEP 25 41
FT CHAIN 42 193
FT CHAIN 194 446
FT DOMAIN 47 76
FT DOMAIN 87 123
FT DOMAIN 128 169
FT DOMAIN 194 446
FT SITE 193 194
FT ACT_SITE 234 234
FT ACT_SITE 283 283
FT ACT_SITE 385 385
FT BINDING 379 379
FT DISULFID 58 63
FT DISULFID 91 102
FT DISULFID 96 111
FT DISULFID 113 122
FT DISULFID 132 143
FT DISULFID 139 153
FT DISULFID 155 168
FT DISULFID 176 303
FT DISULFID 200 205
FT DISULFID 219 235
FT DISULFID 351 370
FT DISULFID 381 409
FT MOD_RES 47 47
FT MOD_RES 48 48
FT MOD_RES 55 55
FT MOD_RES 57 57
FT MOD_RES 60 60
FT MOD_RES 61 61
FT MOD_RES 66 66
FT MOD_RES 67 67
FT MOD_RES 70 70
FT MOD_RES 76 76
FT MOD_RES 104 104
FT CARBOHYD 186 186
FT CARBOHYD 244 244
SQ SEQUENCE 446 AA; 50276 MM; 2512E44A45C0B96E CRC64;

Query Match 61.5%; Score 112; DB 1; Length 446;
Best Local Similarity 54.5%; Pred. No. 1,le-12;
Matches 24; Conservative 1; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLLXLRKGSLLRXCKXQCSFXXAXIFKDAKRTKLFWISY 44
DB 42 ANSLLEELWPGSLERECNEQCSFEARELFFKSPERTKQWIIY 85

RESULT 5
PRTC_PIG STANDARD: PRT; 459 AA.
AC 09GLP2;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
DE (Autoproteolytic IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV).
GN PROC.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.

```

RC TISSUE=Liver:
RA Grimm D.R., Colter M.B., Kim H.K.W.:
RT "Cloning of the complete cDNA sequences encoding porcine factor V and
RL protein C.";
CC Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Protein C is a vitamin K-dependent serine protease that
CC regulates blood coagulation by inactivating factors Va and VIIIa
CC in the presence of calcium ions and phospholipids.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIIa.
CC -1- SUBUNIT: Synthesized as a single chain precursor, which is cleaved
CC into a light chain and a heavy chain held together by a disulfide
CC bond. The enzyme is then activated by thrombin, which cleaves a
CC tetrapeptide from the amino end of the heavy chain; this
CC reaction, which occurs at the surface of endothelial cells, is
CC strongly promoted by thrombomodulin.
CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
CC -1- PFM: The vitamin K-dependent, enzymatic carboxylation of some Glu
CC residues allows the modified protein to bind calcium.
CC -1- MISCELLANEOUS: Calcium also binds, with stronger affinity to
CC another site, beyond the GLA domain. This GLA-independent binding
CC site is necessary for the recognition of the
CC thrombin-thrombomodulin complex.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF191307; AAC28380.1;
DR Interpro: IPR000152; Asx_hydroxyl-
DR Interpro: IPR001314; Chymotrypsin.
DR Interpro: IPR000561; EGF-like.
DR Interpro: IPR001881; EGF_Ca.
DR Interpro: IPR002383; GLA_blood.
DR Interpro: IPR001254; Trypsin.
DR Interpro: IPR000294; VitK_dep-GLA.
DR Pfam: PF00089; trypsin_1
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00181; EGF_2.
DR SMART: SM00001; EGF-like_2.
DR SMART: SM00069; GLA_1.
DR SMART: SM00020; TRYP_SPE; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
KW Blood coagulation; Glycoprotein; Serine protease;
KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
KW EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
FT SIGNAL 1
FT PROPEP 18
FT CHAIN 19 41
FT CHAIN 42 459
FT CHAIN 42 196
FT CHAIN 199 459
FT CHAIN 199 213
FT SITE 213 214
FT DOMAIN 96 131
FT DOMAIN 135 175
FT DOMAIN 214 459
FT MOD_RES 47 47
FT MOD_RES 48 48
FT MOD_RES 48 48
FT MOD_RES 55 55

FT MOD_RES 57 57
FT MOD_RES 60 60
FT MOD_RES 61 61
FT MOD_RES 66 66
FT MOD_RES 67 67
FT MOD_RES 70 70
FT MOD_RES 70 70
FT MOD_RES 112 112
FT MOD_RES 255 255
FT ACT_SITE 301 301
FT ACT_SITE 400 400
FT ACT_SITE 58 63
FT DISULFID 91 110
FT DISULFID 100 105
FT DISULFID 104 119
FT DISULFID 121 130
FT DISULFID 139 150
FT DISULFID 146 159
FT DISULFID 161 174
FT DISULFID 182 321
FT DISULFID 240 256
FT DISULFID 371 385
FT DISULFID 396 424
FT CARBOHYD 138 138
FT CARBOHYD 292 292
FT CARBOHYD 353 353
FT SEQUENCE 459 AA; 51866 MW; 8541AAC14CC16D09 CRC64;
SO
Query Match 54.4%; Score 99; DB 1; Length 459;
Best Local Similarity 45.5%; Pred. No. 2.6e-10;
Matches 20; Conservative 3; Mismatches 21; Indels 0; Gaps 0;
QY 1 ANAEFLXLRKXGSLKRXCKXQCSPFXAXXIFKDXKRTLFMISY 44
Db 42 ANSFLLELRPSLSLECKEKEFCDEFEAREIFQNTENTAFMSKY 85
RESULT 6
PRTC_RAT STANDARD; PRT; 461 AA.
AC P31394;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
DE (Autoproteolytic IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV).
CN PROC.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=Liver;
RX MEDLINE=92329550; PubMed=1627650;
RA Okaeji T., Maekawa K., Nawa K., Marumoto Y.;
RT "The cDNA cloning and mRNA expression of rat protein C.";
RL Biochim. Biophys. Acta 1131:329-332(1992).
CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIa
CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIIa.
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE

RL Br. J. Haematol. 86:590-600(1994).

CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT

CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA

CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.

CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va

CC and VIIIA.

CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED

CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE

CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A

CC TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS

CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS

CC STRONGLY PROMOTED BY THROMBOMODULIN.

CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.

CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAITC CARBOXYLATION OF SOME

CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.

CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO

CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING

CC SITE IS NECESSARY FOR THE RECOGNITION OF THE

CC THROMBIN-THROMBOMODULIN COMPLEX.

CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE

CC TRIPSIN FAMILY.

CC -----

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CC -----

CC EMBL: D10445; BAA01235.1; -

CC EMBL: AF034569; AAC33795.1; -

CC EMBL: JX0210; BAA07812.1; -

CC PIR: JX0210; JX0210.

CC HSSP: P04070; 1PCU.

CC MEROPS: S01.218; -.

CC MGD: MG1.97771; Proc.

DR InterPro: IPR000152; Asx_hydroxyl.

DR InterPro: IPR001314; Chymotrypsin.

DR InterPro: IPR000561; EGF-like.

DR InterPro: IPR001881; EGF-Ca.

DR InterPro: IPR002383; GLA_blood.

DR InterPro: IPR001254; Trypsin.

DR InterPro: IPR000284; Vitk_dep_GLA.

DR Pfam: PF00008; EGF_2.

DR Pfam: PF00594; gla; 1.

DR Pfam: PF00089; trypsin; 1.

DR PRINTS: PR00722; CHYMOTRYPSIN.

DR PRINTS: PR00001; GLABLOOD.

DR SMART: SM00179; EGF_CA; 1.

DR SMART: SM00001; EGF_Like; 1.

DR SMART: SM00069; GLA; 1.

DR SMART: SM00020; TRYP_SPC; 1.

DR PROSITE: PS00010; ASX_HYDROXYL; 1.

DR PROSITE: PS00022; EGF_1; 1.

DR PROSITE: PS01186; EGF_2; 2.

DR PROSITE: PS01187; EGF_CA; 1.

DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.

DR PROSITE: PS00240; TRYPSIN_DOM; 1.

DR PROSITE: PS00134; TRYPSIN_HIS; 1.

DR PROSITE: PS00135; TRYPSIN_SER; 1.

KM Blood coagulation; Glycoprotein; Serine protease;

KM Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;

KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.

FT SIGNAL 1 33

FT PROPEP 34 41

FT CHAIN 42 196

FT PEPTIDE 199 461

FT SITE 212 213

FT DOMAIN 96 131

FT DOMAIN 135 175

EGF-LIKE 1.

EGF-LIKE 2.

FT DOMAIN 213 461

FT MOD_RES 47 47

FT MOD_RES 48 48

FT MOD_RES 55 55

FT MOD_RES 57 57

FT MOD_RES 60 60

FT MOD_RES 61 61

FT MOD_RES 66 66

FT MOD_RES 67 67

FT MOD_RES 70 70

FT MOD_RES 112 112

FT ACT_SITE 253 253

FT ACT_SITE 299 299

FT ACT_SITE 402 402

FT DISULFID 58 63

FT DISULFID 91 110

FT DISULFID 100 105

FT DISULFID 104 119

FT DISULFID 121 130

FT DISULFID 139 150

FT DISULFID 146 159

FT DISULFID 161 174

FT DISULFID 182 319

FT DISULFID 238 254

FT DISULFID 373 387

FT DISULFID 398 426

FT CARBOHYD 214 214

FT CARBOHYD 290 290

FT CARBOHYD 355 355

FT CARBOHYD 328 328

FT CONFLICT 393 393

FT SEQUENCE 461 AA; 51945 MW; 53FAAD05B194D6E CRC64;

Query Match 53.8%; Score 98; DB 1; Length 461;

Best Local Similarity 45.5%; Pred. No. 4e-10;

Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLRXKCKXXQCSFYXAXXIFKAXXRTKLPWISY 44

DB 42 ANSFLEMRGSLERECMEICDFEEAQELFQNVEDTLAWIKY 85

RESULT 9

FA10_HUMAN STANDARD; PRT; 488 AA.

AC P00742; O14340; 01, Created)

DT 21-JUL-1986 (Rel. 12, Last sequence update)

DT 01-OCT-1989 (Rel. 40, Last annotation update)

DE 16-OCT-2001 (Rel. 40, Last annotation update)

DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).

GN F10.

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91216473; PubMed=1902434;

RA Messier T.L., Pittman D.D., Long G.L., Kaufman R.J., Church W.R.;

RT Cloning and expression in COS-1 cells of a full-length cDNA encoding

RL human coagulation factor X.*;

RL Gene 99:291-294(1991).

[2]

RP SEQUENCE FROM N.A.
RX MEDLINE=87026600; PubMed=3768336;
RA Leytus S.P., Foster D.C., Kurachi K., Davie E.W.;
RT "Gene for human factor X: a blood coagulation factor whose gene
RT organization is essentially identical with that of factor IX and
RT protein C.";
RL Biochemistry 25:5098-5102(1986).
RN [3]
RP SEQUENCE OF 13-488 FROM N.A.
RX MEDLINE=85216545; PubMed=2582420;
RA Fung M.R., Hay C.W., McGillivray R.T.A.;
RT "Characterization of an almost full-length cDNA coding for human
RT blood coagulation factor X.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).
RN [4]
RP SEQUENCE OF 19-488 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=86221713; PubMed=3011603;
RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;
RT "Isolation and characterization of human blood-coagulation factor X
RT cDNA.";
RL Gene 41:311-314(1986).
RN [5]
RP SEQUENCE OF 41-179.
RX MEDLINE=83257207; PubMed=6671167;
RA McMullen B.A., Fujikawa K., Kistiel W., Sasagawa T., Howald W.N.,
RA Kwa E.Y., Weinstein B.;
RT "Complete amino acid sequence of the light chain of human blood
RT coagulation factor X: evidence for identification of residue 63 as
RT beta-hydroxyaspartic acid.";
RL Biochemistry 22:2875-2884(1983).
RN [6]
RP SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=Liver;
RX MEDLINE=84222026; PubMed=6587384;
RA Leytus S.P., Chung D.W., Kistiel W., Kurachi K., Davie E.W.;
RT "Characterization of a cDNA coding for human factor X.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702(1984).
RN [7]
RP SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=94062825; PubMed=8243461;
RA Inoue K., Morita T.;
RT "Identification of O-linked oligosaccharide chains in the activation
RT peptides of blood coagulation factor X. The role of the carbohydrate
RL moieties in the activation of factor X.";
RL Eur. J. Biochem. 218:153-163(1993).
RN [8]
RP SEQUENCE OF 1-23 FROM N.A.
RX MEDLINE=90128299; PubMed=2612918;
RA Jagadeeswaran P., Reddy S.V., Rao K.J., Hamsabhusanam K., Lyman G.;
RT "Cloning and characterization of the 5' end (exon 1) of the gene
RT encoding human factor X.";
RL Gene 84:517-519(1989).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.
RX MEDLINE=93360277; PubMed=8355279;
RA Padmanabhan K., Padmanabhan K.P., Tulinsky A., Park C.H., Bode W.,
RA Huber R., Blankenship D.T., Cardin A.D., Kistiel W.;
RT "Structure of human des(1-45) factor Xa at 2.2-A resolution.";
RL J. Mol. Biol. 232:947-966(1993).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.
RX MEDLINE=96283982; PubMed=9618463;
RA Kamata K., Kawamoto H., Honma T., Imama T., Kim S.H.;
RT "Structural basis for chemical inhibition of human blood coagulation
RT factor Xa.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).
RN [1]
RP CONVERTS PROTHROMBIN TO THROMBIN IN THE PRESENCE OF FACTOR VA,
CC CA⁺⁺, AND PHOSPHOLIPID DURING BLOOD CLOTTING.
CC -1 CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
CC Arg-|-Ile bonds in prothrombin to form thrombin.
CC -1 SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR

CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
CC MORE DISULFIDE BONDS.
CC -1 TISSUE SPECIFICITY: Plasma; synthesized in the liver.
CC -1 PTM: THE VITAMIN K-DEPENDENT, ENZYMIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM.
CC -1 PTM: N- AND O-GLYCOSYLATED.
CC -1 PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
CC -1 SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: K03194; AAA52490.1; -;
CC EMBL: M57285; AAA52421.1; -;
CC EMBL: L29433; AAA52764.1; -;
CC EMBL: L00390; AAA52764.1; JOINED.
CC EMBL: L00391; AAA52764.1; JOINED.
CC EMBL: L00392; AAA52764.1; JOINED.
CC EMBL: L00393; AAA52764.1; JOINED.
CC EMBL: L00394; AAA52764.1; JOINED.
CC EMBL: L00395; AAA52764.1; JOINED.
CC EMBL: L00396; AAA52764.1; JOINED.
CC EMBL: M2613; AAA51984.1; -;
CC EMBL: K01886; AAA52486.1; -;
CC EMBL: M33297; AAA52636.1; -;
CC PIR: A00924; EXHU.
CC PIR: A25853; A25853.
CC PIR: A24478; A24478.
CC PDB: 1HCG; 08-MAY-95.
CC PDB: 1FAX; 29-OCT-97.
CC PDB: 1FXV; 17-JUN-98.
CC PDB: 1XKA; 23-MAR-99.
CC PDB: 1XKB; 23-MAR-99.
CC MEROPS: S01.216; -;
CC CarDBank; CCSD:29393; -;
CC GlycoSuiteDB; P00742; -;
CC MIM: 134530; -;
CC MIM: 227600; -;
CC InterPro: IPR000152; Asx_hydroxyl.
CC InterPro: IPR001314; Chymotrypsin.
CC InterPro: IPR000561; EGF-like.
CC InterPro: IPR000742; EGF_2.
CC InterPro: IPR001881; EGF_Ca.
CC InterPro: IPR002383; GLA_blood.
CC InterPro: IPR001254; Trypsin.
CC InterPro: IPR00294; VitK_dep_GLA.
CC Pfam: PF00008; EGF_2.
CC Pfam: PF00594; gla; 1.
CC Pfam: PF00089; trypsin; 1.
CC PRINTS: PR00722; CHYMOTRYPSIN.
CC PRINTS: PR00001; GLABLOOD.
CC SMART: SM00179; EGF_CA.1.
CC SMART: SM00001; EGF_like; 1.
CC SMART: SM00069; GLA; 1.
CC SMART: SM00020; Tryp_spec; 1.
CC PROSITE: PS00010; ASX_HYDROXYL; 1.
CC PROSITE: PS00022; EGF_1; 1.
CC PROSITE: PS01186; EGF_2; 2.
CC PROSITE: PS01187; EGF_CA; 1.
CC PROSITE: PS00011; GLU_CARBOXYLATION; 1.
CC PROSITE: PS50240; TRYPSIN_DOM; 1.
CC PROSITE: PS00134; TRYPSIN_HIS; 1.
CC PROSITE: PS00135; TRYPSIN_SER; 1.
CC GlycoProtein: Hydrolyase; Serine protease; Plasma; Blood coagulation;
KW

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KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
KM Signal; Zymogen; EGF-like domain; Repeat; 3D-structure.
FT SIGNAL 1 31
FT PROPEP 1 40
FT CHAIN 32 179
FT CHAIN 41 488
FT PROPEP 183 488
FT CHAIN 234 488
FT CHAIN 235 488
FT DOMAIN 86 122
FT DOMAIN 125 165
FT DOMAIN 125 165
FT DOMAIN 235 488
FT MOD_RES 46 46
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FT MOD_RES 56 56
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FT MOD_RES 66 66
FT MOD_RES 69 69
FT MOD_RES 72 72
FT MOD_RES 79 79
FT MOD_RES 103 103
FT CARBOHYD 199 199
FT CARBOHYD 211 211
FT CARBOHYD 221 221
FT CARBOHYD 231 231
FT ACT_SITE 276 276
FT ACT_SITE 322 322
FT ACT_SITE 419 419
FT DISULFID 90 101
FT DISULFID 95 110
FT DISULFID 112 121

Query Match 52.7%; Score 96; DB 1; Length 488;
Best Local Similarity 38.6%; Pred. No. 9, 8e-10;
Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLKRXKXQCSFYXAXXIFKDXRTKLEWISY 44
   11:11 :: 11:11 11:11 :: 11:11 11:11
DB 41 ANSFLEMKKGHLRECMETCSYEAREVFEDSDKTNEWMKY 84

RESULT 10
FA10_BOVIN STANDARD; PRT; 492 AA.
ID P00743;
AC 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
GN F10.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE OF 1-487 FROM N.A.
RX MEDLINE-84247315; PubMed-6330671;
RA Fung M.R., Campbell R.M., McGillivray R.T.A.;
RT "Blood coagulation factor X mRNA encodes a single polypeptide chain
   containing a prepro leader sequence."
RL Nucleic Acids Res. 12:4481-4492(1984).
RN [2]
RP SEQUENCE OF 41-180.
RX MEDLINE-80130563; PubMed-6766735;
RA Enfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
RA Titani K.;
RT "Amino acid sequence of the light chain of bovine factor XI (Stuart
   factor).";

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RL Biochemistry 19:659-667(1980).
RN [3]
RP REVISION TO 103.
RX MEDLINE-83308813; PubMed-6688526;
RA McMullen B.A., Fujikawa K., Kistiel W.;
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
   K-dependent blood coagulation zymogens."
RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
RN [4]
RP SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RX MEDLINE-76053069; PubMed-1059093;
RA Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,
RA Neurath H.;
RT "Bovine factor XI (Stuart factor): amino-acid sequence of heavy
   chain."
RL Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).
RN [5]
RP SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE-94062825; PubMed-8243461;
RA Inoue K., Morita T.;
RT "Identification of O-linked oligosaccharide chains in the activation
   peptides of blood coagulation factor X. The role of the carbohydrate
   moieties in the activation of factor X."
RL Eur. J. Biochem. 218:153-163(1993).
RN [6]
RP ACTIVE SITE.
RX MEDLINE-73053314; PubMed-4264286;
RA Titani K., Hermanson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
RA Neurath H., Davie E.W.;
RT "Bovine factor XIa (activated Stuart factor). Evidence of homology
   with mammalian serine proteases."
RL Biochemistry 11:4899-4903(1972).
RN [7]
RP PROCESSING.
RX MEDLINE-76053121; PubMed-1059122;
RA Fujikawa K., Titani K., Davie E.W.;
RT "Activation of bovine factor X (Stuart factor): conversion of factor
   Xa-alpha to factor Xa-beta."
RL Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
RN [8]
RP CALCIUM-BINDING DATA.
RX MEDLINE-84185716; PubMed-6546930;
RA Sugo T., Bjorker I., Holmgren A., Stenflo J.;
RT "Calcium-binding properties of bovine factor X lacking the gamma-
   carboxyglutamic acid-containing region."
RL J. Biol. Chem. 259:5705-5710(1984).
RN [9]
RP SULFATION.
RX MEDLINE-86140210; PubMed-3949800;
RA Morita T., Jackson C.M.;
RT "Localization of the structural difference between bovine blood
   coagulation factors XI and X2 to tyrosine 18 in the activation
   peptide."
RL J. Biol. Chem. 261:4008-4014(1986).
RN [10]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE-91084463; PubMed-2261466;
RA Selander M., Persson E., Stenflo J., Drakenberg T.;
RT "1H NMR assignment and secondary structure of the Ca2(+)-free form of
   the amino-terminal epidermal growth factor like domain in coagulation
   factor X."
RL Biochemistry 29:8111-8118(1990).
RN [11]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE-92329412; PubMed-1627540;
RA Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,
RA Telman O.;
RT "Three-dimensional structure of the apo form of the N-terminal
   EGF-like module of blood coagulation factor X as determined by NMR
   spectroscopy and simulated folding."
RL Biochemistry 31:5974-5983(1992).
RN [12]
RP STRUCTURE BY NMR OF 85-126.

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RX MEDLINE=97406922; PubMed=1527084;
RA Selandner-Sunnenhagen M., Ullner M., Persson E., Telemann O.,
RA Stenflo J., Drakenberg T.;
RT "How an epidermal growth factor (EGF)-like domain binds calcium. High
RT resolution NMR structure of the calcium form of the NH2-terminal EGF-
RT like domain in coagulation factor X.";
RL J. Biol. Chem. 267:19642-19649(1992).
RN [13]
RP STRUCTURE BY NMR OF 41-126.
RX MEDLINE=96387194; PubMed=8794734;
RA Sunnenhagen M., Olah G.A., Stenflo J., Forsen S., Drakenberg T.,
RA Trewhella J.;
RT "The relative orientation of Gla and EGF domains in coagulation
RT factor X is altered by Ca2+ binding to the first EGF domain. A
RT combined NMR-small angle X-ray scattering study.";
RL Biochemistry 35:11547-11559(1996).
CC -1- FUNCTION: FACTOR XA IS A VITAMIN K-DEPENDENT GLYCOPROTEIN THAT
CC CONVERTS PROTHROMBIN TO THROMBIN IN THE PRESENCE OF FACTOR VA,
CC CA++ AND PHOSPHOLIPID DURING BLOOD CLOTTING.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-1-Thr and then
CC Arg-1-Ile bonds in prothrombin to form thrombin.
CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
CC MORE DISULFIDE BONDS.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM.
CC -1- PTM: N- AND O-GLYCOSYLATED.
CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
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CC -----
DR EMBL: X00673; CAA25286.1; -.
DR PIR: A00925; EXBO.
DR PDB: IAPQ; 31-JAN-94.
DR PDB: ICGF; 31-MAY-94.
DR PDB: 1WHE; 15-MAY-97.
DR PDB: 1WHR; 15-MAY-97.
DR MEROPS: S01.216; -.
DR CarBank: CCSD:7747; -.
DR CarBank: CCSD:7899; -.
DR CarBank: CCSD:11508; -.
DR GlycoSuiteDB: P00743; -.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF 2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; trypsin.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF; 2.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00001; EGF_like; 1.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; Tryp_Spc; 1.

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DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU CARBOXYLATION; 1.
DR PROSITE: PS02040; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
KW Signal; Zymogen; EGF-like domain; Repeat; Sulfation; 3D-structure.
FT SIGNAL: 1 23
FT PROPEP 24 40
FT CHAIN 41 180
FT CHAIN 183 492
FT PROPEP 183 233
FT CHAIN 234 492
FT PROPEP 476 492
FT DOMAIN 86 122
FT DOMAIN 125 165
FT DOMAIN 234 492
FT ACT_SITE 275 275
FT ACT_SITE 321 321
FT ACT_SITE 418 418
FT MOD_RES 46 46
FT MOD_RES 47 47
FT MOD_RES 54 54
Query Match 52.2%; Score 95; DB 1; Length 492;
Best Local Similarity 40.9%; Pred. No. 1.5e-09;
Matches 18; Conservative 7; Mismatches 19; Indels 0; Gaps 0;
Oy 1 ANAFLLXLRKSGSLRXKXCCSFYXAXXIFKADARTLFTSY 44
Db 41 ANSFLEEVKQGNLERECLEFACSLSEAREVFEDAQTEFNSKY 84
RESULT 11
TMGLI_HUMAN STANDARD; PRT; 218 AA.
AC 014668:
DE 01-MAR-2002 (Rel. 41, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE Transmembrane gamma-carboxyglutamic acid protein 1 precursor (Proline-
DE rich Gla protein 1) (Proline-rich gamma-carboxyglutamic acid protein
DE 1)
GN PRG1 OR TMG1 OR PRG1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97404347; PubMed=9256434;
RA Kulmac J.D., Harris J.E., Haldeman B.A., Davie E.W.;
RT "Primary structure and tissue distribution of two novel proline-rich
RT gamma-carboxyglutamic acid proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997).
CC -1- TISSUE SPECIFICITY: Highly expressed in the spinal cord.
CC -1- PTM: Gla residues are produced after subsequent posttranslational
CC modifications of glutamic acid by a vitamin K-dependent gamma-
CC carboxylase.
CC -----
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DR EMBL: AF009242; AAB67070.1; -.
DR MIM: 604428; -.
DR HSSP: P00740; ICFH.
DR InterPro: IPR000294; VitK_dep_GLA.
DR InterPro: IPR002383; GLA_blood.
DR Pfam: PF00594; gla; 1.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00069; GLA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
KW Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
FT PROPEP 1 20
FT CHAIN 21 218
FT DOMAIN 21 83 TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
FT TRASNMEM 84 106 PROTEIN 1.
FT DOMAIN 107 218 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 107 218 POTENTIAL.
FT DOMAIN 24 61 CTOPOLASTIC (POTENTIAL).
FT DOMAIN 131 135 GLA-RICH.
FT DOMAIN 131 135 POLY-PRO.
SQ SEQUENCE 218 AA; 24947 MW; 26538A61AB0AEB98 CRC64;

Query Match 51.1%; Score 93; DB 1; Length 218;
Best Local Similarity 38.6%; Pred. No. 1.6e-09;
Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLLXLRXGSLRXCKXXQCSFXXAXIIFDAXRTKLFWISY 44
DB 21 ANGFEEIRQGNIERCKEEFCTFEARAEAFENNEXTKEFWSTY 64

RESULT 12
PRTC_BOVIN STANDARD; PRT; 456 AA.
AC P00745;
DR 21-JUL-1986 (Rel. 01, Created)
DR 13-AUG-1987 (Rel. 05, Last sequence update)
DR 16-OCT-2001 (Rel. 40, Last annotation update)
DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
DE (Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV) (Fragment).
DE PROC.
GN Bos taurus (Bovine).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014826; PubMed=6091100;
RA Long G.L., Balagaje R.M., McGillivray R.T.A.;
RT "Cloning and sequencing of liver cDNA coding for bovine protein C.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).
RN [2]
RP SEQUENCE OF 40-194.
RX MEDLINE=83007325; PubMed=6896876;
RA Fernlund P., Stenflo J.;
RT "Amino acid sequence of the light chain of bovine protein C.";
RL J. Biol. Chem. 257:12170-12179(1982).
RN [3]
RP REVISION TO 110.
RX MEDLINE=83169769; PubMed=6572939;
RA Drakenberg T., Fernlund P., Roepstorff P., Stenflo J.;
RT "Beta-hydroxyaspartic acid in vitamin K-dependent protein C.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).
RN [4]
RP SEQUENCE OF 197-456.
RX MEDLINE=83007326; PubMed=6896877;
RA Stenflo J., Fernlund P.;
RT "Amino acid sequence of the heavy chain of bovine protein C.";
RL J. Biol. Chem. 257:12180-12190(1982).
RN [5]
RP PROCESSING, AND CALCIUM-BINDING DATA.
RX MEDLINE=83213513; PubMed=6304092;

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RA Esmon N.L., Debault L.E., Esmon C.T.;
RT "proteolytic formation and properties of gamma-carboxyglutamic acid-
RT domainless protein C.";
RL J. Biol. Chem. 258:5548-5553(1983).
RN [6]
RP PROCESSING, AND CALCIUM-BINDING DATA.
RX MEDLINE=83213514; PubMed=6406503;
RA Johnson A.E., Esmon N.L., Lane T.M., Esmon C.T.;
RT "Structural changes required for activation of protein C are induced
RT by Ca2+ binding to a high affinity site that does not contain gamma-
RT carboxyglutamic acid.";
RL J. Biol. Chem. 258:5554-5560(1983).
CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VILLA
CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and villa.
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC STRONGLY PROMOTED BY THROMBOMODULIN.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC THROMBIN-THROMBOMODULIN COMPLEX.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRIPSIN FAMILY.
CC -----
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CC -----
DR EMBL: R02435; AAA30685.1; -.
DR PIR: A00928; KXBO.
DR HSSP: P04070; IPCU.
DR MEROPS: S01.218; -.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001254; Trypsin.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF; 2.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00089; trypsin; 1.
DR SMART: SM00181; EGF; 2.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; Tryp_Spc; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_Ca; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; FALSE_NEG.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Blood coagulation; Glycoprotein; Serine protease;
KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
FT NON_TER 1 1
FT SIGNAL <1 29
FT PROPEP 30 39
FT CHAIN 40 194
FT CHAIN 197 456

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PROTEIN C LIGHT CHAIN.
PROTEIN C HEAVY CHAIN.


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CC      C++ , AND PHOSPHOLIPID DURING BLOOD CLOTTING.
CC      - FUNCTION: VAP CLEAVES THE FUSION PROTEINS OF SENDAI VIRUS, NDV,
CC      AND INFLUENZA VIRUS A AT A SPECIFIC SINGLE ARGININE-CONTAINING
CC      SITE, AND PLAYS A KEY ROLE IN THE VIRAL SPREADING IN THE ALLANTOIC
CC      SAC.
CC      - CATALYTIC ACTIVITY: Preferential cleavage: Arg-1-Thr and then
CC      Arg-1-Ile bonds in prothrombin to form thrombin.
CC      - SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
CC      BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
CC      MORE DISULFIDE BONDS.
CC      - TISSUE SPECIFICITY: LIVER AND CHORIOALLANTOIC MEMBRANE.
CC      - PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
CC      GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC      CALCIUM.
CC      - PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
CC      INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
CC      - SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC      - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC      TRYPSIN FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: D00844; BAA00724.1; -.
CC      PIR: S15838; S15838.
CC      HSSP: P00742; 1HCG.
CC      MEROPS: S01.216; -.
CC      DR      Interpro: IPR000152; Asx_hydroxyl.
CC      DR      Interpro: IPR001314; Chymotrypsin.
CC      DR      Interpro: IPR000561; EGF-like.
CC      DR      Interpro: IPR000742; EGF_2.
CC      DR      Interpro: IPR001881; EGF_Ca.
CC      DR      Interpro: IPR001438; EGF-IT.
CC      DR      Interpro: IPR002383; GLA_blood.
CC      DR      Interpro: IPR000294; Vitk_dep_GLA.
CC      DR      Pfam: PF00008; EGF_2.
CC      DR      Pfam: PF00059; gla; 1.
CC      DR      Pfam: PF00089; trypsin; 1.
CC      DR      PRINTS: PRO0722; CHYMOTRYPsin.
CC      DR      PRINTS: PRO0010; EGFblood.
CC      DR      PRINTS: PRO0001; GLABlood.
CC      DR      SMART: SM00179; EGF_CA; 1.
CC      DR      SMART: SM00069; GLA; 1.
CC      DR      SMART: SM00020; TYP_Spc; 1.
CC      DR      PROSITE: PS00010; ASX_HYDROXYL; 1.
CC      DR      PROSITE: PS00022; EGF_1; 1.
CC      DR      PROSITE: PS01186; EGF_2; 2.
CC      DR      PROSITE: PS01187; EGF_CA; 1.
CC      DR      PROSITE: PS00011; GLU_CARBOXYLATION; 1.
CC      DR      PROSITE: PS00240; TRYPSIN_DOM; 1.
CC      DR      PROSITE: PS00134; TRYPSIN_HTS; 1.
CC      DR      PROSITE: PS00135; TRYPSIN_SER; 1.
CC      DR      Glycoprotein: Hydroxylase; Serine protease; Plasma; Blood coagulation;
CC      Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
CC      Signal; Zymogen; EGF-like domain; Repeat.
CC      FT      SIGNAL 1 20 OR 30, OR 31 (POTENTIAL).
CC      FT      PROPEP 21 40
CC      FT      CHAIN 41 180
CC      FT      CHAIN 186 475
CC      FT      PROPEP 186 241
CC      FT      CHAIN 242 475
CC      FT      DOMAIN 86 122
CC      FT      DOMAIN 125 168
CC      FT      DOMAIN 241 475
CC      FT      MOD_RES 46 46
CC      FT      MOD_RES 47 47
CC      MOD_RES 47 47

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FT      MOD_RES 54 54 (BY SIMILARITY).
FT      MOD_RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID
FT      MOD_RES 59 59 (BY SIMILARITY).
FT      MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID
FT      MOD_RES 65 65 (BY SIMILARITY).
FT      MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID
FT      MOD_RES 69 69 (BY SIMILARITY).
FT      MOD_RES 72 72 GAMMA-CARBOXYGLUTAMIC ACID
FT      MOD_RES 79 79 (BY SIMILARITY).
FT      MOD_RES 103 103 (BY SIMILARITY).
FT      ACT_SITE 282 282 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT      ACT_SITE 328 328 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT      ACT_SITE 425 425 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT      DISULFID 90 101 BY SIMILARITY.
FT      DISULFID 95 110 BY SIMILARITY.
FT      DISULFID 112 121 BY SIMILARITY.
FT      DISULFID 129 140 BY SIMILARITY.
FT      DISULFID 136 152 BY SIMILARITY.
FT      DISULFID 154 167 BY SIMILARITY.
FT      DISULFID 175 348 INTERCHAIN (BY SIMILARITY).
FT      DISULFID 247 252 BY SIMILARITY.
FT      DISULFID 267 283 BY SIMILARITY.
FT      DISULFID 366 410 BY SIMILARITY.
FT      DISULFID 421 449 BY SIMILARITY.
FT      CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      SEQUENCE 475 AA; 53142 MW; 570BF849565C74D CRC64;

Query Match 46.7%; Score 85; DB 1; Length 475;
Best local Similarity 36.4%; Pred. No. 9 4e-08;
Matches 16; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLLXLRXGSLRXKXQCSFXKXKXIFKDKRTKLEWISY 44
DB 41 ANSFLERMKGNIERECNEERCSKEAREAFEDNEETEEWNIY 84

RESULT 15
THRB_HUMAN STANDARD; PRT; 622 AA.
AC P00734;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Prothrombin precursor (EC 3.4.21.5) (Coagulation factor II).
GN F2.
OS Homo sapiens (Human).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RX MEDLINE=88077877; PubMed=2825773;
RA Degen S.J.F., Davie E.W.;
RL "Nucleotide sequence of the gene for human prothrombin.";
RL Biochemistry 26:6165-6177(1987).
RP [2]
RP SEQUENCE OF 8-622 FROM N.A.
RP MEDLINE=83231469; PubMed=6305407;
RA Degen S.J.F., McGallivray R.T.A., Davie E.W.;

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RT "Characterization of the complementary deoxyribonucleic acid and gene
RT coding for human prothrombin.";
RL Biochemistry 22:2087-2097(1983).
RN [3]
RP SEQUENCE OF 44-314.
RX MEDLINE=7719364; PubMed=266717;
RA Walz D.A., Hewett-Emmett D., Seegers W.H.;
RT "Amino acid sequence of human prothrombin fragments 1 and 2.";
RL Proc. Natl. Acad. Sci. U.S.A. 74:1969-1972(1977).
RN [4]
RP SEQUENCE OF 315-622.
RX MEDLINE=77207112; PubMed=873923;
RA Burkowski R.J., Ellison J., Downing M.R., Mann K.G.;
RT "Primary structure of human prothrombin 2 and alpha-thrombin.";
RL J. Biol. Chem. 252:4942-4957(1977).
RN [5]
RP PROCESSING.
RX MEDLINE=87008532; PubMed=3759958;
RA Rabiet M.J., Blashill A., Furie B., Furie B.C.;
RT "Prothrombin fragment 1 X 2 X 3, a major product of prothrombin
RL activation in human plasma.";
RL J. Biol. Chem. 261:13210-13215(1986).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=90059942; PubMed=2583108;
RA Bode W., Mayr I., Baumann U., Huber R., Stone S.R., Hofsteenge J.;
RT "The refined 1.9 A crystal structure of human alpha-thrombin:
RT interaction with D-Phe-Pro-Arg chloromethylketone and significance of
RT the Tyr-Pro-Tyr insertion segment.";
RL EMBO J. 8:3467-3475(1989).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX MEDLINE=90327074; PubMed=2374926;
RA Rygel T.J., Ravichandran K.G., Tulinsky A., Bode W., Huber R.,
RA Roltsch C., Fenton J.W. II;
RT "The structure of a complex of recombinant hirudin and human alpha-
RT thrombin.";
RL Science 249:277-280(1990).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=94350942; PubMed=8071320;
RA Rygel T.J., Yin M., Padmanabhan K.P., Blankenship D.T., Carolin A.D.,
RA Correa P.E., Fenton J.W. II, Tulinsky A.;
RT "Crystallographic structure of human gamma-thrombin.";
RL J. Biol. Chem. 269:22000-22006(1994).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX MEDLINE=97357286; PubMed=9214615;
RA van de Locht A., Bode W., Huber R., Le Bonniec B.F., Stone S.R.,
RA Eason C.T., Stubbs M.T.;
RT "The thrombin E192Q-BPTI complex reveals gross structural
RT rearrangements: Implications for the interaction with antithrombin
RT and thrombomodulin.";
RL EMBO J. 16:2977-2984(1997).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 328-601.
RX MEDLINE=99162521; PubMed=10051558;
RA Guinto E.R., Caccia S., Rose T., Fuetterer K., Waksman G., di Cera E.;
RT "Unexpected crucial role of residue 225 in serine proteases.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:1852-1857(1999).
RN [11]
RP VARIANT BARCELONA.
RX MEDLINE=87033739; PubMed=3771562;
RA Rabiet M.-J., Furie B.C., Furie B.;
RT "Molecular defect of prothrombin Barcelona. Substitution of cysteine
RT for arginine at residue 273.";
RL J. Biol. Chem. 261:15045-15048(1986).
RN [12]
RP VARIANT FRANKFURT.
RX MEDLINE=95313001; PubMed=7792730;
RA Degen S.J.F., McDowell S.A., Sparks L.M., Scharrer I.;
RT "Prothrombin Frankfurt: a dysfunctional prothrombin characterized by
RT substitution of Glu-466 by Ala.";

RL Thromb. Haemost. 73:203-209(1995).
RN [13]
RP VARIANTS HIMI-1 AND HIMI-2.
RX MEDLINE=93043342; PubMed=1421398;
RA Morishita E., Saito M., Kumabashiri I., Asakura H., Matsuda T.,
RA Yamaguchi K.;
RT "Prothrombin Himi: a compound heterozygote for two dysfunctional
RT prothrombin molecules (Met-337->Thr and Arg-388->His).";
RL Blood 80:2275-2280(1992).
RN [14]
RP VARIANT PADUA-1.
RX MEDLINE=95169898; PubMed=7865694;
RA James H.L., Kim D.J., Zheng D.-Q., Girolami A.;
RT "Prothrombin Padua I: incomplete activation due to an amino acid
RT substitution at a factor Xa cleavage site.";
RL Blood Coagul. Fibrinolysis 5:841-844(1994).
RN [15]
RP VARIANT QUICK-1.
RX MEDLINE=89207504; PubMed=3242619;
RA Henriksen R.A., Mann K.G.;
RT "Identification of the primary structural defect in the dysprothrombin
RT thrombin Quick I: substitution of cysteine for arginine-382.";
RL Biochemistry 27:9160-9165(1988).
RN [16]
RP VARIANT QUICK-2.
RX MEDLINE=89247398; PubMed=2719946;
RA Henriksen R.A., Mann K.G.;
RT "Substitution of valine for glycine-558 in the congenital dysprothrombin
RT thrombin Quick II alters primary substrate specificity.";
RL Biochemistry 28:2078-2082(1989).
RN [17]
RP VARIANT SALAKTA.
RX MEDLINE=92378975; PubMed=1354985;
RA Miyata T., Aruga R., Uneyama H., Bezeaud A., Guillain M.-C.,
RA Iwanaga S.;
RT "Prothrombin Salakta: substitution of glutamic acid-466 by alanine
RT reduces the fibrinogen clotting activity and the esterase activity.";
RL Biochemistry 31:7457-7462(1992).
RN [18]
RP VARIANT TOKUSHIMA.
RX MEDLINE=87185407; PubMed=3567158;
RA Miyata T., Morita T., Inomoto T., Kawauchi S., Shirakami A.,
RA Iwanaga S.;
RT "Prothrombin Tokushima, a replacement of arginine-418 by tryptophan
RT that impairs the fibrinogen clotting activity of derived thrombin
RT Tokushima.";
RL Biochemistry 26:1117-1122(1987).
RN [19]
RP VARIANT TOKUSHIMA.
RX MEDLINE=87101511; PubMed=3801671;
RA Inomoto T., Shirakami A., Kawauchi S., Shigekiyo T., Saito S.,
RA Miyoshi K., Morita T., Iwanaga S.;
RT "Prothrombin Tokushima: characterization of dysfunctional thrombin
RT derived from a variant of human prothrombin.";
RL Blood 69:565-569(1987).
RN [20]
RP VARIANT TOKUSHIMA.
RX MEDLINE=92256895; PubMed=1349838;
RA Iwihana H., Yoshimoto K., Shigekiyo T., Shirakami A., Saito S.,
RA Itakura M.;
RT "Detection of a single base substitution of the gene for prothrombin
RT Tokushima. The application of PCR-SSCP for the genetic and molecular
RT analysis of dysprothrombinemia.";
RL Int. J. Hematol. 55:93-100(1992).
RN [21]
RP VARIANT TYPE-3.
RX MEDLINE=83204687; PubMed=6405779;
RA Board P.G., Shaw D.C.;
RT "Determination of the amino acid substitution in human prothrombin
RT type 3 (157 Glu leads to Lys) and the localization of a third
RT thrombin cleavage site.";
RL Br. J. Haematol. 54:245-254(1983).
CC -!- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS


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FT MOD_RES 107 107 (BY SIMILARITY).
FT ACT_SITE 250 250 HYDROXYLATION (BY SIMILARITY).
FT ACT_SITE 296 296 CHARGE RELAY SYSTEM.
FT ACT_SITE 399 399 CHARGE RELAY SYSTEM.
FT DISULFID 53 58 BY SIMILARITY.
FT DISULFID 86 105 BY SIMILARITY.
FT DISULFID 95 100 BY SIMILARITY.
FT DISULFID 99 114 BY SIMILARITY.
FT DISULFID 116 125 BY SIMILARITY.
FT DISULFID 134 145 BY SIMILARITY.
FT DISULFID 141 154 BY SIMILARITY.
FT DISULFID 156 169 BY SIMILARITY.
FT DISULFID 177 316 INTERCHAIN (BY SIMILARITY).
FT DISULFID 235 251 BY SIMILARITY.
FT DISULFID 370 384 BY SIMILARITY.
FT DISULFID 395 423 BY SIMILARITY.
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 458 AA; 51087 MW; D75A5F990C8F29D7 CRC64;

Query Match 45.1%; Score 82; DB 1; Length 458;
Best Local Similarity 40.9%; Pred. NO. 3.2e-07;
Matches 18; Conservative 2; Mismatches 24; Indels 0; Gaps 0;

QY 1 ANAFELXRLXGSLXRCXKXOCSEFXAXXIFKDXAKRTKLFWISY 44
Db 37 ANSFLERPSLRECEVEYCDLEAKKEIRFQSVDDTLAFYKY 80

RESULT 17
PRTC_HUMAN STANDARD; PRT; 461 AA.
AC P04070: Q16001: Q15190: Q15189;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
DE (Autoproteolysis IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV).
GN PROC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=65270390; PubMed=2991887;
RA Foster D.C., Yoshitake S., Davie E.W.;
RT "The nucleotide sequence of the gene for human protein C.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:4673-4677(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=65269639; PubMed=2991859;
RA Beckmann R.J., Schmidt R.J., Santerre R.F., Plutsky J., Crabtree G.R.,
RA Long G.L.;
RT "The structure and evolution of a 461 amino acid human protein C
RT precursor and its messenger RNA, based upon the DNA sequence of
RT cloned human liver cDNAs.";
RL Nucleic Acids Res. 13:5233-5247(1985).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=6120978; PubMed=3511471;
RA Plutsky J., Hoskins J.A., Long G.L., Crabtree G.R.;
RT "Evolution and organization of the human protein C gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:346-350(1986).
RN [4]
RP SEQUENCE OF 106-461 FROM N.A.
RX MEDLINE=64272714; PubMed=6589623;
RA Foster D.C., Davie E.W.;
RT "Characterization of a cDNA coding for human protein C.";

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RL Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984).
RN [5]
RP CARBOHYDRATE-LINKAGE SITE ASN-371.
RX MEDLINE=90293094; PubMed=1694179;
RA Mielich J.P., Broze G.J. Jr.;
RT "Beta protein C is not glycosylated at asparagine 329. The rate of
RT translation may influence the frequency of usage at asparagine-X-
RT cysteine sites.";
RL J. Biol. Chem. 265:11397-11404(1990).
RN [6]
RP HYDROXYLATION.
RX MEDLINE=92184750; PubMed=1544894;
RA Harris R.J., Ling V.T., Spellman M.W.;
RT "O-linked fucose is present in the first epidermal growth factor
RT domain of factor XII but not protein C.";
RL J. Biol. Chem. 267:5102-5107(1992).
RN [7]
RP 3D-STRUCTURE MODELING OF 175-450.
RX MEDLINE=94272342; PubMed=8003977;
RA Fisher C.L., Greengard J.S., Griffin J.H.;
RT "Models of the serine protease domain of the human antithrombotic
RT plasma factor activated protein C and its zymogen.";
RL Protein Sci. 3:588-599(1994).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 84-461.
RX MEDLINE=97157472; PubMed=9003757;
RA Mather T., Oganessyan V., Hof P., Huber R., Fountelling S., Esmen C.,
RA Bode W.;
RT "The 2.8 A crystal structure of Gla-domainless activated protein C.";
RL EMBO J. 15:6822-6831(1996).
RN [9]
RP REVIEW ON PROC VARIANTS.
RX MEDLINE=93190290; PubMed=8446940;
RA Reitsma P.H., Poort S.R., Bernardi F., Gandrille S., Long G.L.,
RA Sala N., Cooper D.N.;
RT "Protein C deficiency: a database of mutations. For the Protein C & S
RT Subcommittee of the Scientific and Standardization Committee of the
RT Internatinal Society on Thrombosis and Haemostasis.";
RL Thromb. Haemost. 69:77-84(1993).
RN [10]
RP VARIANT CYS-444.
RX MEDLINE=87204221; PubMed=2437584;
RA Romeo G., Haasn H.J., Staempfl S., Roncuuzi L., Clanetti L.,
RA Leonardi A., Vicente V., Mannucci P.M., Bertina R.M., Peschle C.,
RA Cortese R.;
RT "Hereditary thrombophilia: identification of nonsense and missense
RT mutations in the protein C gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:2829-2832(1987).
RN [11]
RP VARIANT TRP-211 (LONDON-1).
RX MEDLINE=90098906; PubMed=2602169;
RA Grundy C.B., Chitlole A., Talbot S., Bevan D., Kakkar V.V.,
RA Cooper D.N.;
RT "Protein C London 1: recurrent mutation at Arg-169 (CGG-->TGG) in
RT the protein C gene causing thrombosis.";
RL Nucleic Acids Res. 17:10513-10513(1989).
RN [12]
RP VARIANT CYS-272.
RX MEDLINE=91329836; PubMed=1868249;
RA Reitsma P.H., Poort S.R., Allaart C.F., Briet E., Bertina R.M.;
RT "The spectrum of genetic defects in a panel of 40 Dutch families with
RT symptomatic protein C deficiency type I: heterogeneity and founder
RT effects.";
RL Blood 78:890-894(1991).
RN [13]
RP VARIANTS ALA-62 (VERMONT-1) AND MET-76.
RX MEDLINE=92190481; PubMed=1347706;
RA Bovill E.G., Tomczak J.A., Grant B., Bhushan F., Pillemer E.,
RA Rainville I.R., Long G.L.;
RT "Protein C Vermont: symptomatic type II protein C deficiency
RT associated with two gla domain mutations.";
RL Blood 79:1456-1465(1992).
RN [14]

```

RP VARIANT ASP-418 (HONG KONG-2).
RX MEDLINE-92305321; PubMed-1611081.
RA Sugahara Y., Miura O., Yuen P., Aoki N.;
RT "Protein C deficiency Hong Kong 1 and 2: hereditary protein C
RT deficiency caused by two mutant alleles, a 5-nucleotide deletion and
RT a missense mutation";
RL Blood 80:126-133(1992).
RN [15]
RP VARIANT LEU-289.
RX MEDLINE-92380660; PubMed-1511988;
RA Grundy C.B., Chisholm M., Kakkar V.V., Cooper D.N.;
RT "A novel homozygous missense mutation in the protein C (PROC) gene
RT causing recurrent venous thrombosis";
RL Hum. Genet. 89:683-684(1992).
RN [16]
RP VARIANTs GLN-220 AND TRP-220.
RX MEDLINE-92380661; PubMed-1511989;
RA Grundy C.B., Schliman S., Tengborn L., Kakkar V.V., Cooper D.N.;
RT "Two different missense mutations at Arg 178 of the protein C (PROC)
RT gene causing recurrent venous thrombosis";
RL Hum. Genet. 89:685-686(1992).
RN [17]
RP VARIANT GLN-220.
RX MEDLINE-93250852; PubMed-1301959;
RA Gandiille S., Vidaud M., Alach M., Alenc-Gelas M., Fischer A.M.,
RA Gouault-Heilmann M., Toulon P., Flessinger J.N., Goossens M.;
RT "Two novel mutations responsible for hereditary type I protein C
RT deficiency: characterization by denaturing gradient gel
RT electrophoresis";
RL Hum. Mutat. 1:491-500(1992).
RN [18]
RP VARIANT SER-334.
RX MEDLINE-92276939; PubMed-1593215;
RA Yamamoto K., Matsushita T., Sugura I., Takamatsu J., Iwasaki E.,
RA Wada H., Deguchi K., Shirakawa S., Saio H.;
RT "Homozygous protein C deficiency: identification of a novel missense
RT mutation that causes impaired secretion of the mutant protein C";
RL J. Lab. Clin. Med. 119:682-689(1992).
RN [19]
RP VARIANTs TRP-38; CYS-42; HIS-42; GLN-271 AND ASN-294.
RX MEDLINE-93313192; PubMed-8324221.
RA Gandiille S., Alenc-Gelas M., Gaussem P., Allaud M.-F., Dupuy E.,
RA Juhán-Vague I., Alach M.;
RT "Five novel mutations located in exons III and IX of the protein C
RT gene in patients presenting with defective protein C anticoagulant
RT activity";
RL Blood 82:159-168(1993).
RN [20]
RP VARIANTs G-14; Q-211; Y-244; Q-253; L-321; C-328; I-385; T-388 AND
RP V-388.
RX MEDLINE-93271391; PubMed-8499565;
RA Poort S.R., Pabinger-Fasching I., Mannhalter C., Retsma P.H.,
RA Bertina R.M.;
RT "Twelve novel and two recurrent mutations in 14 Austrian families
RT with hereditary protein C deficiency";
RL Blood Coagul. Fibrinolysis 4:273-280(1993).
RN [21]
RP VARIANT TRP-57.
RX MEDLINE-93271396; PubMed-8499568;
RA Millier D.S., Grundy C.B., Biggell P., Moffat E.H., Martin R.,
RA Kakkar V.V., Cooper D.N.;
RT "A Gln domain mutation (Arg 15->Trp) in the protein C (PROC) gene
RT causing type 2 protein C deficiency and recurrent venous
RT thrombosis";
RL Blood Coagul. Fibrinolysis 4:345-347(1993).
RN [22]
RP VARIANTs R-145; L-210; W-211; T-243; L-321; M-340 AND Y-426.
RX MEDLINE-94122339; PubMed-8292730;
RA Tsay W., Greengard J.S., Montemayor R.R., McPherson R.A., Fucci J.C.,
RA Koepfer M.A., Coughlin J., Griffin J.H.;
RT "Genetic mutations in ten unrelated American patients with
RT symptomatic type I protein C deficiency";
RL Blood Coagul. Fibrinolysis 4:791-796(1993).

RN [23]
 RP VARIANT SER-423.
 RX MEDLINE=94001606; PubMed=8398832;
 RA Marchetti G., Parracchini P., Gemmati D., Castan G., Rodeghiero F.,
 RA Macey A., Cooper D.N., Tuddenham E.G., Bernardi F.;
 RT "Symptomatic type II protein C deficiency caused by a missense
 RT mutation (Gly 381->Ser) in the substrate-binding pocket."
 RL Br. J. Haematol. 84:285-289(1993).
 RN [24]
 RP SEQUENCE OF 43-64 FROM N.A., AND VARIANT GLY-57 (YONAGO).
 RX MEDLINE=99237511; PubMed=8477066;
 RA Minuro J., Muramatsu S., Kaneko M., Yoshitake S., Iijima K.,
 RA Nakamura K., Sakata Y., Matsuda M.;
 RT "An abnormal protein C (protein C Yonago) with an amino acid
 RT substitution of Gly for Arg-15 caused by a single base mutation of C

Query Match 45.1%; Score 82; DB 1; Length 461;
 Best Local Similarity 43.9%; Pred. No. 3.2e-07;
 Matches 18; Conservative 3; Mismatches 20; Indels 0; Gaps 0

Qy 1 ANAFXXLRXGSLRXCKXXCSPFXAXXIFDAXRTKLFW 41
 Db 43 ANSFLELRHSLRECEIEICDFEAKRIEFPNVDTLAFW 83

RESULT 18
 THRB_RAT
 ID THRB_RAT STANDARD; PRT: 617 AA.
 AC PI8292;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Prothrombin precursor (EC 3.4.21.5).
 F2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
 RX MEDLINE=90332426; PubMed=2377469;
 RA Dhanich M., Monard D.;
 RT "cDNA sequence of rat prothrombin."
 RL Nucleic Acids Res. 18:4251-4251(1990).
 RN [2]
 RP SEQUENCE OF 383-617 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=92212913; PubMed=1557383;
 RA Banfield D.K., Macgillivray R.T.;
 RT "Partial characterization of vertebrate prothrombin cDNAs:
 RT amplification and sequence analysis of the B chain of thrombin from
 RT nine different species."
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
 RN [3]
 RP FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS
 RT FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,
 RT AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.
 RN [4]
 RP FUNCTION: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
 RT RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOAL
 RT ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES
 RT ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY
 RT CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
 RT OF PROTHROMBIN TO THROMBIN.
 RN [5]
 RP MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A
 RT PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &
 RT FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES
 RT THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &
 RT HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR
 RT V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
 RT THROMBIN.
 RN [6]
 RP MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL
 RT FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
 RT BY FACTOR XA.

```

CC -1- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPsin FAMILY.
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CC -----
DR EMBL: X52835; CAAB7017.1; -.
DR EMBL: M81397; AAA42240.1; -.
DR PIR: S10511; S10511.
DR HSP: P00734; IUVS.
DR MEROPS: S01.217; -.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR003966; Prothrombin.
DR InterPro: IPR001254; Trypsin.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00051; kringle; 2.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR PRINTS: PR00018; KRINGLE.
DR PRINTS: PR01505; PROTHROMBIN.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00130; KR; 2.
DR SMART: SM00020; TRYp_Spc; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00021; KRINGLE_1; 2.
DR PROSITE: PS00070; KRINGLE_2; 2.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Blood coagulation; Plasma; Calcium-binding; glycoprotein; Repeat;
KW Vitamin K; zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver;
KW Hydrolyase; Serine protease; Kringle; Signal.
FT SIGNAL 1 24
FT PROPEP 25 43
FT CHAIN 44 617
FT PEPTIDE 44 200
FT PEPTIDE 201 323
FT CHAIN 324 359
FT CHAIN 360 617
FT DOMAIN 109 187
FT DOMAIN 215 292
FT DOMAIN 360 617
FT SITE 200 201
FT SITE 323 324
FT SITE 359 360
FT ACT_SITE 402 402
FT ACT_SITE 458 458
FT ACT_SITE 564 564
FT MOD_RES 50 50
FT MOD_RES 51 51
FT MOD_RES 58 58
FT MOD_RES 60 60
FT MOD_RES 63 63
FT MOD_RES 64 64
FT MOD_RES 69 69
FT MOD_RES 70 70
FT MOD_RES 73 73
FT MOD_RES 76 76
FT CARBOHYD 120 120
FT CARBOHYD 144 144
FT CARBOHYD 412 412
FT CARBOHYD 552 552
FT DISULFID 61 66

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FT DISULFID 91 104 BY SIMILARITY.
FT DISULFID 109 187 BY SIMILARITY.
FT DISULFID 130 170 BY SIMILARITY.
FT DISULFID 158 182 BY SIMILARITY.
FT DISULFID 215 292 BY SIMILARITY.
FT DISULFID 236 276 BY SIMILARITY.
FT DISULFID 264 287 BY SIMILARITY.
FT DISULFID 332 478 INTERCHAIN (BY SIMILARITY).
FT DISULFID 387 403 BY SIMILARITY.
FT DISULFID 532 546 BY SIMILARITY.
FT DISULFID 560 590 BY SIMILARITY.
FT DISULFID 617 AA; 70411 MM; AD27D1B71445DB1D CRC64;
SQ
Query Match 44.5%; Score 81; DB 1; Length 617;
Best Local Similarity 37.2%; Pred. No. 6.5e-07;
Matches 16; Conservative 5; Mismatches 22; Indels 0; Gaps 0;
OY 2 NAFLXLRXGSLRXCKXKXOCSEFXKXIXIFDKAKTKLFWISY 44
Db 46 SGFEELRKGNLRECVCEOCSEYEFAPALESPQDVFWMKY 88
RESULT 19
THRB_MOUSE STANDARD; PRT: 618 AA.
ID THRB_MOUSE
AC P19221;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Prothrombin precursor (EC 3.4.21.5).
GN F2 OR CF2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId:10090;
RN [1]
RP STRAIN=C57BL/6; TISSUE=Liver;
RC MEDLINE=9102551; Pubmed=222810;
RA Fritzeneger Degen S.J., Schaeffer L.A., Jamison C.S., Grant S.G.,
RA Fitzgibbon J.J., Pal J.-A., Chapman V.M., Elliott R.W.,
RT "Characterization of the cDNA coding for mouse prothrombin and
RT localization of the gene on mouse chromosome 2."
RL DNA Cell Biol. 9:487-498(1990).
[2]
SEQUENCE OF 384-618 FROM N.A.
TISSE=Liver;
RC MEDLINE=92212913; Pubmed=1557383;
RA Banfield D.K., Macgillivray R.T.;
RT "Partial characterization of vertebrate prothrombin cDNAs:
RT amplification and sequence analysis of the B chain of thrombin from
RT nine different species."
RL Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
-1- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS
FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VIII, VIII, XIII,
AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.
-1- PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOML
ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES
ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY
CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
OF PROTHROMBIN TO THROMBIN.
-1- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A
PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &
FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS. FACTOR XA REMOVES
THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &
HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR
V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
THROMBIN.
-1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL
FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
BY FACTOR XA.

```

CC -1- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
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 DR EMBL: X52308; CAA36548.1; -;
 DR EMBL: M81394; AAA40435.1; -;
 DR PIR: A35827; A35827.
 DR HSSP: P00734; 1B7X.
 DR MEROPS: S01.217; -;
 DR MGD: MGI:88380; F2.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003866; Prothombin.
 DR InterPro: IPR001254; Trypsin.
 DR InterPro: IPR000294; Vltk_dep_GLA.
 DR Pfam: PF00594; gla; 1.
 DR Pfam: PF00051; kringle; 2.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00011; GLABLOOD.
 DR PRINTS: PR00018; KRINGLE.
 DR PRINTS: PR01505; PROTHROMBIN.
 DR SMART: SM00069; GLA; 1.
 DR SMART: SM00130; KR; 2.
 DR SMART: SM00020; TRYP_Spec; 1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE: PS00021; KRINGLE_1; 2.
 DR PROSITE: PS00070; KRINGLE_2; 2.
 DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 DR Blood coagulation; Plasma; Calcium-binding; Glycoprotein; Repeat;
 KM Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver;
 KM Hydroxylase; Serine protease; Kringle; Signal.
 FT SIGNAL 1 24
 FT PROPEP 25 43
 FT CHAIN 44 618
 FT PEPTIDE 44 200
 FT PEPTIDE 201 324
 FT CHAIN 325 360
 FT CHAIN 361 618
 FT DOMAIN 109 187
 FT DOMAIN 215 292
 FT DOMAIN 361 618
 FT SITE 200 201
 FT SITE 200 325
 FT SITE 360 361
 FT ACT_SITE 403 403
 FT ACT_SITE 459 459
 FT ACT_SITE 565 565
 FT MOD_RES 50 50
 FT MOD_RES 51 51
 FT MOD_RES 58 58
 FT MOD_RES 60 60
 FT MOD_RES 63 63
 FT MOD_RES 64 64
 FT MOD_RES 69 69
 FT MOD_RES 70 70
 FT MOD_RES 73 73
 FT MOD_RES 76 76
 FT DISULFID 61 66
 FT DISULFID 91 104
 FT DISULFID 109 187
 FT DISULFID 130 170

FT DISULFID 158 182 BY SIMILARITY.
 FT DISULFID 215 293 BY SIMILARITY.
 FT DISULFID 236 276 BY SIMILARITY.
 FT DISULFID 264 288 BY SIMILARITY.
 FT DISULFID 333 479 BY SIMILARITY.
 FT DISULFID 388 404 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 533 547 BY SIMILARITY.
 FT DISULFID 561 591 BY SIMILARITY.
 FT CARBOHD 122 122 N-LINKED (GLCNAC. . .).
 FT CARBOHD 144 144 N-LINKED (GLCNAC. . .).
 FT CARBOHD 413 413 N-LINKED (GLCNAC. . .).
 FT CARBOHD 553 553 N-LINKED (GLCNAC. . .).
 SQ SEQUENCE 618 AA; 70268 MW; B89F719AAMD601E0 CRC64;
 Query Match 44.5%; Score 81; DB 1; Length 618;
 Best Local Similarity 37.2%; Pred. No. 6.5e-07;
 Matches 16; Conservative 5; Mismatches 22; Indels 0; Gaps 0;
 QY 2 NAFLLXLRGSLXRRCKXQCSFXXAXXIFKDAKTKLFWISY 44
 DB 46 SGELELRKGNLRECVBECSCYEAFALBESPDITDFWARY 88
 RESULT 20
 ID FA9_BOVIN STANDARD; PRT; 416 AA.
 AC P00741.
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Coagulation factor IX (EC 3.4.21.22) (Christmas factor).
 GN F9.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=80056619; PubMed=291916;
 RA Katayama K., Ericsson L.H., Enfield D.L., Walsh K.A., Neurath H.,
 RA Davie E.W., Titani K.;
 RT "Comparison of amino acid sequence of bovine coagulation Factor IX
 RT (Christmas factor) with that of other vitamin K-dependent plasma
 RT proteins.";
 RT Proc. Natl. Acad. Sci. U.S.A. 76:4990-4994(1979).
 RL [2]
 RP REVISION TO 64.
 RX MEDLINE=83308813; PubMed=6688526;
 RA McKullen B.A., Fujikawa K., Kisiel W.;
 RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
 RT K-dependent blood coagulation zymogens.";
 RT Biochem. Biophys. Res. Commun. 115:8-14(1983).
 RN [3]
 RP SEQUENCE OF 51-111 FROM N.A.
 RX MEDLINE=82272386; PubMed=6287289;
 RA Choo K.H., Gould K.G., Rees D.J.G., Brownlee G.G.;
 RT "Molecular cloning of the gene for human anti-haemophilic factor IX.";
 RT Nature 299:178-180(1982).
 RN [4]
 RP STRUCTURE OF CARBOHYDRATE ON SER-53.
 RX MEDLINE=89213999; PubMed=3149637;
 RA Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T.,
 RA Miyata T., Iwanaga S., Takao T., Shimomishi Y., Ikenaka T.;
 RT "A new trisaccharide sugar chain linked to a serine residue in bovine
 RT blood coagulation factors VII and IX.";
 RT J. Biochem. 104:867-868(1988).
 RN [5]
 RP STRUCTURE OF CARBOHYDRATE ON SER-53.
 RX MEDLINE=91344709; PubMed=2129367;
 RA Iwanaga S., Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T.;
 RT "A new trisaccharide sugar chain linked to a serine residue in the

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RT first EGF-like domain of clotting factors VII and IX and protein Z." ;
RL Adv. Exp. Med. Biol. 281:121-131(1990).
RX [6]
RX STRUCTURE OF CARBOHYDRATE ON SER-53.
RX MEDLINE=90130422; PubMed=2105311;
RA Hasee S., Nishimura H., Kawabata S., Iwanaga S., Ikenaka T.;
RA "The structure of (xylose)2glucose-O-serine 53 found in the first
RT epidermal growth factor-like domain of bovine blood clotting factor
RT IX." ;
RL J. Biol. Chem. 265:1858-1861(1990).
CC -1- FUNCTION: FACTOR IX IS A VITAMIN K-DEPENDENT PLASMA PROTEIN THAT
CC PARTICIPATES IN THE INTRINSIC PATHWAY OF BLOOD COAGULATION BY
CC CONVERTING FACTOR X TO ITS ACTIVE FORM IN THE PRESENCE OF CA++
CC IONS, PHOSPHOLIPIDS, AND FACTOR VIII.
CC -1- CATALYTIC ACTIVITY: Hydrolyses one Arg-1-Ile bond in factor X to
CC form factor xa.
CC -1- SUBUNIT: FACTOR IX IS ACTIVATED BY FACTOR XIA, WHICH EXCISES THE
CC ACTIVATION PEPTIDE AND THUS PRODUCES A MOLECULE CONSISTING OF 2
CC CHAINS HELD TOGETHER BY ONE OR MORE DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CALCIUM BINDS TO THE GAMMA-CARBOXYGLUTAMIC ACID
CC (GLA) RESIDUES AND, WITH STRONGER AFFINITY, TO ANOTHER SITE,
CC BEYOND THE GLA DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
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DR EMBL; J00007; AAA0520.1; -.
DR PIR; A00923; KFB0.
DR HSSP; P00740; ICFH.
DR MEROPS; S01.214; -.
DR GlycoSuiteDB; P00741; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF-2.
DR InterPro; IPR001881; EGF-Ca.
DR InterPro; IPR001438; EGF-II.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Trypsin.
DR InterPro; IPR000294; Vltk_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFBL00D.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA_1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYP_sec; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF-2_2.
DR PROSITE; PS01187; EGF_CA_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Blood coagulation; Plasma; Serine protease; Calcium-binding;
KW Hydroxylase; Glycoprotein; Vitamin K; Gamma-carboxyglutamic acid;
KW Hemophilias; Hydroxylation; Zymogen; EGF-like domain.
FT CHAIN 1 146 FACTOR IXA (ACTIVE FORM) LIGHT CHAIN.
FT PROPEP 147 181 ACTIVATION PEPTIDE.
FT CHAIN 182 416 FACTOR IXA (ACTIVE FORM) HEAVY CHAIN.
FT DOMAIN 47 83 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).

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FT	DOMAIN	84	125	EGF-LIKE 2.
FT	DOMAIN	182	416	SERINE PROTEASE.
FT	SITE	146	147	CLEAVAGE (BY FACTOR X1A).
FT	SITE	181	182	CLEAVAGE (BY FACTOR X1A).
FT	MOD_RES	7		GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	8	8	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	15	15	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	17	17	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	20	20	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	21	21	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	26	26	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	27	27	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	30	30	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	33	33	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	36	36	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	40	40	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	64	64	HYDROXYLATION.
FT	DISULFID	18	23	BY SIMILARITY.
FT	DISULFID	51	62	BY SIMILARITY.
FT	DISULFID	56	71	BY SIMILARITY.
FT	DISULFID	73	82	BY SIMILARITY.
FT	DISULFID	88	99	BY SIMILARITY.
FT	DISULFID	95	109	BY SIMILARITY.
FT	DISULFID	111	124	BY SIMILARITY.
FT	CARBOHYD	53	53	O-LINKED (GLC . .).
FT	CARBOHYD	158	158	/FTID-CAR_000008.
FT	CARBOHYD	168	168	N-LINKED (GLCNAC . .).
FT	CARBOHYD	173	173	N-LINKED (GLCNAC . .).
FT	CARBOHYD	261	261	N-LINKED (GLCNAC . .).
FT	ACT_SITE	222	222	CHARGE RELAY SYSTEM.
FT	ACT_SITE	270	270	CHARGE RELAY SYSTEM.
FT	ACT_SITE	366	366	CHARGE RELAY SYSTEM.
FT	VARIANT	64	64	D -> T (IN REF. 1).
SO	SEQUENCE	416 AA;	46785 MM;	34A7DEF916330662 CRC64;
Query Match 44.0%; Score 80; DB 1; Length 416;				
Best Local Similarity 41.2%; Pred. No. 6; e-07;				
Matches 14; Conservative 6; Mismatches 14; Indels 0; Gaps 0;				
Qy	11	GLIKRCKXXKCSFXXAKXIFKDAKRTLFKISY 44		
	1:1	1:1	1:1	1:1
Db	12	GNLEKCKEKKCSFEAREVEFTEKTEFWKQY 45		
RESULT 21				
FA10_TROCA STANDARD; PRI: 376 AA.				
ID	FA10_TROCA			
AC	P81428;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Coagulation factor X (EC 3.4.21.6) (Trocetin prothrombin activator).			
OS	Tropiuchis carinatus (Australian rough-scaled snake).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Lepidodermata; Squamata; Scleroglossa; Serpentes; Colubroidae;			
OC	Elapidae; Tropiuchis.			
OX	NCBI_TaxID=10989;			
RN	[1]			
RP	SEQUENCE, AND CHARACTERIZATION.			
RC	TISSUE=Venom;			
RX	MEDLINE=99326314; PubMed=10397729;			
RA	"Jung J.S., Chung M.C.M., Jayaseelan K., Kim R.M.;			
RT	"Amino acid sequence of trocetin, a prothrombin activator from			
RT	Tropiuchis carinatus venom: Its structural similarity to coagulation			
RT	factor Xa.";			
RL	Blood 94:621-631(1999).			
CC	-1- FUNCTION: FACTOR XA IS A VITAMIN K-DEPENDENT GLYCOPROTEIN THAT			
CC	CONVERTS PROTHROMBIN TO THROMBIN IN THE PRESENCE OF FACTOR VA,			
CC	CALCIUM, AND PHOSPHOLIPID DURING BLOOD CLOTTING. ACTS AS A TOXIN			
CC	IN VENOM.			
CC	-1- CATALYTIC ACTIVITY: Preferential cleavage: Arg- -Thr and then			

RP SEQUENCE OF 444-461 FROM N.A.
RX MEDLINE=94054330; PubMed=8236150.
RA de la Salle C., Charmanlier J.L., Baas M.J., Schwartz A.,
RA Wiesel M.L., Grunedaum L., Cazenave J.-P.;
RT "A deletion located in the 3' non translated part of the factor IX
RT gene responsible for mild haemophilia B.";
RL Thromb. Haemost. 70:370-371(1993).
RN [8]
RP SEQUENCE OF 47-461 (VARIANT NAGORA).
RX MEDLINE=90078229; PubMed=2592373.
RA Suehiro K., Kawabata S.-I., Miyata T., Takeya H., Takamatsu J.,
RA Oota K., Kamiya T., Saito H., Niho Y., Iwanaga S.;
RT "Blood clotting factor IX BM Nagoya. Substitution of arginine 180 by
RT tryptophan and its activation by alpha-chymotrypsin and rat mast cell
RT chymase.";
RL J. Biol. Chem. 264:21257-21265(1989).
RN [9]
RP HYDROXYLATION OF ASP-110.
RX MEDLINE=83308813; PubMed=6688526.
RA McMullen B.A., Fujikawa K., Kistiel W.;
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
RT K-dependent blood coagulation zymogens.";
RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
RN [10]
RP PROCESSING, ACTIVE SITE, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=78194509; PubMed=659613;
RA di Scipio R.G., Kurachi K., Davie E.W.;
RT "Activation of human factor IX (Christmas factor).";
RL J. Clin. Invest. 61:1528-1538(1978).
RN [11]
RP CALCIUM-BINDING DATA.
RX MEDLINE=84185715; PubMed=6425296.
RA Morita T., Isaacs B.S., Esmon C.T., Johnson A.E.;
RT "Derivatives of blood coagulation factor IX contain a high affinity
RT Ca2+-binding site that lacks gamma-carboxyglutamic acid.";
RL J. Biol. Chem. 259:5698-5704(1984).
RN [12]
RP ERRATUM.
RA Morita T., Isaacs B.S., Esmon C.T., Johnson A.E.;
RL J. Biol. Chem. 260:2583-2583(1985).
RN [13]
RP SIGNAL SEQUENCE CLEAVAGE SITE.
RX MEDLINE=86189947; PubMed=3009023.
RA Bentley A.K., Rees D.J.G., Rizza C., Brownlee G.G.;
RT "Defective propeptide processing of blood clotting factor IX caused
RT by mutation of arginine to glutamine at position -4.";
RL Cell 45:343-348(1986).
RN [14]
RP STRUCTURE OF CARBOHYDRATE ON SER-99.
RX MEDLINE=90062160; PubMed=2511201.
RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T., Takao T.,
RA Shimonishi Y., Iwanaga S.;
RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first
RT epidermal growth factor-like domain of human factors VII and IX and
RT protein Z and bovine protein Z.";
RL J. Biol. Chem. 264:20320-20325(1989).
RN [15]
RP STRUCTURE OF CARBOHYDRATE ON SER-99.
RX MEDLINE=91344709; PubMed=2129367.
RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.,
RT "A new trisaccharide sugar chain linked to a serine residue in the
RT first EGF-like domain of clotting factors VII and IX and protein Z.";
RL Adv. Exp. Med. Biol. 281:121-131(1990).
RN [16]
RP STRUCTURE OF CARBOHYDRATE ON SER-107.
RX MEDLINE=92388094; PubMed=1517205.
RA Nishimura H., Takao T., Hase S., Shimonishi Y., Iwanaga S.;
RT "Human factor IX has a tetrasaccharide O-glycosidically linked to
RT serine 61 through the fucose residue.";
RL J. Biol. Chem. 267:17520-17525(1992).
RN [17]
RP PHOSPHORYLATION OF SER-114.
RA Harris R.J., Papac D.I., Truong L., Smith K.J.;
RT "Partial phosphorylation of serine-68 in EGF-1 of human factor IX.";
RL (in) Abstracts of Xith International conference on methods in protein
RL structure analysis, pp.50-50, Anney (1996).
RN [18]
RP POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=20575397; PubMed=11133752.
RA Arruda V.R., Hagstrom J.N., Deitch J., Helman-Patterson T.,
RA Camire R.M., Chu K., Fields P.A., Herzog R.W., Couto L.B.,
RA Larson P.J., High K.A.;
RT "Posttranslational modifications of recombinant myotube-synthesized
RT human factor IX.";
RL Blood 97:130-138(2001).
RN [19]
RP STRUCTURE BY NMR OF 47-93.
RX MEDLINE=95229607; PubMed=7713897.
RA Freedman S.J., Furie B.C., Furie B., Baleja J.D.;
RT "Structure of the metal-free gamma-carboxyglutamic acid-rich membrane
RT binding region of factor IX by two-dimensional NMR spectroscopy.";
RL J. Biol. Chem. 270:7980-7987(1995).
RN [20]
RP STRUCTURE BY NMR OF 47-93.
RX MEDLINE=96032604; PubMed=7547952.
RA Freedman S.J., Furie B.C., Furie B., Baleja J.D.;
RT "Structure of the calcium ion-bound gamma-carboxyglutamic acid-rich
RT domain of factor IX.";
RL Biochemistry 34:12126-12137(1995).
RN [21]
RP STRUCTURE BY NMR OF 47-93.
RX MEDLINE=96279169; PubMed=8663165.
RA Freedman S.J., Blostein M.D., Baleja J.D., Jacobs M., Furie B.C.,
RA Furie B.;
RT "Identification of the phospholipid binding site in the vitamin K-
RT dependent blood coagulation protein factor IX.";
RL J. Biol. Chem. 271:16227-16236(1996).
RN [22]
RP STRUCTURE BY NMR OF 47-93.
RX MEDLINE=97199336; PubMed=9047312.
RA Li L., Darden T.A., Freedman S.J., Furie B.C., Furie B., Baleja J.D.,
RA Smith H., Hlskey R.G., Pedersen L.G.;
RT "Refinement of the NMR solution structure of the
RT gamma-carboxyglutamic acid domain of coagulation factor IX using
RT molecular dynamics simulation with initial Ca2+ positions determined
RT by a genetic algorithm.";
RL Biochemistry 36:2132-2138(1997).
RN [23]
RP STRUCTURE BY NMR OF 91-133.
RX MEDLINE=91308127; PubMed=1854745.
RA Huang L.H., Cheng H., Pardi A., Tam J.P., Sweeney W.V.;
RT "Sequence-specific 1H NMR assignments, secondary structure, and
RT location of the calcium binding site in the first epidermal growth
RT factor like domain of blood coagulation factor IX.";
RL Biochemistry 30:7402-7409(1991).
RN [24]
RP STRUCTURE BY NMR OF 92-130.
RX MEDLINE=93284090; PubMed=1304885.
RA Baron M., Norman D.G., Harvey T.S., Handford P.A., Mayhew M.,
RA Tee A.G.D., Brownlee G.G., Campbell I.D.C.;
RT "The three-dimensional structure of the first EGF-like module of
RT human factor IX: comparison with EGF and TGF-alpha.";
RL Protein Sci. 1:81-90(1992).
RN [25]
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 92-130.
RX MEDLINE=95330802; PubMed=7606779.
RA Rao Z., Handford P., Mayhew M., Knott V., Brownlee G.G., Stuart D.;
RT "The structure of a Ca(2+)-binding epidermal growth factor-like
RT domain: its role in protein-protein interactions.";
RL Cell 82:131-141(1995).
RN [26]
RP MOLECULAR PATHOLOGY OF HEMOPHILIA B.

Query Match 42.3%; Score 77; DB 1; Length 461;
Best Local Similarity 41.2%; Pred. No. 2.6e-06;

Matches 14; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 11 GSLXKCKKXXCSEFXAXIIFKDXKTKLFWISY 44
DB 58 GNLERCEMEKCSFEAREVFENTERTEFTFEMKQY 91

RESULT 23

TMG2_HUMAN STANDARD; PRT; 202 AA.

AC 014669;
DT 01-MAR-2002 (rel. 41, Created)
DT 01-MAR-2002 (rel. 41, Last sequence update)
DT 01-MAR-2002 (rel. 41, Last annotation update)
DE Transmembrane gamma-carboxylutamic acid protein 2 precursor (Proline-rich Gla protein 2) (Proline-rich gamma-carboxylutamic acid protein 2).
GN PRG2 OR TMG2 OR PRGP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97404347; PubMed=9256434;
RA Kulman J.D., Harris J.E., Haldeman B.A., Davie E.W.;

"Primary structure and tissue distribution of two novel proline-rich gamma-carboxylutamic acid proteins."
Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997).
-1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- TISSUE SPECIFICITY: Highly expressed in the thyroid.
-1- PTM: Gla residues are produced after subsequent posttranslational modifications of glutamic acid by a vitamin K-dependent gamma-carboxylase.

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DR EMBL: AF009243; AAB67071.1; -.
DR MIM: 604429; -.
DR HSSP: P00740; 1CFH.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00594; gla; 1.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00069; GLA; 1.
DR PROSITE: PS00011; GLD-CARBOXYLATION; 1.
KW Gamma-carboxylutamic acid; Vitamin K; Transmembrane; Signal.
FT SIGNAL 1 23
FT PROPEP 24 49
FT CHAIN 50 202
FT DOMAIN 50 109
FT DOMAIN 110 132
FT DOMAIN 133 202
FT DOMAIN 54 91
FT DOMAIN 161 173
FT DOMAIN 191 194
SQ SEQUENCE 202 AA; 22393 MW; BC79400C98492060 CRC64;

Query Match 40.7%; Score 74; DB 1; Length 202;

Best Local Similarity 40.0%; Pred. No. 4.1e-06;
Matches 16; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

QY 5 LXXLRKGSLLKCKKXXCSEFXAXIIFKDXKTKLFWISY 44
DB 55 LELUTPGNLERCEKCSFEAREVFENTERTEFTFEMKQY 94

RESULT 24

FA9_CANFA STANDARD; PRT; 452 AA.

AC P19540;
DT 01-FEB-1991 (rel. 17, Created)
DT 01-FEB-1991 (rel. 17, Last sequence update)
DT 01-NOV-1997 (rel. 35, Last annotation update)
DE Coagulation factor IX precursor (FC 3.4.21.22) (Christmas factor).
GN F9.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=90311364; PubMed=2367529;
RA Axelrod J.H., Read M.S., Brinkhaus K.M., Verma I.M.;

"Phenotypic correction of factor IX deficiency in skin fibroblasts of hemophilic dogs."
Proc. Natl. Acad. Sci. U.S.A. 87:5173-5177(1990).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89323338; PubMed=2752110;
RA Evans J.P., Matzke H.H., Ware J.L., Stafford D.W., High K.A.;

"Molecular cloning of a cDNA encoding canine factor IX."
Blood 74:207-212(1989).
[3]
RP VARIANT HEMOPHILIA B GLU-418.
RX MEDLINE=9009303; PubMed=2481310;
RA Evans J.P., Brinkhaus K.M., Brayer G.D., Reisner H.M., High K.A.;

"Canine hemophilia B resulting from a point mutation with unusual consequences."
Proc. Natl. Acad. Sci. U.S.A. 86:10095-10099(1989).
-1- FUNCTION: FACTOR IX IS A VITAMIN K-DEPENDENT PLASMA PROTEIN THAT PARTICIPATES IN THE INTRINSIC PATHWAY OF BLOOD COAGULATION BY CONVERTING FACTOR X TO ITS ACTIVE FORM IN THE PRESENCE OF CA++ IONS, PHOSPHOLIPIDS, AND FACTOR VIII.
-1- CATALYTIC ACTIVITY: Hydrolyses one Arg-I-Ile bond in factor X to form factor xa.
-1- SUBUNIT: FACTOR IX IS ACTIVATED BY FACTOR XIa, WHICH EXCISES THE ACTIVATION PEPTIDE AND THUS PRODUCES A MOLECULE CONSISTING OF 2 CHAINS HELD TOGETHER BY ONE OR MORE DISULFIDE BONDS.
-1- DISEASE: HEMOPHILIA B IS DUE TO DEFECTS IN FACTOR IX.
-1- MISCELLANEOUS: CALCIUM BINDS TO THE GAMMA-CARBOXYGLUTAMIC ACID (GLA) RESIDUES AND, WITH STRONGER AFFINITY, TO ANOTHER SITE, BEYOND THE GLA DOMAIN.
-1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.

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DR EMBL: M21757; AAA75006.1; -.
DR EMBL: M33826; AAA30844.1; -.
DR PIR: A30351; A30351.
DR HSSP: P00740; 1CFH.
DR MEROPS: S01.214; -.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF-2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR002383; GLA_blood.

DR InterPro: IPR001254; Trypsin.
 DR InterPro: IPR00294; VitK_dep-GLA.
 DR Pfam: PF00008; EGF_2.
 DR Pfam: PF00594; gla; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00179; EGF_CA; 1.
 DR SMART: SM00069; GLA; 1.
 DR SMART: SM00020; TRYP_SPE; 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; 1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF_CA; 1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 DR Blood coagulation; Plasma; Serine protease; Calcium-binding;
 KM Hydrolase; Glycoprotein; Vitamin K; Gamma-carboxyglutamic acid;
 KM Hemophilia; Hydroxylation; Zymogen; Signal; EGF-like domain;
 KW Repeat; Disease mutation.
 FT SIGNAL 1 21
 FT PROPEP 22 39
 FT CHAIN 40 183
 FT PROPEP 184 217
 FT CHAIN 218 452
 FT DOMAIN 86 122
 FT DOMAIN 123 164
 FT DOMAIN 218 452
 FT SITE 183 184
 FT SITE 217 218
 FT MOD_RES 46 46
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 FT MOD_RES 134 148
 FT MOD_RES 150 163
 FT MOD_RES 197 197
 FT MOD_RES 207 207
 FT MOD_RES 297 297
 FT MOD_RES 258 258
 FT MOD_RES 306 306
 FT MOD_RES 402 402
 FT MOD_RES 418 418
 FT MOD_RES 452 AA; 50827 MW; 1F6537C46A6960ED CRC64;

Query Match 39.6%; Score 72; DB 1; Length 452;
 Best Local Similarity 38.2%; Pred. No. 2e-05;
 Matches 13; Conservative 6; Mismatches 15; Indels 0; Gaps 0;
 11 GSLAKKCKXXCSPFXAXIKDKAKRTKLFMISY 44
 Db 51 GNLERECIEKSCFEEAREFVENTETKTEFMKQY 84
 RESULT 25
 FA9_MOUSE STANDARD: PRT; 459 AA.
 ID FA9_MOUSE
 AC P16294;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Coagulation factor IX precursor (EC 3.4.21.22) (Christmas factor)
 DE (Fragment).
 GN F9 OR CF9.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid=10090.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90215309; PubMed=2323576;
 RA Wu S.-M., Stafford D.W., Ware J.;
 RT "Deduced amino acid sequence of mouse blood-coagulation factor IX.";
 RL Gene 86:275-278(1990).
 RN [2]
 RP SEQUENCE OF 168-451 FROM N.A.
 RX MEDLINE=90152675; PubMed=2303254;
 RA Sarkar G., Koehler D.D., Sommer S.S.;
 RT "Direct sequencing of the activation peptide and the catalytic domain
 of the factor IX gene in six species.";
 RL Genomics 6:133-143(1990).
 CC -1- FUNCTION: FACTOR IX IS A VITAMIN K-DEPENDENT PLASMA PROTEIN THAT
 PARTICIPATES IN THE INTRINSIC PATHWAY OF BLOOD COAGULATION BY
 CONVERTING FACTOR X TO ITS ACTIVE FORM IN THE PRESENCE OF CA++
 IONS, PHOSPHOLIPIDS, AND FACTOR VIII.
 CC -1- CATALYTIC ACTIVITY: Hydrolyses one Arg-Ile bond in factor X to
 form factor xa.
 CC -1- SUBUNIT: FACTOR IX IS ACTIVATED BY FACTOR XIA, WHICH EXCISES THE
 ACTIVATION PEPTIDE AND THUS PRODUCES A MOLECULE CONSISTING OF 2
 CHAINS HELD TOGETHER BY ONE OR MORE DISULFIDE BONDS.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 TRYPSIN FAMILY.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M23109; AAA37629.1; -;
 DR EMBL: M26236; AAA37630.1; -;
 DR PIR: JQ0419; JQ0419.
 DR HSSP: P00740; ICFH.
 DR MGD: MGI:88384; F9.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000742; EGF_2.
 DR InterPro: IPR001881; EGF_CA.
 DR InterPro: IPR001254; Trypsin.
 DR InterPro: IPR000294; VitK_dep-GLA.
 DR Pfam: PF00008; EGF_2.
 DR Pfam: PF00594; gla; 1.
 DR Pfam: PF00089; trypsin; 1.

DR	SMART:		SMD00179;	Egf_CA; 1.
DR	SMART:		SMD0069;	Gla_1.
DR	PROSITE:		PSM0020;	Tryp_Spc; 1.
DR	PROSITE:		PSM0010;	Asx_Hydroxyl; 1.
DR	PROSITE:		PSM0022;	EgF_1; 1.
DR	PROSITE:		PSM1186;	EgF_2; 2.
DR	PROSITE:		PSM1187;	EgF_CA; 1.
DR	PROSITE:		PSM0011;	GLU_CARBOXYLATION; 1.
DR	PROSITE:		PSM0240;	TRYPSIN_DOM; 1.
DR	PROSITE:		PSM0134;	TRYPsinHis; 1.
KW	Blood coagulation:		Plasma; Serine protease; Calcium-binding; Hemophilias; Glycoprotein; Vitamin K; Gamma-carboxyglutamic acid; Hydroxylation; Zymogen; Signal; EgF-like domain;	
KW	Hemophilia:		Hydroxylation; Zymogen; Signal; EgF-like domain;	
KW	Repeat:			
FT	NON_TER	<1	1	
FT	SIGNAL	17	16	
FT	PROPEP	35	34	
FT	CHAIN	181	180	
FT	PROPEP	225	224	
FT	CHAIN	225	459	
FT	DMAIN	81	117	
FT	DOMAIN	118	159	
FT	DOMAIN	225	459	
FT	SITE	180	181	
FT	SITE	224	225	
FT	MOD_RES	41	41	
FT	MOD_RES	42	42	
FT	MOD_RES	49	49	
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FT	MOD_RES	74	74	
FT	MOD_RES	98	98	
FT	ACT_SITE	265	265	
FT	ACT_SITE	313	313	
FT	ACT_SITE	409	409	
FT	DISULFID	52	57	
FT	DISULFID	85	96	
FT	DISULFID	90	105	
FT	DISULFID	107	116	
FT	DISULFID	122	133	
FT	DISULFID	129	143	
FT	DISULFID	145	158	
FT	CARBOHYD	192	192	
FT	CARBOHYD	211	211	
FT	CARBOHYD	304	304	
FT	CONFLICT	363	363	
FT	CONFLICT	388	388	
QO	SEQUENCE	459 AA;	51635 MM;	EF439C840DD6CB1A CRC64; T -> I (IN REF. 2). H -> Q (IN REF. 2).

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Qy      11 GSLRXCXXXQCSFXAXXIFKDXARTKLEWISY 44
         1:1 1 1 1:1 1 1:1 1 1 1
Db      46 GNLERCIIEKRCSEFEAREVFENTETKEETEFMKQY 79
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RESULT	26				
TMG4_HUMAN					
ID	TMG4_HUMAN	STANDARD:	PRT:	226 AA.	
AC	Q9B2D6;				
DT	01-MAR-2002 (Rel. 41, Created)				
DT	01-MAR-2002 (Rel. 41, Last sequence update)				
DT	01-MAR-2002 (Rel. 41, Last annotation update)				
DE	Transmembrane gamma-carboxyglutamic acid protein 4 precursor.				
GN	TMG4.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_Taxid=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=21117044; PubMed=11171957;				
RA	Kulman J.D., Harris J.E., Xie L., Davie E.W.;				
RT	"Identification of two novel transmembrane gamma-carboxyglutamic acid				
RT	proteins expressed broadly in fetal and adult tissues.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 98:1370-1375(2001).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Placenta;				
RC	Strausberg R.;				
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.				
CC	-1 SUBCELLULAR LOCATION: Type I membrane protein.				
CC	-1 TISSUE SPECIFICITY: Expressed in lung, liver, kidney, pancreas and				
CC	Placenta.				
CC	-1 PTM: Glu residues are produced after subsequent posttranslational				
CC	modifications of glutamic acid by a vitamin K-dependent gamma-				
CC	carboxylase.				
CC	-----				
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CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL: AF326351; AAK00956.1; -				
DR	EMBL: BC010052; AAH10052.1; -				
DR	HSSP: P00740; ICFH.				
DR	InterPro: IPR002383; GLA_blood.				
DR	InterPro: IPR000294; VltK_dep_GLA.				
DR	PRINTS: PR00001; GLABLOOD.				
DR	SMART: SM00069; GLA; 1.				
DR	PROSITE: PS00011; GLU_CARBOXYLATION; 1.				
KW	Gamma-carboxyglutamic acid; Vitamin K; Transmembrane; Signal.				
FT	SIGNAL	1	17	POTENTIAL.	
FT	PROPEP	18	49	POTENTIAL.	
FT	CHAIN	50	226	TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID	
FT	DOMAIN	50	113	PROTEIN 4.	
FT	TRANSMEM	114	134	EXTRACELLULAR (POTENTIAL).	
FT	DOMAIN	135	226	POTENTIAL.	
FT	DOMAIN	56	93	CYTOPLASMIC (POTENTIAL).	
FT	DOMAIN	203	208	GLA-RICH.	
FT	SEQUENCE	226 AA;	25403 MW;	POLY-PRO.	
FT	SEQUENCE	226 AA;	45C783E825797EE	CRC64;	

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Query Match      37.4%   Score 68   DB 1; Length 226;
Best Local Similarity 38.2%; Pred NO. 5.5e-05;
Matches 13; Conservative 4; Mismatches 17; Indels 0; Gaps 0;
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RESULT 27
ID THRB_BOVIN STANDARD; PRT; 625 AA.
AC P00735;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Prothrombin precursor (EC 3.4.21.5).
GN F2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88245190; PubMed=3379642;
RA Irwin D.W., Robertson K.A., McGillivray R.T.A.;
RT "Structure and evolution of the bovine prothrombin gene.";
RL J. Mol. Biol. 200;31-45(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=84203525; PubMed=6326805;
RA McGillivray R.T.A., Davie E.W.;
RT "Characterization of bovine prothrombin mRNA and its translation product.";
RL Biochemistry 23:1626-1634(1984).
RN [3]
RP SEQUENCE OF 44-625. DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RA Magnusson S., Sottrup-Jensen L., Petersen T.E., Claess H.;
RL (in) Hemker H.C., Veltkamp J.J. (eds.);
Boehrhae symposium on prothrombin and related coagulation factors,
RL pp.25-46, Leiden University Press, Leiden (1975).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF ACTIVATION PEPTIDE 1.
RX MEDLINE=86296631; PubMed=3741841;
RA Park C.H., Tulinsky A.;
RT "Three-dimensional structure of the kringe sequence: structure of
RT prothrombin fragment 1.";
RL Biochemistry 25:3977-3982(1986).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF ACTIVATION PEPTIDE 1.
RX MEDLINE=91311686; PubMed=1856869;
RA Seshari T.-P., Tulinsky A., Skrzypczak-Jankun E., Park C.H.;
RT "Structure of bovine prothrombin fragment 1 refined at 2.25-A
RT resolution.";
RL J. Mol. Biol. 220:481-494(1991).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF ACTIVATION PEPTIDE 1.
RX MEDLINE=92190185; PubMed=1547238;
RA Soriano-garcia M., Padmanabhan K., de Vos A.M., Tulinsky A.;
RT "The Ca2+ ion and membrane binding structure of the Gla domain of Ca-
RT prothrombin fragment 1.";
RL Biochemistry 31:2554-2566(1992).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX MEDLINE=92218459; PubMed=1560020;
RA Martin P.D., Robertson W., Turk D., Huber R., Bode W., Edwards B.F.P.;
RT "The structure of residues 7-16 of the A alpha-chain of human
RT fibrinogen bound to bovine thrombin at 2.3-A resolution.";
RL J. Biol. Chem. 267:7911-7920(1992).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX MEDLINE=92389319; PubMed=1518046;
RA Brandstetter H., Turk D., Hoeffken H.W., Grosse D., Stuerzebecher J.,
RA Martin P.D., Edwards B.F.P., Bode W.;
RT "Refined 2.3 A x-ray crystal structure of bovine thrombin complexes
RT formed with the benzamidine and arginine-based thrombin inhibitors
RT NADAP, 4-TAPAP and MQPA. A starting point for improving
RT antithrombotics.";
RL J. Mol. Biol. 226:1085-1089(1992).

[9]
RP X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF COMPLEX WITH ORNITHODORIN.
RX MEDLINE=97102783; PubMed=8947023;
RA van de Loch A., Stubbs M.T., Bode W., Friedrich T., Bollschweiler C.,
RA Hoffman W., Huber R.;
RT "The ornithodorin-thrombin crystal structure, a key to the TAP
RT enigma?";
RL EMBO J. 15:6011-6017(1996).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF COMPLEX WITH TRIABIN.
RX MEDLINE=98004486; PubMed=9342325;
RA Fuentes-Prior P., Noeske-Jungblut C., Donner P., Schleuning W.D.,
RA Huber R., Bode W.;
RT "Structure of the thrombin complex with triabin, a lipocalin-like
RT exosite-binding inhibitor derived from a triatomine bug.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:11845-11850(1997).
RN [11]
RP GENE STRUCTURE.
RX MEDLINE=86077733; PubMed=3000440;
RA Irwin D.W., Ahern K.G., Pearson G.D., McGillivray R.T.A.;
RT "Characterization of the bovine prothrombin gene.";
RL Biochemistry 24:6854-6861(1985).
CC -1- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS
CC FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,
CC AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: SYNTHESIZED IN THE LIVER; FOUND IN PLASMA.
CC -1- PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
CC RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOML
CC ENZYME. THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES
CC ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY
CC CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
CC OF PROTHROMBIN TO THROMBIN.
CC -1- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A
CC PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &
CC FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS. FACTOR XA REMOVES
CC THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &
CC HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR
CC V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
CC THROMBIN.
CC -1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL
CC FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
CC BY FACTOR XA.
CC -1- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
CC -1- DATABASE: NAME=prozyme technical fact sheet;
CC WWW="http://www.prozyme.com/technical/thrombindata.html".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: V00135; CAA23451.1; -;
DR EMBL: J00041; AAA30781.1; -;
DR PTR: A00915; THRB.
DR PIR: S02537; S02537.
DR PDB: 1BBR; 3I-JAN-94.
DR PDB: 1ETR; 3I-JAN-94.
DR PDB: 1ETS; 3I-JAN-94.
DR PDB: 1ETT; 3I-JAN-94.
DR PDB: 1HRT; 3I-JAN-94.
DR PDB: 2PF1; 3I-JAN-94.
DR PDB: 2PF2; 3I-JAN-94.
DR PDB: 2SPT; 3I-MAY-94.
DR PDB: 1MKW; 07-JUL-97.
DR PDB: 1MKX; 07-JUL-97.
DR PDB: 1TBO; 14-OCT-96.
DR PDB: 1TBR; 14-OCT-96.

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DR PDB: 1TQC: 23-JUL-97.
DR PDB: 1VIT: 21-APR-97.
DR PDB: 1YCP: 06-MAY-98.
DR PDB: 1A0H: 17-JUN-98.
DR PDB: 1AVG: 16-FEB-99.
DR MEROPS: S01.217; -.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR003966; Prothrombin.
DR InterPro: IPR001254; Trypsin.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00051; kringle; 2.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR PRINTS: PR00018; KRINGLE.
DR PRINTS: PR01505; PROTHROMBIN.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00130; KR; 2.
DR SMART: SM00020; TRYP-SPEC; 1.
DR PROSITE: PS00011; GLU-CARBOXYLATION; 1.
DR PROSITE: PS00021; KRINGLE_1; 2.
DR PROSITE: PS50070; KRINGLE_2; 2.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR Blood coagulation; Plasma; Calcium-binding; Glycoprotein; Repeat;
KW Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver;
KW Hydroxylase; Serine protease; Kringle; Signal; 3D-structure.
FT SIGNAL: 1 24
FT PROPEP: 25 43
FT CHAIN: 44 625
FT PEPTIDE: 44 199
FT PEPTIDE: 200 317
FT CHAIN: 318 366
FT CHAIN: 367 625
FT DOMAIN: 109 187
FT DOMAIN: 214 292
FT DOMAIN: 367 625
FT SITE: 199 200
FT SITE: 317 318
FT SITE: 366 367
FT SITE: 366 367
FT ACT_SITE: 409 409
FT ACT_SITE: 465 465
FT ACT_SITE: 571 571
FT MOD_RES: 51 51
FT MOD_RES: 51 51
FT MOD_RES: 58 58
FT MOD_RES: 60 60
FT MOD_RES: 63 63
FT MOD_RES: 64 64
FT MOD_RES: 69 69
FT MOD_RES: 70 70
FT MOD_RES: 73 73
FT MOD_RES: 76 76
FT CARBOHD: 120 120

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Query Match 35.7%; Score 65; DB 1; Length 625;
 Best Local Similarity 34.1%; Pred. No. 0.00052;
 Matches 14; Conservative 3; Mismatches 24; Indels 0; Gaps 0;

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OY 4 FLXXLRXGLXKXKXKXGCSFYXAXYIFDARKTKLEWISY 44
DB 48 FLEEVKRGKMLERECLSEPCSRBEAFALSLSATDAFMKY 88

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RESULT 28
 PRS_BOVIN STANDARD: PRT; 675 AA.
 AC P07224;
 DT 01-APR-1988 (rel. 07, Created)

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DT 01-APR-1988 (rel. 07, Last sequence update)
DT 01-MAR-2002 (rel. 41, Last annotation update)
DE Vitamin K-dependent protein S precursor.
GN PROS1 OR PROS.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxId=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86233400; PubMed=2940598;
RA Dahlback B., Lundwall A., Stenflo J.;
RT "Primary structure of bovine vitamin K-dependent protein S.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:4199-4203(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX Wydro R., Cohen E., Dackowski W., Stenflo J., Lundwall A.,
RA Dahlback B.;
RL Submitted (FEB-1992) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE OF 42-141.
RX MEDLINE=86168236; PubMed=2937785;
RA Dahlback B., Lundwall A., Stenflo J.;
RT "Localization of thrombin cleavage sites in the amino-terminal region
of bovine protein S.";
RL J. Biol. Chem. 261:5111-5115(1986).
CC -1- FUNCTION: ANTICOAGULANT PLASMA PROTEIN; IT IS A COFACTOR TO
ACTIVATED PROTEIN C IN THE DEGRADATION OF COAGULATION FACTORS VA
AND VIIIA. IT HELP TO PREVENT COAGULATION AND STIMULATING
FIBRINOLYSIS.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- SIMILARITY: CONTAINS 2 LAMININ G-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 4 EGF-LIKE DOMAINS.
-----
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DR EMBL: M13044; AA030757.1; -.
DR EMBL: X12891; CA031382.1; -.
DR PIR: A24759; A24759.
DR HSSP: P00740; 1CFH.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001861; EGF_CA.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001791; Laminin_G.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF; 4.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00054; laminin_G; 1.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 3.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00282; LamG; 2.
DR PROSITE: PS00010; ASX_HYDROXYL; 4.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 3.
DR PROSITE: PS01187; EGF_CA; 3.
DR PROSITE: PS00011; GLU CARBOXYLATION; 1.
DR PROSITE: PS50025; LAM G DOMAIN; 2.
KW Plasma; Gamma-carboxyglutamic acid; Calcium; Vitamin K; Zymogen;
KW Blood coagulation; Hydroxylation; Glycoprotein; Signal; Repeat;
KW EGF-like domain.
FT SIGNAL: 1 24
FT PROPEP: 25 41
FT CHAIN: 42 675

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VITAMIN K-DEPENDENT PROTEIN S.

[illegible]

ID PRIS_HUMAN STANDARD; PRT: 676 AA.
AC P07225; Q15518;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Vitamin K-dependent protein S precursor.
GN PROS1 OR PROS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9108444; Pubmed=2148110;
RA Schmidel D.K., Tatro A.V., Phelps L.G., Tomczak J.A., Long G.L.;
RT "Organization of the human protein S genes.";
RL Biochemistry 29:7845-7852(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Ploos van Amstel H.K.;
RL Submitted (AUG-1987) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 27-676 FROM N.A.
RX MEDLINE=9108444; Pubmed=2148111;
RA Ploos van Amstel H.K., Reitsma P.H., der Logt C.P., Bertina R.M.;
RT "Intron-exon organization of the active human protein S gene PS alpha and its pseudogene PS beta: duplication and silencing during primate evolution.";
RL Biochemistry 29:7853-7861(1990).
RN [4]
RP SEQUENCE OF 1-42 FROM N.A.
RX MEDLINE=88005138; Pubmed=2820795;
RA Ploos van Amstel H.K., van der Zanden A.L., Reitsma P.H.,
RA Bertina R.M.;
RT "Human protein S cDNA encodes Phe-16 and Tyr 222 in consensus sequences for the post-translational processing.";
RL FEBS Lett. 222:186-190(1987).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=87092407; Pubmed=3467362;
RA Hoskins J., Norman D.K., Beckmann R.J., Long G.L.;
RT "Cloning and characterization of human liver cDNA encoding a protein S precursor.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:349-353(1987).
RN [6]
RP SEQUENCE OF 27-676 FROM N.A.
RX MEDLINE=86313649; Pubmed=2944113;
RA Lundvall A., Dackowski W., Cohen E., Shaffer M., Mahr A., Dahlback B.,
RA Scenlio J., Wyder R.;
RT "Isolation and sequence of the cDNA for human protein S, a regulator of blood coagulation.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:6716-6720(1986).
RN [7]
RP VARIANT HEERLEN.
RX MEDLINE=90335440; Pubmed=2143091;
RA Bertina R.M., Ploos van Amstel H.K., van Wijngaarden A.,
RA Coenen J., Leemhuis M.P., Deutz-Terlouw P.P., van der Linden I.K.,
RA Reitsma P.H.;
RT "Heerlen polymorphism of protein S, an immunologic polymorphism due to dimorphism of residue 460.";
RL Blood 76:538-548(1990).
RN [8]
RP VARIANT SER-258.
RA Cooper D.N.;
RL Unpublished observations (SEP-1993).
RN [9]
RP VARIANT TOKUSHIMA.
RX MEDLINE=94129009; Pubmed=8298131;
RA Hayashi T., Nishioke T., Shigekiyo T., Saito S., Suzuki K.;
RT "Protein S Tokushima: abnormal molecule with a substitution of Glu for Lys-155 in the second epidermal growth factor-like domain of protein S.";

RL Blood 83:683-690(1994).
CC -1- FUNCTION: ANTICOAGULANT PLASMA PROTEIN. IT IS A COFACTOR TO
CC ACTIVATED PROTEIN C IN THE DEGRADATION OF COAGULATION FACTORS VA
CC AND VIIIA. IT HELPS TO PREVENT COAGULATION AND STIMULATING
CC FIBRINOLYSIS.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- DISEASE: DEFECTS IN PROS1 ARE ASSOCIATED WITH AN INCREASED RISK TO
CC DEVELOP THROMBOTIC DISEASE (THROMBOPHILIA).
CC -1- SIMILARITY: CONTAINS 2 LAMININ G-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 4 EGF-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL: M57853; AAA60357.1; -;
DR EMBL: M57840; AAA60357.1; JOINED.
DR EMBL: M57841; AAA60357.1; JOINED.
DR EMBL: M57842; AAA60357.1; JOINED.
DR EMBL: M57844; AAA60357.1; JOINED.
DR EMBL: M57845; AAA60357.1; JOINED.
DR EMBL: M57846; AAA60357.1; JOINED.
DR EMBL: M57847; AAA60357.1; JOINED.
DR EMBL: M57848; AAA60357.1; JOINED.
DR EMBL: M57849; AAA60357.1; JOINED.
DR EMBL: M57850; AAA60357.1; JOINED.
DR EMBL: M57851; AAA60357.1; JOINED.
DR EMBL: M57852; AAA60357.1; JOINED.
DR EMBL: M57854; AAA60180.1; -;
DR EMBL: M36551; AAA60180.1; JOINED.
DR EMBL: M36552; AAA60180.1; JOINED.
DR EMBL: M36553; AAA60180.1; JOINED.
DR EMBL: M36554; AAA60180.1; JOINED.
DR EMBL: M36555; AAA60180.1; JOINED.
DR EMBL: M36556; AAA60180.1; JOINED.
DR EMBL: M36557; AAA60180.1; JOINED.
DR EMBL: M36558; AAA60180.1; JOINED.
DR EMBL: M36559; AAA60180.1; JOINED.
DR EMBL: M36560; AAA60180.1; JOINED.
DR EMBL: M36561; AAA60180.1; JOINED.
DR EMBL: M36563; AAA60180.1; JOINED.
DR EMBL: Y00692; CAA68687.1; -;
DR EMBL: M15036; CAA68688.1; ALT_SEQ.
DR PIR: A35610; A35610.
DR PIR: A26157; A26157.
DR PIR: A25891; A25891.
DR PIR: S02424; S02424.
DR PIR: S09519; S09519.
DR HSP: P07204; LEGT.
DR MM: 176880; -;
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001791; Laminin_G.
DR Pfam: PF00008; EGF_4.
DR Pfam: PF00594; gla_1.
DR Pfam: PF00054; laminin_G_1.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 3.
DR SMART: SM00282; Lamg; 2.
DR PROSITE: PS00010; ASX_HYDROXYL; 4.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 3.
DR PROSITE: PS01187; EGF_CA; 3.

FT MOD_RES 27 27 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 30 30 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 33 33 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 36 36 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 40 40 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 64 64 HYDROXYLATION.
FT DISULFID 51 62 BY SIMILARITY.
FT DISULFID 56 71 BY SIMILARITY.
FT DISULFID 73 82 BY SIMILARITY.
FT DISULFID 89 101 BY SIMILARITY.
FT DISULFID 97 110 BY SIMILARITY.
FT DISULFID 112 125 BY SIMILARITY.
FT CARBOHYD 53 53 O-LINKED (GLC. . .).
FT CARBOHYD 59 59 /FTID-CAR_000032.
FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .).
FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .).
SQ SEQUENCE 396 AA; 43112 MW; 04C5D7A35849B116 CRC64;

Query Match 31.3%; Score 57; DB 1; Length 396;
Best Local Similarity 32.5%; Pred. No. 0.0095;
Matches 13; Conservative 5; Mismatches 22; Indels 0; Gaps 0;

OY 5 LXXLRXGSLARXCKXXKXCSFYXAXXIFKDAYRTKLEWISY 44
DB 6 LEELEFEGHLEKECEWCEICVYEAREVEDETDTEFWRTY 45

RESULT 33
PRIS_RAT STANDARD; PRT; 675 AA.
ID PRIS_RAT
AC P53813;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Vitamin K-dependent protein S precursor.
GN PROS1 OR PROS.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=95332263; Pubmed=7608128;
RA Yasuda F., Hayashi T., Tanitame K., Nishioke J., Suzuki K.;
RT "Molecular cloning and functional characterization of rat plasma
protein S".
RL J. Biochem. 117:374-383(1995).
CC - FUNCTION: ANTICOAGULANT PLASMA PROTEIN. IT IS A COFACTOR TO
CC ACTIVATED PROTEIN C IN THE DEGRADATION OF COAGULATION FACTORS VA
CC AND VIIIA. IT HELP TO PREVENT COAGULATION AND STIMULATING
CC FIBRINOLYSIS.
CC - SUBCELLULAR LOCATION: Extracellular.
CC - TISSUE SPECIFICITY: PLASMA.
CC - SIMILARITY: CONTAINS 2 LAMININ G-LIKE DOMAINS.
CC - SIMILARITY: CONTAINS 4 EGF-LIKE DOMAINS.
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CC
CC EMBL: S78744; AAC60704.1; -.
CC HSSP: P00740; ICFH.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_Ca.

DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001791; Laminin_G.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF; 4.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00054; laminin_G; 1.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 3.
DR SMART: SM00001; EGF_Like; 1.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00282; lamg; 2.
DR PROSITE: PS00010; ASX_HYDROXYL; 4.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 3.
DR PROSITE: PS01187; EGF_CA; 3.
DR PROSITE: PS00011; GLU CARBOXYLATION; 1.
DR PROSITE: PS00025; LAM_G_DOMAIN; 1.
KW Plasma; gamma-carboxyglutamic acid; Calcium; Vitamin K; Zymogen;
KW Blood coagulation; Hydroxylation; Glycoprotein; Signal; Repeat;
KW EGF-like domain.
FT SIGNAL 1 24
FT PROPEP 25 41
FT CHAIN 42 675
FT DOMAIN 42 86
FT DOMAIN 87 116
FT DOMAIN 117 155
FT DOMAIN 157 200
FT DOMAIN 201 242
FT DOMAIN 243 283
FT DOMAIN 299 475
FT DOMAIN 484 665
FT MOD_RES 47 47
FT MOD_RES 48 48
FT MOD_RES 55 55
FT MOD_RES 57 57
FT MOD_RES 60 60
FT MOD_RES 61 61
FT MOD_RES 66 66
FT MOD_RES 67 67
FT MOD_RES 70 70
FT MOD_RES 73 73
FT MOD_RES 77 77
FT MOD_RES 121 136
FT DISULFID 121 134
FT DISULFID 126 143
FT DISULFID 145 154
FT DISULFID 161 175
FT DISULFID 171 184
FT DISULFID 186 199
FT DISULFID 205 217
FT DISULFID 212 226
FT DISULFID 228 241
FT DISULFID 247 256
FT DISULFID 252 265
FT DISULFID 267 282
FT CARBOHYD 499 499
FT CARBOHYD 509 509
SQ SEQUENCE 675 AA; 74626 MW; B4338F556846075 CRC64;

Query Match 31.3%; Score 57; DB 1; Length 675;
Best Local Similarity 29.5%; Pred. No. 0.016;


```

AC P42837;
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Hypothetical 101.7 kDa protein in Egr2-KREI intergenic region.
GN YNL125C OR N0330.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / FY1676;
RX MEDLINE=95373280; PubMed=7645347;
RA Matfahl M., Nicaud J.-M., Levesque H., Galliardin C.;
RT "Sequencing analysis of a 15.4 kb fragment of yeast chromosome XIV
RT identifies the RPD3, PAS8 and KRE1 loci, five new open reading
RT frames."
RL Yeast 11:567-572(1995).
CC -1- SIMILARITY: TO YEAST RSD1/SAC1, AND TO HUMAN KIA0274.
CC -1- SIMILARITY: CONTAINS 1 SAC DOMAIN.
CC -----
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CC -----
DR EMBL: 246259; CAA86373.1; -
DR SCD: 271601; CAA96256.1; -
DR SCD: S0005269; YNL325C.
DR InterPro: IPR002013; SYJA_N.
DR Pfam: PF02383; SYJA_N.1.
DR PROSITE: PS50275; SAC: 1.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 101 122 POTENTIAL.
FT DOMAIN 166 528 SAC
SQ SEQUENCE 879 AA; 101745 MW; 872B331104185FA CRC64;

Query Match 24.7%; Score 45; DB 1; Length 879;
Best Local Similarity 60.0%; Pred. No. 3.1;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 30 IRKDAARTKLFWISY 44
DB 165 IRKDLDTKTFYFSY 179
      1111 1111
      |||  |||

RESULT 37
PFLA_STRMU STANDARD: PRT; 263 AA.
AC 068575;
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyruvate formate-lyase activating enzyme (EC 1.97.1.4) (PFL-activating
DE enzyme).
DE ACT OR PFLC.
OS Streptococcus mutans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1309;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT11;
RA Boyd D.A., Hamilton I.R., Cytkovitch D.G., Blotweis A.S.;
RT "Detects in D-alanyl-lipoteichoic acid synthesis in Streptococcus
RT mutans leads to acid sensitivity."
RT Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [2]

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RP SEQUENCE FROM N.A.
RC STRAIN=CS-5;
RA Yamamoto Y., Sato Y., Takahashi-Abbe S., Yamada T., Kizaki H.;
RT "Cloning and characterization of the act gene encoding pyruvate
RT formate-lyase-activating enzyme from Streptococcus mutans."
RT Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ACTIVATION OF PYRUVATE FORMATE-LYASE UNDER ANAEROBIC
CC CONDITIONS BY GENERATION OF AN ORGANIC FREE RADICAL, USING
CC S-ADENOSYLMETHIONINE AND REDUCED FLAVOXYDIN AS COSUBSTRATES TO
CC PRODUCE 5'-DEOXY-ADENOSINE.
CC -1- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + DIHYDROFLAVOXYDIN +
CC [PYRUVATE FORMATE-LYASE]-GLYCINE - 5'-DEOXYADENOSINE + METHIONINE
CC + FLAVOXYDIN + [PYRUVATE FORMATE-LYASE]-GLYCINE RADICAL.
CC -1- COFACTOR: BINDS 1 AFE-4S CLUSTER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE ORGANIC RADICAL ACTIVATING ENZYMES
CC FAMILY.
CC -----
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CC -----
DR EMBL: AF051356; AAC05773.1; -
DR EMBL: AB018417; BAA34998.1; -
DR InterPro: IPR001989; Radical_activat.
DR Pfam: PF02143; Radical_activat: 1.
DR ProDom: PD004758; Radical_activat: 1.
DR PROSITE: PS01087; RADICAL_ACTIVATING: 1.
KW Oxidoreductase; Iron-sulfur; 4Fe-4S.
FT METAL 37 37 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 41 41 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 44 44 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 44 44 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ SEQUENCE 263 AA; 30150 MW; 5754053EE248EFC CRC64;

Query Match 23.6%; Score 43; DB 1; Length 263;
Best Local Similarity 37.5%; Pred. No. 2.2;
Matches 9; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 18 KXXQSEFXXAXXFKDAXRTKLFW 41
DB 53 KNDRTERTAGDVFKEALRKDFW 76
      | : : : | : | | | | | |
      YOL3_CAEFL

RESULT 38
YOL3_CAEFL STANDARD: PRT; 322 AA.
AC 009292;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Hypothetical 35.9 kDa protein C5667.3 in chromosome III.
GN C5667.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2.
RA Percy C.;
RT Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
REVISED.
RA Jones S.J.M.;
RT Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: Z46793; CAA86771.1; -.
DR MornRep; C5667.3; CE17608.
KM Hypothetical protein.
SQ SEQUENCE 322 AA; 35890 MW; 4B0ADB6F5D27AFCA CRC64;

Query Match 22.8%; Score 41.5; DB 1; Length 322;
Best Local Similarity 25.0%; Pred. No. 5;
Matches 9; Conservative 5; Mismatches 19; Indels 3; Gaps 1;

Qy 4 FLXLRKXSLKXRC---KXQCSPFXKXKXIFKDKXR 36
Db 262 FFSAIHSAMCRFCSYKSKCTLANQTITSEITR 297

RESULT 39
MD12_YEAST STANDARD; PRT; 271 AA.
AC 092328; 008064;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Mitochondrial inheritance component MD12.
GN MDM12 OR YOL009C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97177134; PubMed=9024686;
RA Berger K.H., Sogo L.F., Yaffe M.P.;
RT "Mdm12p, a component required for mitochondrial inheritance that is
RT conserved between budding and fission yeast.";
RL J. Cell Biol. 136:545-553(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Hughes B., Pohl T.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: REQUIRED FOR NORMAL MITOCHONDRIAL MORPHOLOGY.
CC -!- SUBCELLULAR LOCATION: Mitochondrial outer membrane.
CC -!- SIMILARITY: TO S. POMBE MDM12.
CC -----
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CC -----
DR EMBL: U62252; AAB1867.1; -.
DR EMBL: Z74751; CAA99008.1; -.
DR SGD: S0005369; MDM12.
KM Mitochondrion; Outer membrane; Transmembrane.
FT CONFLICT 91 91 V -> I (IN REF. 2).
FT CONFLICT 269 269 D -> G (IN REF. 2).
SQ SEQUENCE 271 AA; 30772 MW; 39279549C652AF01 CRC64;

Query Match 21.4%; Score 39; DB 1; Length 271;
Best Local Similarity 53.3%; Pred. No. 12;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 30 IFKDAKRTKLFWISY 44
Db 247 IFKDLKRLKWLAMPWM 261

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RESULT 40
ID Y788_BORBU STANDARD; PRT; 440 AA.
AC 051728;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein BB0788.
GN BB0788.
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RX MEDLINE=98065943; PubMed=9403685;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman C.,
RA Uterback T., Matthey L., McDonald L., Artach P., Bowman C.,
RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochete, Borrelia
RT burgdorferi.";
RL Nature 390:580-586(1997).
CC -!- SIMILARITY: BELONGS TO THE UPF0072 (MST/YCF62) FAMILY.
CC -----
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CC -----
DR EMBL: AE001177; AAC67121.1; -.
DR TIGR: BB0788; -.
KM Hypothetical protein; Complete proteome.
SQ SEQUENCE 440 AA; 51472 MW; C44D22E566D92E3 CRC64;

Query Match 21.4%; Score 39; DB 1; Length 440;
Best Local Similarity 30.4%; Pred. No. 19;
Matches 7; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

Qy 22 CSFXKXIFKDAKRTKLFWISY 44
Db 368 CSYEFKFFKDRKAKKFFSKF 390

RESULT 41
ID YJJI_HAEN STANDARD; PRT; 514 AA.
AC P44744;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein HI0521.
GN HI0521.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

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RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-I., Giodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.W., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhmann J.L., Geoghagen N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus
 RT influenzae Rd.";
 RL Science 269:496-512(1995).
 RN [2]
 RP IDENTIFICATION BY MASS SPECTROMETRY.
 RX MEDLINE=20137488; PubMed=10675023;
 RA Langen H., Takacs B., Evers S., Berndt P., Lahm H.W., Wipf B.,
 RA Gray C., Fountoulakis M.;
 RT "Two-dimensional map of the proteome of Haemophilus influenzae.";
 RL Electrophoresis 21:411-429(2000).
 CC -1 SIMILARITY: STRONG, TO E.COLI YJUI.
 CC -----
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 CC -----
 DR EMBL: U32734; AAC22179.1; -.
 DR TIGR: HI0521; -.
 DR Complete proteome.
 KW SEQUENCE 514 AA; 58159 MW; 69472E231F9B746 CRC64;

Query Match 21.4%; Score 39; DB 1; Length 514;
 Best Local Similarity 50.0%; Pred. No. 22;
 Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Oy 5 LXXLRXSLRXCK 18
 Db 244 LTRRLGTATCK 257

RESULT 42
 VE1_BPv2 STANDARD: PRT; 604 AA.
 ID VE1_BPv2
 AC P11298;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Replication protein El.
 GN El.
 OS Bovine papillomavirus type 2.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10560;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA Groff D.E., Mitra R., Lancaster W.D.;
 RL Submitted (MAY-1988) to the EMBL/Genbank/DBJ databases.
 CC -1 FUNCTION: ATP-DEPENDENT DNA HELICASE REQUIRED FOR INITIATION OF
 CC VIRAL DNA REPLICATION. IT FORMS A COMPLEX WITH THE VIRAL E2
 CC PROTEIN. THE E1-E2 COMPLEX BINDS TO THE REPLICATION ORIGIN WHICH
 CC CONTAINS BINDING SITES FOR BOTH PROTEINS.
 CC -1 SUBCELLULAR LOCATION: Nuclear.
 CC -----
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 CC -----

DR EMBL: M20219; AAA66833.1; -.
 DR PIR: C31169; W1WLB2.
 DR InterPro: IPR001177; Papillom_E1.
 DR Pfam: PF00519; El_1.
 DR Pfam: PF00524; El_N; 1.
 KW Early protein; DNA replication; Helicase; ATP-binding; DNA-binding;
 FT Nuclear protein.
 RT NP_BIND 432 439 ATP (POTENTIAL).
 RL SEQUENCE 604 AA; 68077 MW; D2D7036ADE88A9DD CRC64;

Query Match 21.4%; Score 39; DB 1; Length 604;
 Best Local Similarity 33.3%; Pred. No. 26;
 Matches 7; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

Oy 22 CSFXXAXXIFKDXRRTKLEWI 42
 Db 172 CSFHDLTRLFKNDKTTNOQWV 192

RESULT 43
 VE1_BPv1 STANDARD: PRT; 605 AA.
 ID VE1_BPv1
 AC P03116; Q9WMH1;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Replication protein El.
 GN El.
 OS Bovine papillomavirus type 1.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10559;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=83012974; PubMed=6289124;
 RA Chen E.Y., Howley P.M., Levinson A.D., Seeburg P.H.;
 RT "The primary structure and genetic organization of the bovine
 RT papillomavirus type 1 genome.";
 RL Nature 299:529-534(1982).
 RN [2]
 RP REQUIREMENT FOR REPLICATION.
 RX MEDLINE=91122053; PubMed=1846806;
 RA Ustav M., Stenlung A.;
 RT "Transient replication of BPV-1 requires two viral polypeptides
 RT encoded by the E1 and E2 open reading frames.";
 RL EMBO J. 10:449-457(1991).
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE=93281701; PubMed=8389467;
 RA Yang L., Mohr I., Fouts E., Lim D.A., Nohalie M., Botchan M.;
 RT "The E1 protein of bovine papilloma virus 1 is an ATP-dependent DNA
 RT helicase.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:5086-5090(1993).
 CC -1 FUNCTION: ATP-DEPENDENT DNA HELICASE REQUIRED FOR INITIATION OF
 CC VIRAL DNA REPLICATION. IT FORMS A COMPLEX WITH THE VIRAL E2
 CC PROTEIN. THE E1-E2 COMPLEX BINDS TO THE REPLICATION ORIGIN WHICH
 CC CONTAINS BINDING SITES FOR BOTH PROTEINS.
 CC -1 SUBCELLULAR LOCATION: Nuclear.
 CC -----
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 CC -----
 DR EMBL: X02346; CAB46511.1; -.
 DR PIR: A03663; W1WLB.
 DR InterPro: IPR001177; Papillom_E1.
 DR Pfam: PF00519; El_1.
 DR Pfam: PF00524; El_N; 1.

KW Early protein: DNA replication; Helicase; ATP-binding; DNA-binding;
 KM Nuclear protein.
 FT NP_BIND 433 440 ATP (POTENTIAL).
 SQ SEQUENCE 605 AA; 68190 MW; C8400B78BF6060B CRC64;

Query Match 21.4%; Score 39; DB 1; Length 605;
 Best Local Similarity 33.3%; Pred. NO. 26;
 Matches 7; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 22 CSFXXAXXIFKDXRTKLEFWI 42
 111 :11: 1:
 Db 173 CSFHDITRLEFKNDKTTNQOWV 193

RESULT 44
 IF39_HUMAN
 ID IF39_HUMAN STANDARD; PRT; 814 AA.
 AC P55884;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Eukaryotic translation initiation factor 3 subunit 9 (eif-3 eta) (eif3 p16) (eif3 p110).
 GN EIF3S9.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eultheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98049567; PubMed=9388245;
 RA Chaudhuri J., Chakrabarti A., Maitra U.;
 RT Biochemical characterization of mammalian translation initiation factor 3 (eif3). Molecular cloning reveals that p10 subunit is the mammalian homologue of Saccharomyces cerevisiae protein Pti1.;
 RT J. Biol. Chem. 272:30975-30983(1997).
 RL [2]

RP SEQUENCE FROM N.A.
 RC Tissue=Neuroblastoma;
 RA Strausberg R.;
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: BINDS TO THE 40S RIBOSOME AND PROMOTES THE BINDING OF METHIONYL-TRNAI AND MRNA.
 CC -1- SUBUNIT: EIF-3 IS COMPOSED OF AT LEAST 10 DIFFERENT SUBUNITS.
 CC -1- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
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 CC -----
 DR EMBL: U78525; AAC99479.1; -;
 DR EMBL: BC001173; AAH01173.1; -;
 DR MIM: 603917; -;
 DR InterPro: IPR000504; RRM.
 DR Pfam: PF00076; rrm; 1.
 DR SMART: SMO0360; RRM; 1.
 DR PROSITE: PSS0102; RRM; 1.
 DR PROSITE: PSS00030; RRM_RNP_1; 1.
 DR Initiation factor; protein biosynthesis; RNA-binding.
 KM DOMAIN 185 268 RNA-BINDING (RRM).
 SQ SEQUENCE 814 AA; 92491 MW; 9ECSHC04687562C3 CRC64;

Query Match 21.4%; Score 39; DB 1; Length 814;
 Best Local Similarity 50.0%; Pred. NO. 35;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 30 IFKDXRTKLEFW 41

Db 309 IFESGRTSIFW 320

RESULT 45
 YN99_YEAST
 ID YN99_YEAST STANDARD; PRT; 1333 AA.
 AC P53756;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Probable ATP-dependent transporter YNR070W.
 GN YNR070W OR N3568.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Andre B., Traqui Houssein I., Urrestazu L.A., Vissers S.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP SEQUENCE OF 1-1054 FROM N.A.
 RA Duesterhoeft A., Floeth M., Fritz C., Heuss-Netzel D.,
 RA Hilbert H., Moestl D.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. PDR5 SUBFAMILY.
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 CC -----

DR EMBL: Z71685; CAA96352.1; -;
 DR EMBL: Z71686; CAA96354.1; -;
 DR SGD: S0005353; YNR070W.
 DR InterPro: IPR003593; AAA.
 DR InterPro: IPR003439; ABC_transporter.
 DR InterPro: IPR001687; ATP_GTP_A.
 DR Pfam: PF00005; ABC_tran; 2.
 DR SMART: SMO0382; AAA; 1.
 DR PROSITE: PSS0211; ABC_TRANSPORTER; 1.
 KM Hypothetical protein; ATP-binding; Transmembrane; Glycoprotein;
 KW Transport.

FT TRANSMEM 13 33 POTENTIAL.
 FT TRANSMEM 392 412 POTENTIAL.
 FT TRANSMEM 425 445 POTENTIAL.
 FT TRANSMEM 474 494 POTENTIAL.
 FT TRANSMEM 499 519 POTENTIAL.
 FT TRANSMEM 534 554 POTENTIAL.
 FT TRANSMEM 642 662 POTENTIAL.
 FT TRANSMEM 1071 1091 POTENTIAL.
 FT TRANSMEM 1092 1112 POTENTIAL.
 FT TRANSMEM 1150 1170 POTENTIAL.
 FT TRANSMEM 1178 1198 POTENTIAL.
 FT TRANSMEM 1210 1230 POTENTIAL.
 FT TRANSMEM 1235 1255 POTENTIAL.
 FT NP_BIND 765 772 POTENTIAL.
 FT CARBOHYD 48 48 N-LINKED (GLCNAC).
 FT CARBOHYD 144 144 N-LINKED (GLCNAC).
 FT CARBOHYD 205 205 N-LINKED (GLCNAC).
 FT CARBOHYD 350 350 N-LINKED (GLCNAC).
 FT CARBOHYD 697 697 N-LINKED (GLCNAC).
 FT CARBOHYD 733 733 N-LINKED (GLCNAC).
 FT CARBOHYD 958 958 N-LINKED (GLCNAC).
 FT CARBOHYD 1320 1320 N-LINKED (GLCNAC).
 SQ SEQUENCE 1333 AA; 149749 MW; 61B4758E0245CB70 CRC64;

OS Brachydanio rerio (zebrafish) (zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Keen T.J., Ingolearn C.F.;
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20525589; Pubmed-11071763;
 RA Chin A.J., Tsang M., Weinberg E.S.;
 RT "Heart and gut chiralities are controlled independently from initial
 RT heart position in the developing zebrafish.";
 RL Dev. Biol. 227:403-421(2000).
 CC -1- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CLAUDIN FAMILY.
 CC -----
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 CC -----
 DR EMBL; AJ011788; CAA09776.1; -;
 DR EMBL; AF260240; AAG24512.1; -;
 DR ZFIN; ZDB-GENE-001103-5; cldn7.
 DR InterPro; IPR001833; Claudin.
 DR InterPro; IPR004031; PMP22_Claudin.
 DR PRINTS; PR01077; CLAUDIN.
 DR PROSITE; PS01346; CLAUDIN.1.
 DR TIGHT JUNCTION: Transmembrane.
 KM TRANSMEM 8 28 POTENTIAL.
 FT TRANSMEM 82 102 POTENTIAL.
 FT TRANSMEM 118 138 POTENTIAL.
 FT TRANSMEM 163 183 POTENTIAL.
 SQ SEQUENCE 215 AA; 22865 MW; BC04870B75B8CB9D CRC64;
 OY 1 ANAFLLXLRKSGKXKXKXCS 23
 DB 170 AGAFLDIMGGMGLASSCSKGOSS 192
 Query Match 20.9%; Score 38; DB 1; Length 215;
 Best Local Similarity 39.1%; Pred. NO. 15;
 Matches 9; Conservative 1; Mismatches 13; Indels 0; Gaps 0;
 RESULT 48
 LXL1_PHOLE STANDARD; PRT; 354 AA.
 ID LXL1_PHOLE
 AC P09140;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alkanal monooxygenase alpha chain (EC 1.14.14.3) (Bacterial luciferase
 DE alpha chain).
 GN LUXA.
 OS Photobacterium leiognathi.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae;
 OC Photobacterium.
 OX NCBI_TaxID=658;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-554;
 RX MEDLINE-89041570; Pubmed-3186447;
 RA Iliarionov B.A., Protopopova M.V., Karginov V.A., Mertvelsov N.P.,
 RA Gltelson J.I.;

RT "Nucleotide sequence of part of Photobacterium leiognathi lux
 RT region.";
 RL Nucleic Acids Res. 16:9855-9855(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-554;
 RX MEDLINE-88251495; Pubmed-3382442;
 RA Iliarionov B.A., Protopopova M.V., Karginov V.A., Mertvelsov N.P.,
 RA Gltelson J.I.;
 RT "Nucleotide sequence of genes for alpha- and beta-subunits of
 RT luciferase from Photobacterium leiognathi.";
 RL Bioorg. Khim. 14:412-415(1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-554;
 RX MEDLINE-90185252; Pubmed-2311938;
 RA Iliarionov B.A., Bilnov V.M., Donchenko A.P., Protopopova M.V.,
 RA Karginov V.A., Mertvelsov N.P., Gltelson J.I.;
 RT "Isolation of bioluminescent functions from Photobacterium
 RT leiognathi: analysis of luxA, luxB, luxG and neighboring genes.";
 RL Gene 86:89-94(1990).
 CC -1- FUNCTION: LIGHT-EMITTING REACTION IN LUMINOUS BACTERIA.
 CC -1- CATALYTIC ACTIVITY: RCHO + FMN(2) + O(2) -> RCOOH + FMN + H(2)O +
 CC light.
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC -----
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 CC -----
 DR EMBL; X08036; CAA30831.1; -;
 DR PIR; S01697; S01697.
 DR PIR; JQ0413; JQ0413.
 DR PIR; S06369; S06369.
 DR HSP; P07740; IBRL.
 DR InterPro; IPR002103; Bac_Luciferase.
 DR Pfam; PF00296; bac_luciferase.1.
 DR PRINTS; PR00089; LUCIFERASE.
 DR PROSITE; PS00494; BACTERIAL_LUCIFERASE.1.
 KW Photoprotein; Luminescence; Oxidoreductase; Monooxygenase;
 KW Flavoprotein; FMN.
 FT DOMAIN 100 115 REGION OF ACTIVE CENTER-1 (BY
 FT DOMAIN SIMILARITY).
 FT DOMAIN 279 294 REGION OF ACTIVE CENTER-2 (BY
 FT DOMAIN SIMILARITY).
 SQ SEQUENCE 354 AA; 40370 MW; 569f6EB903C7B90 CRC64;
 OY 23 SFXXAXXIFKDXRTK 38
 DB 252 SYTNATNIFKDSNOTR 267
 Query Match 20.9%; Score 38; DB 1; Length 354;
 Best Local Similarity 43.8%; Pred. NO. 24;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 RESULT 49
 NCAP_IHNV STANDARD; PRT; 413 AA.
 ID NCAP_IHNV
 AC P19691;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-MAY-1992 (Rel. 22, Last annotation update)
 DE Nucleocapsid protein (Nucleoprotein).
 GN N.
 OS Infectious hematopoietic necrosis virus (strain Round Butte) (IHNV).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Rhabdoviridae; unclassified Rhabdoviridae.

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OM protein - protein search, using sw model

Run on: September 3, 2002, 15:15:27 : Search time 41.95 Seconds
(without alignments)
181.449 Million cell updates/sec

Title: US-09-302-239-3-COPY
Perfect score: 182
Sequence: 1 ANAFLLXLRGSLRXKCKXX.....XXAXXIFKDXRTKLFWISY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapect 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mbc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriophage:*
17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	157	86.3	701	4 Q96PQ8	Q96PQ8 homo sapien
2	112	61.5	446	11 Q61109	Q61109 mus musculu
3	98	53.8	460	11 Q91WN8	Q91WN8 mus musculu
4	93	51.1	218	4 Q14668	Q14668 homo sapien
5	92	50.5	460	11 Q99PC6	Q99PC6 mus musculu
6	91	50.0	456	6 Q9TTR0	Q9TTR0 canis famili
7	90	49.5	482	11 Q63207	Q63207 ratius norv
8	88	48.4	469	6 Q9GMD9	Q9GMD9 ornithorhyn
9	88	48.4	481	11 Q88947	Q88947 mus musculu
10	88	48.4	481	11 Q54740	Q54740 mus musculu
11	88	48.4	481	11 Q99132	Q99132 mus musculu
12	85	46.7	100	4 Q15253	Q15253 homo sapien
13	85	46.7	231	4 Q95BD7	Q95BD7 homo sapien
14	80	44.0	49	6 Q95ME8	Q95ME8 bos taurus
15	77	42.3	456	4 Q14316	Q14316 homo sapien
16	77	42.3	461	6 Q95ND7	Q95ND7 pan troglod

17	77	42.3	461	6 Q95ND6	Q95ND6 pan troglod
18	74	40.7	202	4 Q14669	Q14669 homo sapien
19	73	40.1	138	6 Q28994	Q28994 sus scrofa
20	70	38.5	433	13 Q90YK1	Q90YK1 brachydanio
21	68	37.4	226	4 Q9BZD6	Q9BZD6 homo sapien
22	63	34.6	98	13 P82807	P82807 notechis sc
23	63	34.6	608	13 Q9PTW7	Q9PTW7 struthio ca
24	63	34.6	648	6 Q29094	Q29094 sus scrofa
25	60	33.0	399	11 Q9COW3	Q9COW3 mus musculu
26	60	33.0	607	13 Q91001	Q91001 gallus gall
27	58	31.9	650	4 Q9NSD0	Q9NSD0 homo sapien
28	58	31.9	650	4 Q16519	Q16519 homo sapien
29	57.5	31.6	492	10 Q9SMW7	Q9SMW7 cicier ariet
30	56.5	31.0	196	10 Q04284	Q04284 selaginella
31	56.5	31.0	431	10 Q94EV5	Q94EV5 arabidopsis
32	56.5	31.0	543	10 Q9MB23	Q9MB23 arabidopsis
33	56.5	31.0	576	10 Q9C9U4	Q9C9U4 arabidopsis
34	56.5	31.0	589	10 Q9LMS2	Q9LMS2 arabidopsis
35	54.5	29.9	459	10 Q9SE22	Q9SE22 oryza sativ
36	53.5	29.4	506	10 Q9SPF0	Q9SPF0 oryza sativ
37	53.5	29.4	506	10 Q9SE23	Q9SE23 oryza sativ
38	53	28.1	25	11 Q9QVH6	Q9QVH6 rattus sp.
39	52.5	28.8	510	10 Q9MB22	Q9MB22 arabidopsis
40	52.5	28.8	619	10 Q9LV37	Q9LV37 arabidopsis
41	51.5	28.3	594	10 Q9SUG9	Q9SUG9 arabidopsis
42	51.5	28.3	603	10 Q9LPG7	Q9LPG7 arabidopsis
43	51.5	28.3	606	10 Q945F8	Q945F8 arabidopsis
44	50.5	27.7	575	10 Q94E17	Q94E17 oryza sativ
45	50.5	27.7	588	10 Q9LWC3	Q9LWC3 arabidopsis
46	50.5	27.7	593	10 Q9LUC3	Q9LUC3 arabidopsis
47	49.5	27.2	608	10 Q9XF36	Q9XF36 medicago sa
48	49	26.9	673	11 Q61592	Q61592 mus musculu
49	49	26.9	674	11 Q99K57	Q99K57 mus musculu
50	47	25.8	674	11 Q63772	Q63772 rattus sp.

ALIGNMENTS

RESULT	ID	Q96PQ8	PRELIMINARY:	PRT:	701 AA.
AC	Q96PQ8:	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)				
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE	FACTOR VII ACTIVE SITE MUTANT IMMUNOCONJUGATE.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=21477448; PubMed=11593034;				
RA	Hu Z., Garen A.;				
RT	"Targeting tissue factor on tumor vascular endothelial cells and tumor				
RT	cells for immunotherapy in mouse models of prostatic cancer.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).				
DR	EMBL; AF272774; AAK58686.1;				
SO	SEQUENCE 701 AA; 77826 MW; 94AC6CEBA2CC992F CRC64;				

Query Match 86.3%; Score 157; DB 4; Length 701;
Best Local Similarity 72.7%; Pred. No. 6.3e-21;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY	1 ANAFLLXLRGSLRXKCKXXCSEFXAXXIFKDXRTKLFWISY 44
DB	61 ANAFLELRPGSLERCKEQQCSFEPAELTFDAERTKLFWISY 104
RESULT	2 Q61109

```
ID 061109 PRELIMINARY: PRT: 446 AA.
AC 061109
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE COAGULATION FACTOR VII.
GN F7 OR FVII.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER.
RX MEDLINE=96276538; PubMed=8701412;
RA Idsogile E., Rosen E., Geng J.P., Carmeliet P., Collen D.,
RA Castellino F.J.;
RT "Characterization of a cDNA encoding murine coagulation factor VII.";
RL Thromb. Haemost. 75:481-487(1996).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL: U44795; AAC52570.1; -.
DR HSSP: P08709; IFAK.
DR MGD: MGI:109325; F7.
DR InterPro: IPR002086; Aldehyde_dehydr.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR001064; Crystallin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Trypsin.
DR InterPro: IPR002294; VitK_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; gla_1.
DR Pfam: PF00089; trypsin_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA_1.
DR SMART: SM00001; EGF_Like_1.
DR SMART: SM00069; GLA_1.
DR SMART: SM00020; TRYP_SPC_1.
DR PROSITE: PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR PROSITE: PS00022; EGF_L; UNKNOWN_1.
DR PROSITE: PS01187; EGF_CA_1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ SEQUENCE 446 AA; 50318 MW; 482FD09BEFDA6870 CRC64;

Query Match 61.5%; Score 112; DB 11; Length 446;
Best Local Similarity 54.5%; Pred. No. 1.2e-12;
Matches 24; Conservative 1; Mismatches 19; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRXGSLRXCKXXCSPFXAXXIFKDXARTKLFWISY 44
Db 42 ANSLLEELPGLSLRECKECCFEAEARIFKSPERTKQFWIYV 85

RESULT 3
ID 091WN8 PRELIMINARY: PRT: 460 AA.
AC 091WN8
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE SIMILAR TO PROTEIN C.
```

```
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER.
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC013896; AAH13896.1; -.
SQ SEQUENCE 460 AA; 51818 MW; 0117F26E68FCC274 CRC64;

Query Match 53.8%; Score 98; DB 11; Length 460;
Best Local Similarity 45.5%; Pred. No. 5.4e-10;
Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRXGSLRXCKXXCSPFXAXXIFKDXARTKLFWISY 44
Db 42 ANSFLEEMRPGSLRECKMEICDFEAEQIFQWVEDTLAFWIKY 85

RESULT 4
ID 014668 PRELIMINARY: PRT: 218 AA.
AC 014668
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE PROLINE-RICH GLA PROTEIN 1.
DE PRCP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97404347; PubMed=9256434;
RA Kulman J.D., Harris J.E., Haldeman B.A., Davie E.W.;
RT "Primary structure and tissue distribution of two novel proline-rich
RT gamma-carboxyglutamic acid proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997).
DR EMBL: AF009242; AAB67070.1; -.
DR HSSP: P00740; ICEH.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR002294; VitK_dep_GLA.
DR Pfam: PF00594; gla_1.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00069; GLA_1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
SQ SEQUENCE 218 AA; 24947 MW; 26538A61AB0AEB98 CRC64;

Query Match 51.1%; Score 93; DB 4; Length 218;
Best Local Similarity 38.6%; Pred. No. 2.1e-09;
Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRXGSLRXCKXXCSPFXAXXIFKDXARTKLFWISY 44
Db 21 ANGFEEELRGQNIERCKEERCCTFEAEARFENNEKTRKFWSTY 64

RESULT 5
ID 099PC6 PRELIMINARY: PRT: 460 AA.
AC 099PC6
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE ANTI-COAGULANT PROTEIN C.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```


OK NCBI_TaxID=10090;
RP [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL;
RA Korf I.;
RT "Complete sequence of UC72A01."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -! SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE TRYPSIN FAMILY.
DR EMBL: AF318182; AAK07918.1; -
DR HSSP: P04070; 1PCU.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Trypsin.
DR InterPro: IPR00294; VitK_dep_GLA.
DR Pfam: PF00089; trypsin_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00181; EGF_2.
DR SMART: SM00001; EGF_like; 2.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; tryp_spec; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_Ca; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KW Hydroxylation; Repeat; Serine protease.
KW SEQUENCE 460 AA; 51784 MW; 0293BC25E9D3ED16 CRC64;
SQ

Query Match 50.5%; Score 92; DB 11; Length 460;
Best Local Similarity 43.2%; Pred. No. 7.2e-09;
Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLRXKXKXCCSFXXAXIFKDAKRTKLFMISY 44
DB 42 ANSFLEMRPGSLERECMEICDLEAQEIFQNVDTLAFWKY 85

RESULT 6
O9TTR0 PRELIMINARY; PRT; 456 AA.
AC O9TTR0:
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE PROTEIN C PRECURSOR.
GN PROC.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Leeb T., Kopp T., Deppe A., Breen M., Mattis U., Brunberg L.,
RA Breig B.;
RT "Molecular characterization and chromosomal assignment of the canine
RT protein C gene."
RL Mann. Genome 10:135-139(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99371952; PubMed=10443005;
RA Leeb T., Pfeiffer I., Kopp T., Deppe A., Breig B.;
RT "Analysis of canine protein C gene polymorphisms."
RL Anim. Genet. 30:237-238(1999).

CC -! SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE TRYPSIN FAMILY.
CC EMBL: AJ001979; CA05126.1; -
DR HSSP: P04070; 1PCU.
DR MEROPS: S01.218; -;
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Trypsin.
DR InterPro: IPR00294; VitK_dep_GLA.
DR Pfam: PF00008; EGF; 2.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00089; trypsin_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00181; EGF; 2.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; tryp_spec; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_Ca; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KW Hydroxylation; Repeat; Serine protease; Signal.
FT SIGNAL 1 42
FT CHAIN 43 192 PROTEIN C LIGHT CHAIN.
FT CHAIN 193 194 PROTEIN C CONNECTING DIPEPTIDE.
FT CHAIN 195 456 PROTEIN C HEAVY CHAIN.
SQ SEQUENCE 456 AA; 50813 MW; 7AD3A8C1C34E59FF CRC64;
SQ

Query Match 50.0%; Score 91; DB 6; Length 456;
Best Local Similarity 40.9%; Pred. No. 1.1e-08;
Matches 18; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLRXKXKXCCSFXXAXIFKDAKRTKLFMISY 44
DB 43 ANSFLEMRPGSLERECMEICDLEAQEIFQNVDTLAFWKY 86

RESULT 7
O63207 PRELIMINARY; PRT; 482 AA.
AC O63207:
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE FACTOR X.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=96093366; PubMed=8578539;
RA Stanton C., Ross R.P., Hutson S., Wallin R.;
RT "Evidence for competition between vitamin K-dependent clotting factors
RT for intracellular processing by the vitamin K-dependent gamma-
RT carboxylase."
RL Thromb. Res. 80:63-73(1995).
CC -! SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE TRYPSIN FAMILY.
CC EMBL: X79807; CAAS6202.1; -
DR HSSP: P00742; 1XKA.
DR MEROPS: S01.216; -;
DR InterPro: IPR000152; Asx_hydroxyl.

Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRKSLXKCKXXCQSFXXAXXIFKDAKRTLEWISY 44
Db 41 ANSFEFEKKGKGLRECEMEICSYEEVREIFEDEKTEKWEYTKY 84

RESULT 12
Q15253 ID Q15253 PRELIMINARY; PRT; 100 AA.

AC Q15253;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE THROMBIN PRECURSOR (FRAGMENT).
GN F2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-87182874; Pubmed-3471151;
RX McGillivray R.T., Irwin D.M., Guineto E.R., Stone J.C.;
RT "Recombinant genetic approaches to functional mapping of thrombin.";
RL Ann. N. Y. Acad. Sci. 485:73-79(1986).
DR EMBL; M3031; AAA60220.1; -.
DR HSSP; P00735; 2PFI.
DR InterPro; IPR002383; GLA_blood.
DR Pfam; PF00594; gla: 1.
DR PRINTS; PR0001; GLABLOOD.
DR SMART; SM00069; GLA: 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
KW SIGNAL.
FT CHAIN 1 43 POTENTIAL.
FT NON_TER 44 >100 POTENTIAL.
SQ SEQUENCE 100 AA; 11302 MW; PD0E5D0174E1F6EE CRC64;

Query Match 46.7%; Score 85; DB 4; Length 100;
Best Local Similarity 36.4%; Pred. No. 3e-08;
Matches 16; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRKSLXKCKXXCQSFXXAXXIFKDAKRTLEWISY 44
Db 44 ANTFLEEVKRGKGLRECEMEICSYEEVREIFEDEKTEKWEYTKY 87

RESULT 13
Q9BZD7 ID Q9BZD7 PRELIMINARY; PRT; 231 AA.

AC Q9BZD7;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE TRANSEMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID PROTEIN 3 TMG3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPINAL CORD;
RX MEDLINE-21117044; Pubmed-11171957;
RA Kulman J.D., Harris J.E., Xie L., Davie E.W.;
RT "Identification of two novel transmembrane gamma-carboxyglutamic acid
RT proteins expressed broadly in fetal and adult tissues.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:1370-1375(2001).
DR EMBL; AF326350; AAK00955.1; -.
DR HSSP; P00740; ICFH.
DR InterPro; IPR002383; GLA_blood.

DR InterPro; IPR000294; VltK_dep-GLA.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA: 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
SQ SEQUENCE 231 AA; 25848 MW; 8A373E4848490D81 CRC64;

Query Match 46.7%; Score 85; DB 4; Length 231;
Best Local Similarity 36.4%; Pred. No. 7.3e-08;
Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRKSLXKCKXXCQSFXXAXXIFKDAKRTLEWISY 44
Db 20 ANFLEELRQGTIERECEMEICSYEEVREIFEDEKTEKWEYTKY 63

RESULT 14
Q95ME8 ID Q95ME8 PRELIMINARY; PRT; 49 AA.

AC Q95ME8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE COAGULATION FACTOR IX (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizlaria M.N., Amara E.J.;
RT "Partial sequence of bovine F9 coding gene.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF394598; AAK7556.1; -.
FT NON_TER 1 1
FT NON_TER 49 49
SQ SEQUENCE 49 AA; 6023 MW; D15C6DE9CCBA4A14 CRC64;

Query Match 44.0%; Score 80; DB 6; Length 49;
Best Local Similarity 41.2%; Pred. No. 1.3e-07;
Matches 14; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy 11 GSLXKCKXXCQSFXXAXXIFKDAKRTLEWISY 44
Db 15 GNLEBECKEKCQSFEEAREVEENKTEKTEPFKQY 48

RESULT 15
Q14316 ID Q14316 PRELIMINARY; PRT; 456 AA.

AC Q14316;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-AUG-1999 (TREMBLrel. 11, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE F9 (COAGULATION FACTOR IX (PLASMA THROMBOPLASTIC COMPONENT, CHRISTMAS
DE DISEASE, HAEMOPHILIA B)) (FACTOR IX).
GN F9 OR FACTOR IX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bird C.;
RN Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 3-19 FROM N.A.
RX MEDLINE-88327116; Pubmed-3416069;
RA Bettsma P.A., Bertina R.M., Ploos van Amstel J.K., Riemens A.,
RA Briet E.;
RT "The putative factor IX gene promoter in hemophilia B Leyden.";

RL Blood 72:1074-1076(1988).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 DR EMBL; AL033403; CAA21954.1; -.
 DR EMBL; X53008; CAB38245.2; -.
 DR HSSP; P00740; ICFH.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000742; EGF-2.
 DR InterPro: IPR001881; EGF-Ca.
 DR InterPro: IPR001438; EGF-II.
 DR InterPro: IPR002383; GLA blood.
 DR InterPro: IPR001254; Trypsin.
 DR InterPro: IPR000294; Vitk_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00594; gla; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00010; EGFBLOOD.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01186; EGF-2; 2.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
 KW Serine protease.
 SQ SEQUENCE 456 AA; 51149 MW; 54E20A1B3964E234 CRC64;

Query Match 42.3%; Score 77; DB 4; Length 456;
 Best Local Similarity 41.2%; Pred. No. 4.9e-06;
 Matches 14; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 11 GSLXRCKXXQCSFYXAXXIFRDAXRTKLFWISY 44
 ID 095ND7 PRELIMINARY; PRT; 461 AA.
 AC 095ND7.
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE COAGULATION FACTOR XI.
 GN F9.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
 DE NCBI_TaxID=9598;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=504;
 RC Saita Y.;
 RA "Comparison of DNA and protein polymorphisms between humans and
 RT chimpanzees.";
 RL Genes Genet. Syst. 0:0-0(2001).
 DR EMBL; AB062470; BAB58885.1; -.
 DR EMBL; AB062458; BAB58885.1; JOINED.
 DR EMBL; AB062460; BAB58885.1; JOINED.
 DR EMBL; AB062462; BAB58885.1; JOINED.
 DR EMBL; AB062464; BAB58885.1; JOINED.
 DR EMBL; AB062466; BAB58885.1; JOINED.
 DR EMBL; AB062468; BAB58885.1; JOINED.

SQ SEQUENCE 461 AA; 51764 MW; 30CF857C0F77F45 CRC64;

Query Match 42.3%; Score 77; DB 6; Length 461;
 Best Local Similarity 41.2%; Pred. No. 4.9e-06;
 Matches 14; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 11 GSLXRCKXXQCSFYXAXXIFRDAXRTKLFWISY 44
 ID 095ND6 PRELIMINARY; PRT; 461 AA.
 AC 095ND6.
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE COAGULATION FACTOR XI.
 GN F9.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
 DE NCBI_TaxID=9598;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=505;
 RC Saita Y.;
 RA "Comparison of DNA and protein polymorphisms between humans and
 RT chimpanzees.";
 RL Genes Genet. Syst. 0:0-0(2001).
 DR EMBL; AB062471; BAB58886.1; -.
 DR EMBL; AB062459; BAB58886.1; JOINED.
 DR EMBL; AB062461; BAB58886.1; JOINED.
 DR EMBL; AB062463; BAB58886.1; JOINED.
 DR EMBL; AB062465; BAB58886.1; JOINED.
 DR EMBL; AB062467; BAB58886.1; JOINED.
 DR EMBL; AB062469; BAB58886.1; JOINED.
 SQ SEQUENCE 461 AA; 51695 MW; 8F5A69A525DF65B5 CRC64;

Query Match 42.3%; Score 77; DB 6; Length 461;
 Best Local Similarity 41.2%; Pred. No. 4.9e-06;
 Matches 14; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 11 GSLXRCKXXQCSFYXAXXIFRDAXRTKLFWISY 44
 ID 014669 PRELIMINARY; PRT; 202 AA.
 AC 014669.
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PROLINE-RICH GLA PROTEIN 2.
 GN PRGP2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 DE NCBI_TaxID=9606;
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=97404347; PubMed=9256434;
 RX Kulman J.D., Harris J.E., Haldeman B.A., Davie E.W.;
 RT "Primary structure and tissue distribution of two novel proline-rich
 RT gamma-carboxyglutamic acid proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997).
 DR EMBL; AF009243; AAB67071.1; -.
 DR HSSP; P00740; ICFH.

Db 48 FLEMLKGNLEKLEECIEYEAFALESTARTPEEFMSKY 88

RESULT 24

ID Q29094 PRELIMINARY; PRT; 648 AA.

AC Q29094;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE PROTEIN S (FRAGMENT).

GN PROS.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=LIVER;

RX MEDLINE=95134217; PubMed=7832752;

RA Greenard J.S., Fernandez J.A., Radtke K.P., Griffin J.H.;

RT "Identification of candidate residues for interaction of protein S with C4b binding protein and activated protein C.";

RL Biochem. J. 305:397-403(1995).

DR EMBL: L31379; AAA70382.1; -.

DR HSP: P00740; ICFH.

DR InterPro: IPR000152; Asx_hydroxyl.

DR InterPro: IPR000561; EGF-like.

DR InterPro: IPR001881; EGF_Ca.

DR InterPro: IPR002383; GLA_blood.

DR InterPro: IPR001791; Laminin.G.

DR InterPro: IPR000294; Vltk_dep_GLA.

DR Pfam: PF00008; EGF_4.

DR Pfam: PF00594; gla; 1.

DR Pfam: PF00054; laminin.G; 1.

DR PRINTS: PR00001; GLABLOOD.

DR SMART: SM000179; EGF_CA; 3.

DR SMART: SM00001; EGF-like; 1.

DR SMART: SM00069; GLA; 1.

DR SMART: SM00282; LamG; 2.

DR PROSITE: PS00010; ASX_HYDROXYL; 4.

DR PROSITE: PS00022; EGF_1; UNKNOWN_1.

DR PROSITE: PS01186; EGF_2; 3.

DR PROSITE: PS01187; EGF_CA; 3.

DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.

DR Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.

KW NON_TER

FT SEQUENCE 648 AA; 71914 MW; 4BDF9AB13872136 CRC64;

SO

Query Match 34.6%; Score 63; DB 6; Length 648;

Best Local Similarity 31.8%; Pred. No. 0.003;

Matches 14; Conservative 9; Mismatches 21; Indels 0; Gaps 0;

Y 1 ANAFLLXLRGSLXKXKXXQCSFXAXXIFKDXARKLFWISY 44

Db 15 ANSLERKQGNLEKLEECIEYEAFALESTARTPEEFMSKY 58

RESULT 25

ID Q9COW3 PRELIMINARY; PRT; 399 AA.

AC Q9COW3;

DT 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE 1300015806RIK PROTEIN.

GN 1300015806RIK.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=STOMACH, AND LIVER;

RX MEDLINE=C57BL/6J; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arai K., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kiehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schiraldi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carrinci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,

RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohetsuki S.,

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPsin FAMILY

CC

DR EMBL: AK008619; BAB25912.1; -.

DR EMBL: AK005011; BAB23744.1; -.

DR HSP: P00740; ICFH.

DR MGD: MGI:1914151; 1300015806RIK.

DR InterPro: IPR000152; Asx_hydroxyl.

DR InterPro: IPR001314; Chymotrypsin.

DR InterPro: IPR000561; EGF-like.

DR InterPro: IPR000742; EGF_2.

DR InterPro: IPR001881; EGF_Ca.

DR InterPro: IPR002383; GLA_blood.

DR InterPro: IPR001254; Trypsin.

DR InterPro: IPR000294; Vltk_dep_GLA.

DR Pfam: PF00089; trypsin; 1.

DR PRINTS: PR00722; CHYMOTRYPSIN.

DR SMART: SM00011; GLABLOOD.

DR SMART: SM00179; EGF; 2.

DR SMART: SM00069; GLA; 1.

DR SMART: SM00020; TRYP_Spc; 1.

DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.

DR PROSITE: PS50240; TRYPSIN_DOM; 1.

KW Hydrolase; Serine protease.

SO

SEQUENCE 399 AA; 44304 MW; 4FC65C9598F27E03 CRC64;

Query Match 33.0%; Score 60; DB 11; Length 399;

Best Local Similarity 29.3%; Pred. No. 0.0067;

Matches 12; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

Y 4 FLXLLRGSLXKXKXXQCSFXAXXIFKDXARKLFWISY 44

Db 45 FLEEIFQGNLEKLEECIEYEAFALESTARTPEEFMSKY 85

RESULT 26

ID Q91001 PRELIMINARY; PRT; 607 AA.

AC Q91001;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE THROMBIN.

GN Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

OX NCBI_TaxID=9031;

RN [1]


```
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Banfield D.K.; Macgillivray R.T.;
RT "Partial characterization of vertebrate prothrombin cDNAs:
RT amplification and sequence analysis of the B chain of thrombin from
RT nine different species.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE-94223694; PubMed-7513365;
RA Banfield D.K., Irwin D.M., Walz D.A., Macgillivray R.T.;
RT "Evolution of prothrombin: isolation and characterization of the cDNAs
RT encoding chicken and haflish prothrombin.";
RL J. Mol. Evol. 38:177-187(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Banfield D.K.;
RT Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.
DR EMBL; M81391; AAA21619.1; -.
DR HSSP; P00734; 10VS.
DR MEROPS; S01.217; -.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR003966; Prothrombin.
DR InterPro: IPR001254; Trypsin.
DR InterPro: IPR000294; Vitk_dep_GLA.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00051; Kringle; 2.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00130; KR; 2.
DR SMART; SM00020; TRYP_SPE; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00021; KRINGLE_1; 2.
DR PROSITE; PS50070; KRINGLE_2; 2.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydrolase; Serine protease.
SQ SEQUENCE 607 AA; 69110 MW; 002F3606EA36270F CRC64;

Query Match 33.0%; Score 60; DB 13; Length 607;
Best Local Similarity 29.3%; Pred. No. 0.01;
Matches 12; Conservative 5; Mismatches 24; Indels 0; Gaps 0;

OY 4 FLXLLRSGSLRXKXKXCSFXAXXIFKDAKRTKLFWISY 44
DB 48 FLEEMIKGNLERBCLERTCNVEBAFALSTYDTDAFWAKY 88

RESULT 27
O9NSDO PRELIMINARY; PRT; 650 AA.
AC O9NSDO;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-DEC-2000 (TREMBLrel. 19, last annotation update)
DE PROTEIN S PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
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```
RC TISSUE=LIVER;
RA Wydro R., Cohen E., Dackowski W., Stenflo J., Lundwall A.,
RA Dahlback B.;
RT Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; X12892; CAA31383.1; -.
DR HSSP; P00740; 1CFH.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_CA.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001791; Laminin_G.
DR InterPro: IPR000294; Vitk_dep_GLA.
DR Pfam; PF00054; laminin_G; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 3.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00282; Lamg; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat;
KW SIGNAL.
FT SIGNAL 1 15 POTENTIAL.
FT CHAIN 16 650 POTENTIAL.
SQ SEQUENCE 650 AA; 72480 MW; C67345CEB8645174 CRC64;

Query Match 31.9%; Score 58; DB 4; Length 650;
Best Local Similarity 29.5%; Pred. No. 0.027;
Matches 13; Conservative 8; Mismatches 23; Indels 0; Gaps 0;

OY 1 ANAFLLXLRSGSLRXKXKXCSFXAXXIFKDAKRTKLFWISY 44
DB 16 ANSLLEETKQGNLERECIELCKKEARVFPENDPTDYFPKY 59

RESULT 28
O16519 PRELIMINARY; PRT; 650 AA.
ID O16519;
AC O16519;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE PROTEIN S PRECURSOR (FRAGMENT).
GN PROSL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-86313649; PubMed-2944113;
RA Lundwall A., Dackowski W., Cohen E., Shaffer M., Mahr A., Dahlback B.,
RA Stenflo J., Wydro R.;
RT "Isolation and sequence of the cDNA for human protein S, a regulator
RT of blood coagulation.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:6716-6720(1986).
DR EMBL; M14338; AAG60181.1; -.
DR HSSP; P00740; 1CFH.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_CA.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001791; Laminin_G.
DR InterPro: IPR000294; Vitk_dep_GLA.
DR Pfam; PF00008; EGF; 4.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00054; laminin_G; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 3.
DR SMART; SM00069; GLA; 1.
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DR SMART: SM00282; LamG; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS00011; G1U_CARBOXYLATION; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat;
KW Signal.
FT NON_TER 1 1
FT SIGNAL <1 15 POTENTIAL.
FT CHAIN 16 650 PROTEIN S.
SQ SEQUENCE 650 AA; 72462 MW; 9A8C04C503BF474 CRC64;

Query Match 31.9%; Score 58; DB 4; Length 650;
Best Local Similarity 29.5%; Pred. No. 0.027;
Matches 13; Conservative 8; Mismatches 23; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLXRCCKXXQCSFYXAXXIFKDXARTKLEWISY 44
DB 16 ANSLLEETKQGNLEKCEIEELCNKEAREVEFENDPETDYFYPKY 59

RESULT 29
Q9SMJ7 PRELIMINARY; PRT; 492 AA.

AC Q9SMJ7;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE MAP KINASE PROTEIN (FRAGMENT).
OS Cicer arietinum (Chickpea) (Garbanzo).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Ciceraceae; Cicer.
OX NCBI_TaxID=3827;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. CASTELLANA; TISSUE=ETIOLATED EPICOTYLS;
RA Doppio B., Esteban R., Labrador E.;
RT "A MAP kinase is expressed in chickpea epicotyls";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ275316; CAB61750.1; -.
DR HSSP; Q16539; IWFC.
DR InterPro; IPR000719; Euk_Pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Transferase.
FT NON_TER 1
SQ SEQUENCE 492 AA; 55638 MW; 8791EF3635A6811 CRC64;

Query Match 31.6%; Score 57.5; DB 10; Length 492;
Best Local Similarity 42.9%; Pred. No. 0.025;
Matches 12; Conservative 1; Mismatches 14; Indels 1; Gaps 1;

QY 17 CKXXQCSFYXAXXIFKDXARTKLEWISY 44
DB 51 CKLVKCDGFLARVAFNDA-PTSIWFTDY 77

RESULT 30
O04284 PRELIMINARY; PRT; 196 AA.

AC O04284;
DT 01-JUL-1997 (TREMblrel. 04, Created)
DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE MAP KINASE-LIKE PROTEIN (FRAGMENT).
SDHN-6R.
GN Selaginella lepidophylla.
OS Selaginella lepidophylla.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Lycopodiophyta; Isoetesida; Selaginellales; Selaginellaceae;

OC Selaginella.
OX NCBI_TaxID=59777;
RN [1]
RP SEQUENCE FROM N.A.
RA Choi D.-W., Close T.J., Iturriaga G.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U96716; AAB57843.1; -.
DR HSSP; P27703; IERK.
DR InterPro; IPR000719; Euk_Pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR PROSITE; PS01351; MAPK; UNKNOWN_1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Transferase.
FT NON_TER 196
SQ SEQUENCE 196 AA; 22852 MW; 11417FA4E31CF72D CRC64;

Query Match 31.0%; Score 56.5; DB 10; Length 196;
Best Local Similarity 34.1%; Pred. No. 0.014;
Matches 15; Conservative 2; Mismatches 14; Indels 13; Gaps 2;

QY 1 ANAFLLXLRGSLXRCCKXXQCSFYXAXXIFKDXARTKLEWISY 44
DB 150 ANAY-----CKLKICDFGLARVAFNDA-PTAIWFTDY 180

RESULT 31
Q94EY5 PRELIMINARY; PRT; 431 AA.

AC Q94EY5;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE PUTATIVE MAP KINASE.
GN F25P22.9.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Lam B., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Barch J., Carlincl P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kanlaya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinzaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF387019; AK62464.1; -.
KW Kinase.
SQ SEQUENCE 431 AA; 49425 MW; 471AAF18FD524C4 CRC64;

Query Match 31.0%; Score 56.5; DB 10; Length 431;
Best Local Similarity 34.8%; Pred. No. 0.033;
Matches 16; Conservative 4; Mismatches 23; Indels 3; Gaps 2;

QY 1 ANAFLLXLRGSL--XRXCKXXQCSFYXAXXIFKDXARTKLEWISY 44
DB 210 ANVEHRLDKPKNLIANADCKLKICDFGLARVAFNDA-PTAIWFTDY 254

RESULT 32
Q9MB23 PRELIMINARY; PRT; 543 AA.

AC Q9MB23;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE ATP8.

OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA.
 RA Mizoguchi T., Ichimura K., Shinozaki K.,
 RT "Arabidopsis thaliana mRNA for MAP kinase."
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB038693; BAA92222.1; -
 DR HSSP: P24941; 1HCL.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003527; MAP_kin.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PS01351; MAPK; UNKNOWN_1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR ATP-binding; Transferase.
 KW SEQUENCE 543 AA; 61513 MW; 60D508FFD40A94E9 CRC64;

Query Match 31.0%; Score 56.5; DB 10; Length 543;
 Best Local Similarity 34.8%; Pred. No. 0.042; Indels 3; Gaps 2;
 Matches 16; Conservative 4; Mismatches 23;

OY 1 ANAFXXLRKXSL--XRCKXXQCSFXXXIFKDXRTKLFWSY 44
 || | : : : || | | | | | | : | | |
 DB 224 ANVFHRLKPKNIILNADCKLKICDGLARVSFND-PTAIRWTDY 268

RESULT 33
 O9C9U4 PRELIMINARY: PRT: 576 AA.
 AC O9C9U4.
 DT 01-JUN-2001 (TRMBLrel. 17, Created)
 DT 01-JUN-2001 (TRMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TRMBLrel. 19, Last annotation update)
 DE PUTATIVE MAP KINASE.
 GN F25P22.9.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RL MEDLINE=21016719; PubMed=1130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Altarfi H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Cressy T.H., Dewar K.,
 RA Dunn P., Elgu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultzer L.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremetska I., Kurtz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
 RA Miltischer J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
 RA Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venner J.C., Davis R.W.,
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 thaliana."
 RL Nature 408:816-820(2000).
 DR EMBL: AC012679; AAG52072.1; -
 DR HSSP: P24941; 1HCL.

DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00220; S_TKC; 1.
 DR SMART: SM00219; Tyrc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR ATP-binding; Kinase; Transferase.
 KW SEQUENCE 576 AA; 65250 MW; FAF429EAF3CF4EE7 CRC64;

Query Match 31.0%; Score 56.5; DB 10; Length 576;
 Best Local Similarity 34.8%; Pred. No. 0.045; Indels 3; Gaps 2;
 Matches 16; Conservative 4; Mismatches 23;

OY 1 ANAFXXLRKXSL--XRCKXXQCSFXXXIFKDXRTKLFWSY 44
 || | : : : || | | | | | | : | | |
 DB 210 ANVFHRLKPKNIILNADCKLKICDGLARVSFND-PTAIRWTDY 254

RESULT 34
 O9LMS2 PRELIMINARY: PRT: 589 AA.
 AC O9LMS2.
 DT 01-OCT-2000 (TRMBLrel. 15, Created)
 DT 01-OCT-2000 (TRMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TRMBLrel. 19, Last annotation update)
 DE T10F20.15 PROTEIN (PUTATIVE ATPK8 PROTEIN).
 GN T10F20.15.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RA Sakano H., Liu S.X., Elgu P., Lee J.M., Lenz C., Pham P., Toriumi M.,
 RA Yu G., Chan A., Chung M., Goldsmith A., Liu A., Smith A., Vaysberg M.,
 RA Altarfi H., Brooks S., Buehler E., Chao Q., Conn L., Conway A.B.,
 RA Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M.,
 RA Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W., Ecker J.R.,
 RA Federspiel N.A., Theologis A.,
 RT "The sequence of BAC T10F20 from Arabidopsis thaliana chromosome 1,"
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Pham P.K., Banh J., Dale J.M., Goldsmith A.D.,
 RA Jiang P.X., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M.,
 RA Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,
 RA Hayashizaki Y., Ishida J., Jones T., Kamita A., Karlin-Neumann G.,
 RA Kawai J., Kim C., Koeseema E., Lam B., Lin J., Meyers M.C., Miranda M.,
 RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Sarou M., Seki M.,
 RA Shinn P., Southwick A., Tracy S.E., Shinzaki K., Davis R.W.,
 RA Ecker J.R., Theologis A.,
 RT "Full length cDNA of gene T10F20.15 (GI:9719729)."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC034107; AAF97831.1; -
 DR EMBL: AY045931; AAK76605.1; -
 DR HSSP: P24941; 1HCL.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003527; MAP_kin.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PS01351; MAPK; UNKNOWN_1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW ATP-binding; Transferase.
 SEQUENCE 589 AA; 66231 MW; 96769BA5E164BD74 CRC64;

Query Match 31.0%; Score 56.5; DB 10; Length 589;
Best Local Similarity 34.8%; Pred. No. 0.046;
Matches 16; Conservative 4; Mismatches 23; Indels 3; Gaps 2;

QY 1 ANAFLXLRKGSU--XRXCKXXQCSFXAXXIFKDAKRTKLFWISY 44
DB 224 ANVFHRDLKPKNLIANSCKLKICDFGLARVSFMDA-PTAIFWTDY 268
|| | : : : || | | | | : || |
|| | : : : || | | | | : || |

RESULT 35
Q9SE22 PRELIMINARY; PRT; 459 AA.
AC Q9SE22;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE MAP KINASE HOMOLOG.
GN MAPK2.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Euphorbiaceae; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Euphorbiaceae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Cheong Y.H., Moon B.C., Kim J.K., Cho M.J.;
RT "Novel plant MAP kinases phosphorylate defense-related transcription factors.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF194416; AAF23903.1; -
DR HSSP: P24941; IHCL.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS01351; MAPK; UNKNOWN_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR ATP-binding; Kinase; Transferase.
SQ SEQUENCE 459 AA; 53308 MW; E4B944437373057F CRC64;

Query Match 29.9%; Score 54.5; DB 10; Length 459;
Best Local Similarity 32.6%; Pred. No. 0.084;
Matches 15; Conservative 5; Mismatches 23; Indels 3; Gaps 2;

QY 1 ANAFLXLRKGSU--XRXCKXXQCSFXAXXIFKDAKRTKLFWISY 44
DB 133 ANVFHRDLKPKNLIANSCKLKICDFGLARVSFMDA-PTAIFWTDY 177
|| | : : : || | | | | : || |
|| | : : : || | | | | : || |

RESULT 36
Q9SPF0 PRELIMINARY; PRT; 506 AA.
AC Q9SPF0;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE BLAST AND WOUNDING INDUCED MITOGEN-ACTIVATED PROTEIN KINASE.
GN BMK1.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Euphorbiaceae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-20089141; PubMed-10624015;
RA He C., Fong S.H., Yang D., Wang G.L.;
RT "BMK1, a novel MAP kinase induced by fungal infection and mechanical wounding in rice.";
RL Mol. Plant Microbe Interact. 12:1064-1073(1999).

DR EMBL: AF177392; AAD52659.1; -
DR HSSP: P24941; IHCL.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS01351; MAPK; UNKNOWN_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR ATP-binding; Kinase; Transferase.
SQ SEQUENCE 506 AA; 57955 MW; 0CB538FDEB171F0B CRC64;

Query Match 29.4%; Score 53.5; DB 10; Length 506;
Best Local Similarity 32.6%; Pred. No. 0.14;
Matches 15; Conservative 5; Mismatches 23; Indels 3; Gaps 2;

QY 1 ANAFLXLRKGSU--XRXCKXXQCSFXAXXIFKDAKRTKLFWISY 44
DB 133 ANVFHRDLKPKNLIANSCKLKICDFGLARVSFMDA-PSAIFWTDY 177
|| | : : : || | | | | : || |
|| | : : : || | | | | : || |

RESULT 37
Q9SE23 PRELIMINARY; PRT; 506 AA.
AC Q9SE23;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE MAP KINASE HOMOLOG.
GN MAPK1.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Euphorbiaceae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Cheong Y.H., Moon B.C., Kim J.K., Cho M.J.;
RT "Novel plant MAP kinases phosphorylate defense-related transcription factors.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF194415; AAF23902.1; -
DR HSSP: P24941; IHCL.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS01351; MAPK; UNKNOWN_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR ATP-binding; Kinase; Transferase.
SQ SEQUENCE 506 AA; 57945 MW; B05509010B2673C4 CRC64;

Query Match 29.4%; Score 53.5; DB 10; Length 506;
Best Local Similarity 32.6%; Pred. No. 0.14;
Matches 15; Conservative 5; Mismatches 23; Indels 3; Gaps 2;

QY 1 ANAFLXLRKGSU--XRXCKXXQCSFXAXXIFKDAKRTKLFWISY 44
DB 133 ANVFHRDLKPKNLIANSCKLKICDFGLARVSFMDA-PSAIFWTDY 177
|| | : : : || | | | | : || |
|| | : : : || | | | | : || |

RESULT 38
Q9QVH6 PRELIMINARY; PRT; 25 AA.
AC Q9QVH6;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)

DE FACTOR X LIGHT CHAIN.
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10118;
 RN [1]
 RP MEDLINE=92041742; PubMed=1718949;
 RX Enjuoji K., Miyazaki K., Kato H.;
 RT "Characterization of rat factors X and Xa: demonstration of factor Xa
 in rat plasma.";
 RL J. Biochem. 109:890-898(1991).
 DR HSSP: P00740; ICFH.
 DR InterPro: IPR002383; GLA blood.
 DR PRINTS: PR00001; GLABLOOD.
 SQ SEQUENCE 25 AA; 2932 MW; 657A6E9B57BE56B CRC64;

Query Match 29.1%; Score 53; DB 11; Length 25;
 Best Local Similarity 45.8%; Pred. No. 0.0076;
 Matches 11; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

OY 1 ANAFLXXLRXGSL--XRCKXXQCSFXXXIIFKDXRTKLFWISY 44
 ||| : : : | | | | | : : ||
 DB 1 ANSFEEIKKGNLRECVXICSF 24

RESULT 39
 Q9MB22 PRELIMINARY; PRT; 510 AA.
 AC Q9MB22;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ATPK9.
 OS Arabidopsis thaliana (Mouse-ear cress).
 CC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxId=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA;
 RA Mizoguchi T., Ichimura K., Shinozaki K.;
 RT "Arabidopsis thaliana mRNA for MAP kinase.";
 RL Submitted (Feb-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AB038694; BAA92223.1; -.
 DR HSSP: P27703; IERK.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003527; MAP_kin.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS01351; MAPK; UNKNOWN_1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW ATP-binding; Transferase.
 SQ SEQUENCE 510 AA; 58440 MW; 496BFOF657F53C97 CRC64;

Query Match 28.8%; Score 52.5; DB 10; Length 510;
 Best Local Similarity 32.6%; Pred. No. 0.22;
 Matches 15; Conservative 5; Mismatches 23; Indels 3; Gaps 2;

OY 1 ANAFLXXLRXGSL--XRCKXXQCSFXXXIIFKDXRTKLFWISY 44
 ||| : : : | | | | | : : ||
 DB 143 ANVFHDLKPKNIILNSDCKLKICDFGLARVSFNDA-PSAIRFTDY 187

RESULT 40
 Q9LV37 PRELIMINARY; PRT; 619 AA.
 AC Q9LV37;
 Q9LV37;

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE MAP KINASE.
 OS Arabidopsis thaliana (Mouse-ear cress).
 CC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxId=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA;
 RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
 RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA;
 RX MEDLINE=20363099; PubMed=10907853;
 RA Nakamura Y.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
 TAG and BAC clones.";
 RT DNA Res. 7:217-221(2000).
 DR EMBL: AB020749; BAB02016.1; -.
 DR HSSP: P24941; IHCL.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003527; MAP_kin.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS01351; MAPK; UNKNOWN_1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW ATP-binding; Kinase; Transferase.
 SQ SEQUENCE 619 AA; 70770 MW; 9AB2B461058ED2DB CRC64;

Query Match 28.8%; Score 52.5; DB 10; Length 619;
 Best Local Similarity 32.6%; Pred. No. 0.28;
 Matches 15; Conservative 5; Mismatches 23; Indels 3; Gaps 2;

OY 1 ANAFLXXLRXGSL--XRCKXXQCSFXXXIIFKDXRTKLFWISY 44
 ||| : : : | | | | | : : ||
 DB 252 ANVFHDLKPKNIILNSDCKLKICDFGLARVSFNDA-PSAIRFTDY 296

RESULT 41
 Q9SJG9 PRELIMINARY; PRT; 594 AA.
 AC Q9SJG9;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PUTATIVE MAP KINASE.
 GN ATG42880.
 OS Arabidopsis thaliana (Mouse-ear cress).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxId=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldlyum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
 RA Cronin D.A., Shen M., Vanaken S.E., Umayam L., Talon L.J., Gill J.E.,
 RA Adams M.D., Carreira A.J., Cressy T.H., Goodman H.M., Somerville C.R.,
 RA Copenhaver G.P., Preuss D., Niernan W.C., White O., Eisen J.A.,
 RA Salzberg S.L., Fraser C.M., Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 thaliana.";

RL Nature 402:761-768(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, COLUMBIA;
 RA Lin X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC006931: AAD21721.1; -
 DR HSSP: P24941: 1838.
 DR InterPro: IPR000719: Euk_pkinase.
 DR InterPro: IPR003527: MAP_kin.
 DR InterPro: IPR002290: Ser_thr_pkinase.
 DR Pfam: PF00069: pkinase.1.
 DR SMART: SM00220: S_TKC.1.
 DR PROSITE: PS01351: MAPK; UNKNOWN_1.
 DR PROSITE: PS00107: PROTEIN_KINASE_ATP.1.
 DR PROSITE: PS50011: PROTEIN_KINASE_DOM.1.
 DR ATP-binding: Kinase; Transferase.
 SO SEQUENCE 594 AA; 67275 MW; AEC31D4F90EE871E CRC64;

Query Match 28.3%; Score 51.5; DB 10; Length 594;
 Best Local Similarity 39.3%; Pred. No. 0.41;
 Matches 11; Conservative 1; Mismatches 15; Indels 1; Gaps 1;

OY 17 CKXXQCSFXXAXIFKDXRKLFWISY 44
 DB 151 CKLVCFGLARVAFND-TPTTFWTDY 177

RESULT 42

O9LPG7

ID O9LPG7 PRELIMINARY; PRT; 603 AA.

AC O9LPG7; PRELIMINARY; PRT; 603 AA.
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-DEC-2001 (TREMblrel. 15, Last sequence update)
 DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE T3F20.17 PROTEIN (MAP KINASE ATPMK9, PUTATIVE).
 GN T3F20.17 OR F22G10.12.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, COLUMBIA;
 RA Lee J.M., Vaysberg M., Sakano H., Lenz C., Liu S.X., Pham P.,
 RA Toriumi M., Yu G., Chin C., Chlou J., Choi E., Chung M., Gonzalez A.,
 RA Howng B., Liu A., Altafi H., Brooks S., Buehler E., Chao Q., Conn L.,
 RA Conway A.B., Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B.,
 RA Miranda M., Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W.,
 RA Ecker J.R., Federspiel N.A., Theologis A.;
 RT "The sequence of BAC T3F20 from Arabidopsis thaliana chromosome 1.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, COLUMBIA;
 RC MEDLINE=21016719; Pubmed=11130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 RA Chung M., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
 RA Dunn P., Etyu P., Feildlyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultzer L.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
 RA Millschler J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 RA Sakano H., Salerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
 RA Uterback T., Van Aken S., Vaysberg M., Vysotskaya V.S., Walker M.,

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 thaliana.";
 RL Nature 408:816-820(2000).
 DR EMBL: AC018748: AAF78438.1; -
 DR EMBL: AC024260: AAG51978.1; -
 DR HSSP: P24941: 1HCL.
 DR InterPro: IPR000719: Euk_pkinase.
 DR InterPro: IPR003527: MAP_kin.
 DR InterPro: IPR002290: Ser_thr_pkinase.
 DR Pfam: PF00069: pkinase.1.
 DR SMART: SM00220: S_TKC.1.
 DR PROSITE: PS01351: MAPK; UNKNOWN_1.
 DR PROSITE: PS00107: PROTEIN_KINASE_ATP.1.
 DR PROSITE: PS50011: PROTEIN_KINASE_DOM.1.
 DR ATP-binding: Kinase; Transferase.
 SO SEQUENCE 603 AA; 67951 MW; DDFD955CC372489D CRC64;

Query Match 28.3%; Score 51.5; DB 10; Length 603;
 Best Local Similarity 39.3%; Pred. No. 0.41;
 Matches 11; Conservative 1; Mismatches 15; Indels 1; Gaps 1;

OY 17 CKXXQCSFXXAXIFKDXRKLFWISY 44
 DB 151 CKLVCFGLARVAFND-TPTTFWTDY 177

RESULT 43

O945L8

ID O945L8 PRELIMINARY; PRT; 606 AA.

AC O945L8; PRELIMINARY; PRT; 606 AA.
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE AT2G42860/F7D19.12.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
 RA Bowser L., Carlucci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
 RA Setou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RT "Arabidopsis cDNA clones.";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF412082: AAL06535.1; -
 SO SEQUENCE 606 AA; 68774 MW; F3634BDF6BD78A1 CRC64;

Query Match 28.3%; Score 51.5; DB 10; Length 606;
 Best Local Similarity 39.3%; Pred. No. 0.42;
 Matches 11; Conservative 1; Mismatches 15; Indels 1; Gaps 1;

OY 17 CKXXQCSFXXAXIFKDXRKLFWISY 44
 DB 163 CKLVCFGLARVAFND-TPTTFWTDY 189

RESULT 44

O94E17

ID O94E17 PRELIMINARY; PRT; 575 AA.

AC O94E17; PRELIMINARY; PRT; 575 AA.
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)


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RT protein kinase homolog.;
RL Mol. Plant Microbe Interact. 12:882-893(1999).
DR EMBL: AF129087; AAD28617.1; -.
DR HSSP: P27703; 1ERK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_Chr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS01351; MAPK; UNKNOWN_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR ATP-binding; kinase; transferase.
KW
SEQUENCE 608 AA; 68903 MW; E5FD3A74BD5A8E6 CRC64;

Query Match 27.2%; Score 49.5; DB 10; Length 608;
Best Local Similarity 39.3%; Pred. No. 0.99;
Matches 11; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

QY 17 CKXXQCSEFXAXXIFKDXARTKLEFWSY 44
Db 163 CLKAVCDGGLARVAFND-TPTTFMTDY 189

RESULT 48
061592
AC 061592; PRELIMINARY; PRT; 673 AA.
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GAS6 PROTEIN.
GN GAS6 OR GAS6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Manfioletti G., Brancolini C., Bordo D., Philipson L., Schneider C.;
RT "Growth-arrest is associated with a negative control element in the
RT Mol. Cell. Biol. 13:0-0(1993).
DR EMBL: X59846; CAA42507.1; -.
DR HSSP: P00740; ICFH.
DR MGD: MGI:95660; Gas6.
DR InterPro: IPR000152; ASX_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_CA.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001791; Laminln.G.
DR InterPro: IPR000294; Vitk_dep_GLA.
DR Pfam: PF00008; EGF; 4.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00594; laminln.G; 2.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 3.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00282; LamG; 2.
DR PROSITE: PS00010; ASX_HYDROXYL; 4.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 3.
DR PROSITE: PS01187; EGF_CA; 3.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
KW
SEQUENCE 673 AA; 74512 MW; 6A49B3F004F92815 CRC64;

Query Match 26.9%; Score 49; DB 11; Length 673;
Best Local Similarity 30.6%; Pred. No. 1.4;
Matches 11; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

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QY 9 RXGSLRXKXKXQCSEFXAXXIFKDXARTKLEFWSY 44
Db 54 KOGHLRECVCEVCSKEAREVFENDPETEYFPRY 89

RESULT 49
099K57
AC 099K57; PRELIMINARY; PRT; 674 AA.
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GROWTH ARREST SPECIFIC 6.
GN GAS6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC005444; AAH05444.1; -.
DR HSSP: P00740; ICFH.
DR MGD: MGI:95660; Gas6.
DR InterPro: IPR000152; ASX_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_CA.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001791; Laminln.G.
DR InterPro: IPR000294; Vitk_dep_GLA.
DR Pfam: PF00008; EGF; 4.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00594; laminln.G; 2.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00181; EGF; 4.
DR SMART: SM00179; EGF_CA; 4.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00282; LamG; 2.
DR PROSITE: PS00010; ASX_HYDROXYL; 4.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 3.
DR PROSITE: PS01187; EGF_CA; 3.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
KW
SEQUENCE 674 AA; 74609 MW; 7C41F7693903F401 CRC64;

Query Match 26.9%; Score 49; DB 11; Length 674;
Best Local Similarity 30.6%; Pred. No. 1.4;
Matches 11; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 9 RXGSLRXKXKXQCSEFXAXXIFKDXARTKLEFWSY 44
Db 54 KOGHLRECVCEVCSKEAREVFENDPETEYFPRY 89

RESULT 50
063772
AC 063772; PRELIMINARY; PRT; 674 AA.
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GROWTH POTENTIATING FACTOR PRECURSOR.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=95197586; Pubmed=7890695;

```


RA Nakano T., Higashino K., Kikuchi N., Kishino J., Nomura K., Fujita H.,
 RA Ohara O., Arita H.;
 RT "Vascular smooth muscle cell-derived Gla-containing growth-
 RT potentiating factor for Ca(2+) mobilizing growth factors.";
 RL J. Biol. Chem. 270:5702-5705(1995).
 DR EMBL; D42148; BAA07719.1; -.
 DR HSSP; P00740; ICFH.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001791; Laminin_G.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 4.
 DR Pfam; PF00594; gla; 1.
 DR Pfam; PF00054; laminin_G; 2.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 3.
 DR SMART; SM00001; EGF_like; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00282; LamG; 2.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS01187; EGF_CA; 3.
 DR PROSITE; PS00011; GLI_CARBOXYLATION; 1.
 KM Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat;
 KW Signal.
 FT SIGNAL 1 45
 FT CHAIN 46 674 GROWTH POTENTIATING FACTOR.
 SQ SEQUENCE 674 AA; 74637 MW; FBF8FB8664D6F2E CRC64;

Query Match 25.8%; Score 47; DB 11; Length 674;
 Best Local Similarity 30.6%; Pred. No. 3.3;
 Matches 11; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

OY 9 RKGSLKRXCKXXQCSFXAXXIFKDXRTKLEWISY 44
 DB 54 KQGHLEKCEVEYCKEAREVFNDEPTDYTPRY 89

Search completed: September 3, 2002, 15:21:13
 Job time: 346 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 3, 2002, 15:14:50 ; Search time 51.38 seconds
(without alignments)
95.120 Million cell updates/sec

Title: US-09-302-239-4-COPY

Perfect score: 181
Sequence: 1 ANGFLXLLKXGSLXKRCRX.....XXAXIFRNXXRTQFWSV 44

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%

Listing first 50 summaries

Database :
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2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
3: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
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22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
23: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	154	85.1	44	20 AAY18306
2	154	85.1	44	22 AAB36396
3	122	67.4	44	20 AAY18310
4	122	67.4	44	20 AAY18311
5	121	66.9	44	20 AAY18312
6	121	66.9	44	20 AAY18305
7	121	66.9	44	22 AAB36395
8	121	66.9	401	22 AAB84870
9	121	66.9	401	22 AAB84871
10	121	66.9	406	14 AAR35764
11	121	66.9	406	18 AAW14509

X 2 residues
10 & 28

12	121	66.9	406	18 AAW14510	Modified blood coa
13	121	66.9	406	22 AAM52171	Human FVII SEQ ID
14	121	66.9	406	22 AAM52172	Mammalian expresse
15	121	66.9	406	22 AAM52181	Human FVII mutant
16	121	66.9	406	22 AAM52182	Human FVII mutant
17	121	66.9	406	22 AAM52183	Human FVII mutant
18	121	66.9	406	22 AAM52184	Human FVII mutant
19	121	66.9	406	22 AAM52185	Human FVII mutant
20	121	66.9	406	22 AAM52186	Human FVII mutant
21	121	66.9	406	22 AAM52187	Human FVII mutant
22	121	66.9	406	22 AAB84866	Wild-type human b1
23	121	66.9	406	22 AAB84867	Mutant blood coagu
24	121	66.9	406	22 AAB84868	Mutant blood coagu
25	121	66.9	406	22 AAB84869	Mutant blood coagu
26	121	66.9	444	16 AAR64205	Factor VII - modif
27	121	66.9	444	19 AAW31687	Homo sapiens Ser34
28	121	66.9	444	21 AAB67967	Factor VII SEQ ID
29	121	66.9	444	22 AAB61992	Human Factor VII p
30	121	66.9	466	7 AAP60056	Factor VII peptide
31	121	66.9	466	14 AAR52562	Factor VIII. Homo
32	121	66.9	466	19 AAB69606	Human Factor VIIa.
33	120	66.3	44	20 AAY18302	Modified GLA domai
34	120	66.3	406	18 AAW14507	Modified blood coa
35	118	65.2	406	18 AAW14508	Modified blood coa
36	117	64.6	44	20 AAY18313	Modified GLA domai
37	117	64.6	406	18 AAW14511	Modified blood coa
38	107	59.1	41	16 AAW11904	Factor VII Gla reg
39	104	57.5	345	22 AAU02959	Angiotensin conver
40	104	57.5	406	18 AAW14506	Modified blood coa
41	99	54.7	231	22 AAM3243	Human polypeptide,
42	98	54.1	139	17 AAR95596	Factor x light cha
43	96	53.0	44	20 AAY18308	Modified GLA domai
44	95	52.5	44	20 AAY18304	Bovine protein C g
45	95	52.5	44	22 AAB36403	Bovine protein C g
46	94	51.9	453	7 AAP60057	Factor IX/Factor V
47	93	51.4	250	12 AAR13675	Factor X-IaCTI hybr
48	93	51.4	436	13 AAR22513	Truncated precursor
49	93	51.4	448	14 AAR35762	Factor X (X). Hom
50	93	51.4	448	14 AAR37402	Factor X. Homo sa

ALIGNMENTS

RESULT 1	
ID	AAV18306 standard; peptide; 44 AA.
NC	AAV18306;
XX	17-AUG-1999 (first entry)
DT	
XX	Bovine factor VII GLA domain.
DE	
XX	GLA domain; vitamin K-dependent protein; clotting disorder;
KW	therapy.
XX	
OS	Bos taurus.
XX	
FT	Key Location/Qualifiers
FT	Misc-difference 1..44 "Xaa" gamma-carboxylutamic acid, or glutamic acid"
FT	MO9920767-A1.
XX	
PN	29-APR-1999.
XX	
PD	20-OCT-1998;
XX	
PF	20-OCT-1998;
XX	
PR	23-OCT-1997;
XX	
PA	(MINU) UNIV MINNESOTA.

XX Nelsestuen GL;
XX WPI; 1999-288309/24.
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
XX PT acid domain, useful for treating clotting disorders
XX
XX Disclosure; Page 15; 86pp; English.
XX
XX This sequence is the factor VII GLA (gamma-carboxyglutamic acid)
XX domain. The invention relates to a vitamin K-dependent polypeptide
XX comprising a modified GLA domain containing an amino acid substitution
XX which enhances membrane binding of the modified polypeptide as compared
XX to the native polypeptide. The polypeptide is used to treat a clotting
XX disorder by decreasing or increasing clot formation. Modification of the
XX GLA domain results in a protein which has enhanced membrane binding
XX affinity as compared to the native protein.
XX
XX Sequence 44 AA;

Query Match 85.1%; Score 154; DB 20; Length 44;
Best Local Similarity 95.5%; Pred. No. 1.3e-19;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ANGFLXXLRGSLRXCRXXICSFXXAXXIFRNXXRTRGFWVS 44
DB 1 angflxxlrpslxxrcrxxlcsfxahxifrnxxrtgrfwvsy 44

RESULT 2

AAB36396
ID AAB36396 standard; peptide; 44 AA.

AC AAB36396;

DT 27-FEB-2001 (first entry)

DE Bovine factor VII gamma-carboxyglutamic acid domain SEQ ID NO:4.

XX Vitamin K-dependent protein; factor VII; protein C; GLA domain;

KW gamma-carboxyglutamic acid domain; factor IX; protein S; domain Z;

KM factor X; prothrombin; enhanced membrane binding affinity;

KW clot formation; thrombolytic; haemostatic; bleeding disorder;

KW thrombosis; clotting disorder; haemophilia A; haemophilia B;

KW liver disease.

XX Bos taurus.

OS WO200066753-A2.

PN 09-NOV-2000.

XX 28-APR-2000; 2000WO-US11416.

PF 29-APR-1999; 99US-0302239.

XX (MINU) UNIV MINNESOTA.

PA Nelsestuen GL;

XX WPI; 2001-007226/01.

XX Novel vitamin K-dependent polypeptide useful for treating clotting

XX disorders such as thrombosis and hemophilia, comprises modified

XX gamma-carboxy glutamic acid domain that enhances membrane binding

XX affinity

XX Disclosure; Page 12; 81pp; English.

XX The present invention describes a vitamin K-dependent polypeptide (I)

XX comprising a modified gamma-carboxy glutamic acid (GLA) domain having

CC at least one amino acid substitution, that enhances membrane binding
CC affinity and the activity of the polypeptide relative to a corresponding
CC native vitamin K-dependent polypeptide and inhibits clot formation.
CC (I) can have thrombolytic and haemostatic activities, and can be used
CC as an inhibitor of clot formation. (I) is useful for decreasing clot
CC formation in a mammal, a factor VII or factor IX containing a modified
CC GLA domain is useful for increasing clot formation and for treating a
CC bleeding disorder, including thrombosis and clotting disorders such as
CC haemophilia A, haemophilia B and liver disease. The present sequence
CC represents a wild type bovine factor VII GLA domain sequence, given in
CC the exemplification of the present invention.
XX
XX Sequence 44 AA;

Query Match 85.1%; Score 154; DB 22; Length 44;
Best Local Similarity 95.5%; Pred. No. 1.3e-19;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ANGFLXXLRGSLRXCRXXICSFXXAXXIFRNXXRTRGFWVS 44
DB 1 angflxxlrpslxxrcrxxlcsfxahxifrnxxrtgrfwvsy 44

RESULT 3

AAV18310
ID AAV18310 standard; peptide; 44 AA.

AC AAV18310;

DT 17-AUG-1999 (first entry)

DE Modified GLA domain of vitamin K-dependent protein.

XX GLA domain; mutein; vitamin K-dependent protein; clotting disorder;

KW therapy.

XX Homo sapiens.

OS Synthetic.

XX Key

FT Misc-difference 1..44

FT /note="Xaa- gamma-carboxyglutamic acid, or glutamic

FT acid"

XX WO9920767-A1.

PN 29-APR-1999.

XX 20-OCT-1998; 98WO-US22152.

PF 23-OCT-1997; 97US-0955636.

XX (MINU) UNIV MINNESOTA.

PA Nelsestuen GL;

XX WPI; 1999-288309/24.

XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic

XX PT acid domain, useful for treating clotting disorders

XX Disclosure; Page 80; 86pp; English.

XX This sequence represents a modified GLA (gamma-carboxyglutamic acid)

XX domain. The invention relates to a vitamin K-dependent polypeptide

XX comprising a modified GLA domain containing an amino acid substitution

XX which enhances membrane binding of the modified polypeptide as compared

XX to the native polypeptide. The polypeptide is used to treat a clotting

XX disorder by decreasing or increasing clot formation. Modification of the

XX GLA domain results in a protein which has enhanced membrane binding

XX affinity as compared to the native protein.


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XX OS Homo sapiens.
XX XX
XX XX Key Location/Qualifiers
XX FT MISC-difference 1..44
XX FT /note= "Xaa gamma-carboxyglutamic acid, or glutamic
XX FT acid"
XX PN WO9920767-A1.
XX PD 29-APR-1999.
XX PE 20-OCT-1998; 98WO-US22152.
XX PR 23-OCT-1997; 97US-0955636.
XX XX (MINU ) UNIV MINNESOTA.
XX PI Nelsestuen GL;
XX DR WPI: 1999-288309/24.
XX PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
XX PT acid domain, useful for treating clotting disorders
XX PS Disclosure; Page 15; 86pp; English.
XX XX
XX CC This sequence is the factor VII GLA (gamma-carboxyglutamic acid)
XX CC domain. The invention relates to a vitamin K-dependent polypeptide
XX CC comprising a modified GLA domain containing an amino acid substitution
XX CC which enhances membrane binding of the modified polypeptide as compared
XX CC to the native polypeptide. The polypeptide is used to treat a clotting
XX CC disorder by decreasing or increasing clot formation. Modification of the
XX CC GLA domain results in a protein which has enhanced membrane binding
XX CC affinity as compared to the native protein.
XX SO Sequence 44 AA;

Query Match 66.9%; Score 121; DB 20; Length 44;
Best Local Similarity 75.0%; Pred. No. 7,4e-14;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLRXRCXXLCSPFXAXXIFRNXXRTQEFWVS 44
Db ||||||| |||||||: |||||||: |||: |||: |||:
1 anaflxlrpslrxrcxxgcsfxarxrlfkdxrklfwlsy 44

RESULT 7
AAB36395
ID AAB36395 standard; peptide: 44 AA.
XX AC AAB36395;
XX XX
XX DT 27-FEB-2001 (first entry)
XX XX
XX DE Human factor VII gamma-carboxyglutamic acid domain SEQ ID NO:3.
XX XX
XX KW Vitamin K-dependent protein; factor VII; protein C; GLA domain;
XX KW gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
XX KW factor X; prothrombin; enhanced membrane binding affinity;
XX KW clot formation; thrombolytic; haemostatic; bleeding disorder;
XX KW thrombosis; clotting disorder; haemophilia A; haemophilia B;
XX KW liver disease.
XX XX
XX OS Homo sapiens.
XX PN WO200066753-A2.
XX XX
XX PD 09-NOV-2000.
XX PF 28-APR-2000; 2000WO-US11416.
XX XX
```

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PR 29-APR-1999; 99US-0302239.
XX XX
XX XX (MINU ) UNIV MINNESOTA.
XX PA
XX XX Nelsestuen GL;
XX PI
XX XX WPI: 2001-007226/01.
XX DR
XX PT Novel vitamin K-dependent polypeptide useful for treating clotting
XX PT disorders such as thrombosis and hemophilia, comprises modified
XX PT gamma-carboxy glutamic acid domain that enhances membrane binding
XX PT affinity
XX XX
XX PS Disclosure; Page 12; 81pp; English.
XX XX
XX CC The present invention describes a vitamin K-dependent polypeptide (I)
XX CC comprising a modified gamma-carboxy glutamic acid (GLA) domain having
XX CC at least one amino acid substitution, that enhances membrane binding
XX CC affinity and the activity of the polypeptide relative to a corresponding
XX CC native vitamin K-dependent polypeptide and inhibits clot formation.
XX CC (I) can have thrombolytic and haemostatic activities, and can be used
XX CC as an inhibitor of clot formation. (I) is useful for decreasing clot
XX CC formation in a mammal, a factor VII or factor IX containing a modified
XX CC GLA domain is useful for increasing clot formation and for treating a
XX CC bleeding disorder, including thrombosis and clotting disorders such as
XX CC haemophilia A, haemophilia B and liver disease. The present sequence
XX CC represents a wild type human factor VII GLA domain sequence, given in
XX CC the exemplification of the present invention.
XX SO Sequence 44 AA;

Query Match 66.9%; Score 121; DB 22; Length 44;
Best Local Similarity 75.0%; Pred. No. 7,4e-14;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLRXRCXXLCSPFXAXXIFRNXXRTQEFWVS 44
Db ||||||| |||||||: |||||||: |||: |||: |||:
1 anaflxlrpslrxrcxxgcsfxarxrlfkdxrklfwlsy 44

RESULT 8
AAB84870
ID AAB84870 standard; Protein; 401 AA.
XX AC AAB84870;
XX XX
XX DT 31-JUL-2001 (first entry)
XX XX
XX DE Mutant blood coagulant factor VII (FVII-31).
XX DE
XX KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
XX KW mutant; muteln.
XX XX
XX OS Homo sapiens.
XX OS Synthetic.
XX XX
XX FT Key Location/Qualifiers
XX FT MISC-difference 311..317
XX FT /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp
XX FT -Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"
XX PN JP2001061479-A.
XX XX
XX PD 13-MAR-2001.
XX XX
XX PF 24-AUG-1999; 99JP-0237610.
XX XX
XX PR 24-AUG-1999; 99JP-0237610.
XX XX
XX PA (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX XX
XX DR WPI: 2001-310677/33.
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DR N-PSDB; AAH19463.

XX Mutant of blood coagulant factor VII, used for substitution therapy in

PT the treatment of hemophilia -

XX

PS Claim 14; Page 20-21; 29pp; Japanese.

CC The present invention relates to mutants of blood coagulant factor VII

CC (FVII) or activated blood coagulant factor VII (FVIIa). The present

CC sequence is one such mutant FVII: VII-31. The mutants can be used as an

CC agent for the substitution therapy of haemophilia inhibitor patients.

XX

SQ Sequence 401 AA;

Query Match 66.9%; Score 121; DB 22; Length 401;

Best Local Similarity 52.3%; Pred. No. 6.2e-13;

Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

OY 1 ANGFLXLRXGSLXRCXRXLCSFXXAXXIFNNXXRTQFWWSY 44

Db 1 anafllelrpslreckeegcsfeareilfxdaerklfwlisy 44

RESULT 9

AAB84871

ID AAB84871 standard; Protein: 401 AA.

AC AAB84871;

XX

DT 31-JUL-2001 (first entry)

XX

DE Mutant blood coagulant factor VII (FVII-39).

XX

KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;

KW mutant; mutain.

XX

OS Homo sapiens.

OS Synthetic.

XX

XX Key Location/Qualifiers

FT MISC-difference 235..239

FT /note= "Wild-type Val-Pro-Gly-Thr-Thr substituted by

FT Asp-Arg-Lys-Thr-Leu"

FT MISC-difference 311..317

FT /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp

FT -Ser-Pro-Asn substituted by Gln-Ala-Ser-Tyr-Pro-Gly-Lys"

XX

PN JP2001061479-A.

XX

PD 13-MAR-2001.

XX

PE 24-AUG-1999; 99JP-0237610.

XX

PR 24-AUG-1999; 99JP-0237610.

XX

XX (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.

XX

DR WPI; 2001-310677/33.

DR N-PSDB; AAH19464.

XX

PT Mutant of blood coagulant factor VII, used for substitution therapy in

PT the treatment of hemophilia -

XX

PS Claim 16; Page 23-24; 29pp; Japanese.

XX

CC The present invention relates to mutants of blood coagulant factor VII

CC (FVII) or activated blood coagulant factor VII (FVIIa). The present

CC sequence is one such mutant FVII: VII-39. The mutants can be used as an

CC agent for the substitution therapy of haemophilia inhibitor patients.

XX

SQ Sequence 401 AA;

Query Match 66.9%; Score 121; DB 22; Length 401;

Best Local Similarity 52.3%; Pred. No. 6.2e-13;

Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

OY 1 ANGFLXLRXGSLXRCXRXLCSFXXAXXIFNNXXRTQFWWSY 44

Db 1 anafllelrpslreckeegcsfeareilfxdaerklfwlisy 44

RESULT 10

AAR35764

ID AAR35764 standard; protein: 406 AA.

AC AAR35764;

XX

DT 24-SEP-1993 (first entry)

XX

DE Factor VII (VII).

XX

KW PC; protein C; IX; Factor IX; X; Factor X; PT; prothrombin; VII;

KW Factor VII; CT; chymotrypsinogen; SP; serine protease; binding;

KW exosite; catalytic activity.

XX

OS Homo sapiens.

XX

XX Key Location/Qualifiers

FT Region 1..152

FT /note= "Factor VII light chain"

FT Region 153..406

FT /note= "Factor VII heavy chain"

FT Peptide 374..388

FT /note= "exosite 1"

FT Peptide 290..310

FT /note= "exosite 2"

FT Peptide 290..310

FT /note= "pref. PC polypeptide; claim 2, page 136"

FT Peptide 374..388

FT /note= "pref. PC polypeptide; claim 2, page 136"

FT Peptide 289..304

FT /note= "pref. PC polypeptide; claim 4, page 137"

FT Peptide 290..304

FT /note= "pref. PC polypeptide; claim 4, page 137"

FT Peptide 245..266

FT /note= "claim 9, page 138-139 describes an antibody

FT that reacts with Factor VII; fragments

FT 289-304, 290-304, 290-310, 374-388 and

FT 400-414 but not with fragment 245-266"

XX

PN WO9309804-A.

XX

PD 27-MAY-1993.

XX

PE 18-NOV-1992; 92WO-US10242.

XX

PR 18-NOV-1991; 91US-0793989.

XX

XX (SCRI) SCRIPPS RES INST.

XX

PA GriffIn JH, Masters RM;

XX

PI

XX WPI; 1993-182244/22.

DR

XX

PT Serine protease derived-polypeptide(s) and anti-peptide

PT antibodies - for inhibiting coagulation and assaying for the

PT presence of serine protease in fluid samples

XX

PS Disclosure; Page 133-135; 149pp; English.

XX

CC The PC polypeptides indicated in the features Table inhibit

CC coagulation (they prevent binding of serine protease to natural

CC substrates), esp. when admin. to give an intravascular blood

CC concn. of 0.1-100 (pref. 0.5-10) microm.

ID AAM52183 standard; Protein; 406 AA.
 AC AAM52183;
 XX
 DT 07-FEB-2002 (first entry)
 DE Human FVII mutant V253N.
 XX
 KW Factor VII; FVII; Factor VIIa; haemostatic; thrombolytic;
 KW cardiatic; hepatotropic; cerebroprotective; haemophilia; liver disease;
 KW myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;
 KW mutuin.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key
 FT Misc-difference 6 Location/Qualifiers
 FT /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxylutamic acid"
 FT
 FT Misc-difference 7
 FT /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxylutamic acid"
 FT
 FT Misc-difference 14
 FT /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxylutamic acid"
 FT
 FT Misc-difference 16
 FT /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxylutamic acid"
 FT
 FT Misc-difference 19
 FT /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxylutamic acid"
 FT
 FT Misc-difference 20
 FT /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxylutamic acid"
 FT
 FT Misc-difference 25
 FT /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxylutamic acid"
 FT
 FT Misc-difference 26
 FT /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxylutamic acid"
 FT
 FT Misc-difference 29
 FT /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxylutamic acid"
 FT
 FT Misc-difference 35
 FT /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxylutamic acid"
 FT
 FT Modified-site 52
 FT /note= "O-glycosylated"
 FT
 FT Modified-site 60
 FT /note= "O-glycosylated"
 FT
 FT Modified-site 145
 FT /note= "N-glycosylated"
 FT
 FT Cleavage-site 152..153
 FT /note= "proteolytic cleavage site converting FVII zymogen
 FT to an activated form, comprising two chains
 FT linked by a single disulphide bridge"
 FT
 FT Misc-difference 253
 FT /note= "Wild-type Val substituted by Asn"
 FT
 FT Modified-site 322
 FT /note= "N-glycosylated"
 FT
 XX
 PN WO200158935-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 12-FEB-2001; 2001WO-DK00094.
 XX
 PR 11-FEB-2000; 2000DK-0000218.
 PR 18-OCT-2000; 2000DK-0001558.
 XX
 PA (MAXY-) MAXYGEN APS.
 XX

PI Andersen KV, Pedersen AH, Bornaes C;
 XX
 DR WPI: 2001-581807/65.
 XX
 PT New conjugate, useful for treating Factor VIIa related diseases or
 PT disorders such as haemophilia, liver disease, myocardial infarction and
 PT deep-vein thrombosis, comprises non-polypeptide group covalently
 PT attached to polypeptide group -
 XX
 PS Example 3; Page -: 89pp; English.
 XX
 CC The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
 CC polypeptide conjugates, comprising at least one non-polypeptide group
 CC covalently attached to a polypeptide, where the amino acid sequence of
 CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
 CC least one amino acid residue containing an attachment group for the
 CC non-polypeptide group has been introduced or removed. The FVIIa
 CC conjugates have haemostatic, thrombolytic, cardiatic, hepatotropic and
 CC cerebroprotective activity and are useful for treating FVIIa/TF-related
 CC diseases or disorders such as haemophilia, liver disease, myocardial
 CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
 CC have increased functional in vivo half life and/or increased plasma half
 CC life, increased bioavailability and/or reduced sensitivity to proteolytic
 CC degradation. Consequently medical treatment using the conjugates has a
 CC number of advantages over currently available such as longer duration
 CC between injections. The present sequence is that of a human FVII mutant,
 CC having an addition in vivo glycosylation site and tested for its
 CC amidolytic activity.
 CC
 CC Note: The present sequence is not shown in the specification but is
 CC derived from the human wild-type FVII sequence shown in SEQ ID NO 1
 CC (AAM52171).
 XX
 SQ Sequence 406 AA;
 XX
 Query Match 66.9%; Score 121; DB 22; Length 406;
 Best Local Similarity 75.0%; Pred. No. 6.3e-13;
 Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 OY 1 ANGFLXLRGSLRXRCRXXCSPFXAXXIFRNXXRTQRFWVS 44
 II IIIII IIIIIII IIIII IIIII IIIII IIIII IIIII
 DB 1 anaflxxlrpgslrxrcxxgcsfxaxxifdxartkifwisy 44
 XX
 RESULT 18
 AAM52184
 ID AAM52184 standard; Protein; 406 AA.
 AC
 XX AAM52184;
 XX
 DT 07-FEB-2002 (first entry)
 XX
 DE Human FVII mutant R290N/A292T.
 XX
 KW Factor VII; FVII; Factor VIIa; haemostatic; thrombolytic;
 KW cardiatic; hepatotropic; cerebroprotective; haemophilia; liver disease;
 KW myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;
 KW mutuin.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key
 FT Misc-difference 6 Location/Qualifiers
 FT /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxylutamic acid"
 FT
 FT Misc-difference 7
 FT /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxylutamic acid"
 FT
 FT Misc-difference 14
 FT /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxylutamic acid"
 FT
 FT Misc-difference 16
 FT /note= "OTHER = gamma carboxylutamic acid"
 FT


```

FT      /note= "N-glycosylated"
FT      152..153
FT      Cleaveage-site
FT      /note= "proteolytic cleavage site converting FVII zymogen
FT      to an activated form, comprising two chains
FT      linked by a single disulphide bridge"
FT      Misc-difference 291
FT      /note= "Wild-type Gly substituted by Asn"
FT      Modified-site
FT      322
FT      /note= "N-glycosylated"
FT      XX
FT      W0200158935-A2.
FT      XX
FT      16-AUG-2001.
FT      XX
FT      12-FEB-2001; 2001WO-DK00094.
FT      XX
FT      11-FEB-2000; 2000DK-0000218.
FT      18-OCT-2000; 2000DK-0001558.
FT      XX
FT      (MAXY-) MAXYGEN APS.
FT      XX
FT      PI      Andersen KV, Pedersen AH, Bornaes C;
FT      DR      WPI; 2001-581807/65.
FT      XX
FT      New conjugate, useful for treating Factor VIIa related diseases or
FT      disorders such as haemophilia, liver disease, myocardial infarction and
FT      deep-vein thrombosis, comprises non-polypeptide group covalently
FT      attached to polypeptide group -
FT      XX
FT      XX
FT      Example 3; Page -: 89pp; English.
FT      XX
CC      The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
CC      polypeptide conjugates, comprising at least one non-polypeptide group
CC      covalently attached to a polypeptide, where the amino acid sequence of
CC      polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
CC      least one amino acid residue containing an attachment group for the
CC      non-polypeptide group has been introduced or removed. The FVIIa
CC      conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and
CC      cerebroprotective activity and are useful for treating FVIIa/TF-related
CC      diseases or disorders such as haemophilia, liver disease, myocardial
CC      infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
CC      have increased functional in vivo half life and/or increased plasma half
CC      life, increased bioavailability and/or reduced sensitivity to proteolytic
CC      degradation. Consequently medical treatment using the conjugates has a
CC      number of advantages over currently available such as longer duration
CC      between injections. The present sequence is that of a human FVII mutant,
CC      having an addition in vivo glycosylation site and tested for its
CC      amidolytic activity.
CC      Note: The present sequence is not shown in the specification but is
CC      derived from the human wild-type FVII sequence shown in SEQ ID NO 1
CC      (AAM52171).
CC      XX
SQ      Sequence 406 AA:

```

```

Query Match 66.9%, Score 121, DB 22, Length 406;
Best Local Similarity 75.0%; Pred. No. 6.3e-13;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

```

```

OY      1 ANGFLXLRGSLRXCRXXLCSEFXAXXIFPNXXRTQFWWSY 44
      ||||||| ||||||| ||||||| |||: |||: |||: |||: |||:
DB      1 anaflxlrpslrxcrxxqscixarxrlfkdxrflklwlsy 44

```

```

RESULT 20
AAM52186
ID      AAM52186 standard; Protein: 406 AA.
XX
XX      AAM52186:
XX
XX      07-FEB-2002 (first entry)
XX

```

```

DE      Human FVII mutant R315N/V317T.
XX      Factor VII: FVII; Factor VIIa: FVIIa; haemostatic; thrombolytic;
XX      cardiant; hepatotrophic; cerebroprotective; haemophilia; liver disease;
XX      myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;
XX      mutein.
XX      Homo sapiens.
XX      OS
XX      Synthetic.
XX
FH      Location/Qualifiers
FT      Misc-difference 6
FT      /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      Misc-difference 7
FT      /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      Misc-difference 14
FT      /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      Misc-difference 16
FT      /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      Misc-difference 19
FT      /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      Misc-difference 20
FT      /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      Misc-difference 25
FT      /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      Misc-difference 26
FT      /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      Misc-difference 29
FT      /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      Misc-difference 35
FT      /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      Modified-site
FT      52
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      Modified-site
FT      60
FT      /note= "O-glycosylated"
FT      Modified-site
FT      145
FT      /note= "O-glycosylated"
FT      Cleavage-site
FT      152..153
FT      /note= "proteolytic cleavage site converting FVII zymogen
FT      to an activated form, comprising two chains
FT      linked by a single disulphide bridge"
FT      Misc-difference 315
FT      /note= "Wild-type Arg substituted by Asn"
FT      Misc-difference 317
FT      /note= "Wild-type Val substituted by Thr"
FT      Modified-site
FT      322
FT      /note= "N-glycosylated"
FT      W0200158935-A2.
FT      XX
FT      16-AUG-2001.
FT      XX
FT      12-FEB-2001; 2001WO-DK00094.
FT      XX
FT      11-FEB-2000; 2000DK-0000218.
FT      18-OCT-2000; 2000DK-0001558.
FT      XX
FT      (MAXY-) MAXYGEN APS.
FT      XX
FT      Andersen KV, Pedersen AH, Bornaes C;
FT      PI      WPI; 2001-581807/65.
FT      DR
FT      XX

```


CC amidolytic activity.

CC Note: The present sequence is not shown in the specification but is
CC derived from the human wild-type FVII sequence shown in SEQ ID NO 1
CC (AAM52171).

SQ Sequence 406 AA;

Query Match 66.9%; Score 121; DB 22; Length 406;
Best Local Similarity 75.0%; Pred. No. 6.3e-13;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;Qy 1 ANGFLXLRXGSLRXRCRXXCXFXAXXIFRNXXRTROFWVS 44
Db 1 anaflexlrpslrxrcxkxgcsfxaxrxifkdxartklfwisy 44

RESULT 22

AAB84866 ID AAB84866 standard; Protein: 406 AA.

AC AAB84866;

DT 31-JUL-2001 (first entry)

DE Wild-type human blood coagulant factor VII (FVII).

KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Disulfide-bond 159..164

XX JP2001061479-A.

XX 13-MAR-2001.

XX PF 24-AUG-1999; 99JP-0237610.

XX PR 24-AUG-1999; 99JP-0237610.

PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.

XX WPI: 2001-310677/33.

DR N-PSDB: AAH19459.

PT Mutant of blood coagulant factor VII, used for substitution therapy in
PT the treatment of hemophilia -

PS Disclosure; Page 8-9; 29pp; Japanese.

XX The present invention relates to mutants of blood coagulant factor VII
CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
CC sequence represents the protein sequence for wild-type human FVII. The
CC mutants can be used as an agent for the substitution therapy of
CC haemophilia inhibitor patients.

SQ Sequence 406 AA;

Query Match 66.9%; Score 121; DB 22; Length 406;
Best Local Similarity 52.3%; Pred. No. 6.3e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;Qy 1 ANGFLXLRXGSLRXRCRXXCXFXAXXIFRNXXRTROFWVS 44
Db 1 anaflexlrpslrxrcxkxgcsfxaxrxifkdxartklfwisy 44RESULT 23
AAB84867

ID AAB84867 standard; Protein: 406 AA.

XX AAB84867;

DT 31-JUL-2001 (first entry)

DE Mutant blood coagulant factor VII (FVII-5).

KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
KW mutant; mutlein.

OS Homo sapiens.

OS Synthetic.

FH Key Location/Qualifiers

FT Misc-difference 159 /note= "Wild-type Cys substituted by Ala"

FT Misc-difference 164 /note= "Wild-type Cys substituted by Ala"

XX JP2001061479-A.

XX 13-MAR-2001.

XX PF 24-AUG-1999; 99JP-0237610.

XX PR 24-AUG-1999; 99JP-0237610.

PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.

XX WPI: 2001-310677/33.

DR N-PSDB: AAH19460.

PT Mutant of blood coagulant factor VII, used for substitution therapy in
PT the treatment of hemophilia -

PS Claim 3; Page 11-12; 29pp; Japanese.

XX The present invention relates to mutants of blood coagulant factor VII
CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
CC sequence is one such mutant FVII: VII-5. In the wild-type protein
CC (AAB84866), there is a disulfide bond (159Cys-164Cys). In the present
CC protein, the disulfide bond is disrupted. The mutants can be used as an
CC agent for the substitution therapy of haemophilia inhibitor patients.

SQ Sequence 406 AA;

Query Match 66.9%; Score 121; DB 22; Length 406;
Best Local Similarity 52.3%; Pred. No. 6.3e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;Qy 1 ANGFLXLRXGSLRXRCRXXCXFXAXXIFRNXXRTROFWVS 44
Db 1 anaflexlrpslrxrcxkxgcsfxaxrxifkdxartklfwisy 44

RESULT 24

AAB84868 ID AAB84868 standard; Protein: 406 AA.

AC AAB84868;

DT 31-JUL-2001 (first entry)

DE Mutant blood coagulant factor VII (FVII-6).

KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
KW mutant; mutlein.

OS Homo sapiens.

OS Synthetic.

XX

```

FH Key Location/Qualifiers
FT MISC-difference 164
FT /note= "Wild-type Cys substituted by Ala"
FT MISC-difference 299
FT /note= "Wild-type Val substituted by Cys"
XX
XX JP2001061479-A.
XX
XX PD 13-MAR-2001.
XX
XX PF 24-AUG-1999; 99JP-0237610.
XX
XX PR 24-AUG-1999; 99JP-0237610.
XX
XX PA (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX
XX DR WPI: 2001-310677/33.
XX DR N-PSDB: AAH19461.
XX
XX PT Mutant of blood coagulant factor VII, used for substitution therapy in
XX the treatment of hemophilia -
XX
XX PS Claim 5; Page 14-15; 29pp; Japanese.
XX
XX CC The present invention relates to mutants of blood coagulant factor VII
XX (FVII) or activated blood coagulant factor VII (FVIIa). The present
XX sequence is one such mutant FVII: VII-6. In the wild-type protein
XX (AAB84866), there is a disulphide bond (159Cys-164Cys). In the present
XX protein, the disulphide bond is disrupted. The mutants can be used as an
XX agent for the substitution therapy of haemophilia inhibitor patients.
XX
XX SQ Sequence 406 AA;

Query Match 66.9%; Score 121; DB 22; Length 406;
Best Local Similarity 52.3%; Pred. No. 6.3e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRXGSLXRCRXKXLCSPFXAXXIFRNXXRTROFWVSY 44
   || || || || || || || || || || || || || || || ||
Db 1 anafllelrpslserckeegcfeearelfkdaerxklfwisy 44

RESULT 25
AAB84869
ID AAB84869 standard; Protein; 406 AA.
XX
XX AAB84869;
AC
XX 31-JUL-2001 (first entry)
XX
XX DE Mutant blood coagulant factor VII (FVII-30).
XX
XX KM Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
XX mutant; mutuin.
XX
XX OS Homo sapiens.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT MISC-difference 235.239
XX FT /note= "Wild-type Val-Pro-Gly-Thr substituted by
XX Asp-Arg-Lys-Thr-Leu"
XX
XX PN JP2001061479-A.
XX
XX PD 13-MAR-2001.
XX
XX PF 24-AUG-1999; 99JP-0237610.
XX
XX PR 24-AUG-1999; 99JP-0237610.
XX
XX PA (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.

```

```

XX
XX DR WPI: 2001-310677/33.
XX DR N-PSDB: AAH19462.
XX
XX PT Mutant of blood coagulant factor VII, used for substitution therapy in
XX the treatment of hemophilia -
XX
XX PS Claim 9; Page 17-18; 29pp; Japanese.
XX
XX CC The present invention relates to mutants of blood coagulant factor VII
XX (FVII) or activated blood coagulant factor VII (FVIIa). The present
XX sequence is one such mutant FVII: VII-30. The mutants can be used as an
XX agent for the substitution therapy of haemophilia inhibitor patients.
XX
XX SQ Sequence 406 AA;

Query Match 66.9%; Score 121; DB 22; Length 406;
Best Local Similarity 52.3%; Pred. No. 6.3e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRXGSLXRCRXKXLCSPFXAXXIFRNXXRTROFWVSY 44
   || || || || || || || || || || || || || || || ||
Db 1 anafllelrpslserckeegcfeearelfkdaerxklfwisy 44

RESULT 26
AAR64205
ID AAR64205 standard; Protein; 444 AA.
XX
XX AAR64205;
AC
XX 18-JUL-1995 (first entry)
XX
XX DE Factor VII - modified forms of this act as an anticoagulant.
XX
XX KW Factor VII; plasma glycoprotein; derivative; tissue factor; TF;
XX inhibition; vascular restenosis; platelet deposition; catalytic centre;
XX factor IX; factor X; inactivation; thrombosis; embolism; stroke; ss.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Active-site 193
XX FT /note= "forms a catalytic triad with Ser344 and Asp242"
XX FT Active-site 242
XX FT /note= "forms catalytic triad with Ser344 and His193"
XX FT Active-site 344
XX FT /note= "forms catalytic triad with Asp242 and His193"
XX FT Cleavage-site 152..153
XX FT /note= "internal cleavage site - cleavage activates
XX the zymogen into active 2-chain Factor VIIa"
XX
XX PN W09427631-A.
XX
XX PD 08-DEC-1994.
XX
XX PF 23-MAY-1994; 94WO-US05779.
XX
XX PR 21-MAY-1993; 93US-0065725.
XX
XX PA (NOVO ) NOVO-NORDISK AS.
XX PA (ZYMO ) ZYMOGENETICS INC.
XX
XX PI Berkner KL, Hart CE, Petersen LC;
XX
XX DR WPI: 1995-022464/03.
XX DR N-PSDB: AAO80296.
XX
XX PT Inhibition of tissue factor, vascular restenosis and platelet
XX deposition - using modifier factor VII unable to activate
XX factors IX and X, e.g. for treating thrombosis, embolism, stroke
XX etc..

```


PT post-ischemic reperfusion -
XX
XX Disclousure; Column 47-50; 34pp; English.
PS
XX The present invention describes a method for the inhibition or
CC minimisation of myocardial injury associated with post-ischaemic
CC reperfusion by administering factor VII, which has at least 1
CC modification in its catalytic triad (therefore inhibiting the ability
CC of factor VII to activate plasma factor X or IX). The method can be
CC used for inhibiting or minimising myocardial injury and for imparting
CC regional myocardial blood flow associated with post-ischaemic
CC reperfusion. It can also be used for inhibiting blood coagulation,
CC platelet deposition, thrombus formation and maintaining or improving
CC vascular potency. Factor VII can be administered at relatively low
CC doses and does not produce undesirable side effects. Further it acts
CC specifically at sites of injury. The present sequence represents
CC Factor VII.
XX
SQ Sequence 444 AA;

Query Match 66.9%; Score 121; DB 21; Length 444;
Best Local Similarity 52.3%; Pred. No. 6.8e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRXGSLRXCRXXLCSEFXXAXIFRNXXRTQFVSVY 44
Db 39 anafllelrpyslereckeqscfeearelfkdaerklfwisy 82

RESULT 29
AAB61992 standard; Protein: 444 AA.
ID AAB61992
XX
AC AAB61992;
XX
DT 14-MAY-2001 (first entry)
XX
DE Human Factor VII polypeptide.
XX
KW Factor VIIa; Thrombus; vascular patency; blood coagulation; Factor X;
KM plasma factor; Factor IX; myocardial injury; human; Factor VII.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..38
FT /note= "signal peptide"
FT Protein 39..444
FT /note= "mature peptide"
FT Misc-difference 10
FT /note= "indicated incorrectly as Trp under sequence
FT listing ID 2"
XX
XX US6183743-B1.
XX
XX 06-FEB-2001.
XX
XX 20-AUG-1999; 99US-0378907.
XX
XX 06-JUN-1997; 97US-0871003.
PR 28-FEB-1991; 91US-0862920.
PR 28-FEB-1992; 92WO-US01636.
PR 21-MAY-1993; 93US-0065725.
PR 23-MAY-1994; 94WO-US05779.
PR 24-OCT-1994; 94US-0327690.
PR 07-JUN-1995; 95US-0475845.
PR 07-JUN-1996; 96US-0660289.
XX
XX (ZYMO) ZYMOGENETICS INC.
PA (NOVO) NOVO NORDISK AS.
XX
XX Hart CE, Petersen LC, Hedner U, Rasmussen ME;

XX
DR WPI; 2001-201993/20.
DR N-PSDB; AAF57099.
XX
XX Use of modified human factor VIIa with a covalent modification in its
PT catalytic center, to inhibit thrombus formation or to maintain vascular
PT patency -
XX
XX Example; Columns 43-48; 34pp; English.
XX
XX The invention relates to the use of modified human Factor VIIa for
CC inhibiting thrombus formation, or maintaining or improving vascular
CC patency in a patient. The modified factor VIIa comprises a covalent
CC modification in its catalytic center which effectively interrupts the
CC blood coagulation cascade. The modifications render Factor VIIa
CC substantially unable to activate plasma factor IX or X. The modified
CC Factor VIIa can be used for preventing or treating myocardial injury
CC associated with post-ischemic reperfusion, for improving regional
CC myocardial blood flow during reperfusion and maintaining or improving
CC vascular patency in a patient. The present sequence represents the
CC human Factor VII polypeptide.
XX
SQ Sequence 444 AA;

Query Match 66.9%; Score 121; DB 22; Length 444;
Best Local Similarity 52.3%; Pred. No. 6.8e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRXGSLRXCRXXLCSEFXXAXIFRNXXRTQFVSVY 44
Db 39 anafllelrpyslereckeqscfeearelfkdaerklfwisy 82

RESULT 30
AAP60056
ID AAP60056 standard; protein: 466 AA.
XX
AC AAP60056;
XX
DT 23-MAY-1991 (first entry)
XX
DE Factor VII peptide encoded by cDNA clone lambda VII2463.
XX
XX Factor VII; Factor VIIa; DNA construct;
KW
XX
XX EP200421-A.
XX
XX 10-DEC-1986.
XX
XX 16-APR-1986; 86EP-0302855.
XX
XX 16-DEC-1985; 85US-0810002.
PR 17-APR-1985; 85US-0724311.
XX
XX (ZYMO-) ZYMOGENETICS INC.
PA
PI Hagen FS, Murry MJ, Berkner KL, Insley MY, Woodbury RG;
PI Gray CL;
XX
XX WPI; 1986-326899/50.
DR N-PSDB; AAN60064.
XX
XX DNA construct used to transfect hosts - to produce protein which
PT activates to give factor VIIa
XX
XX
XX Disclousure; Fig. 1b; 55pp; English.
XX
XX The partial factor VII cDNA sequence encoding the peptide is from
CC cDNA clone lambda VII2463. It is used in a DNA construct which contains
CC a nucleotide sequence encoding a protein which, on activation, has the
CC same biological activity for blood coagulation as factor VIIa. The
CC nucleotide codes at least partially for factor VII and comprises a

CC sequence encoding a calcium binding domain joined to a second sequence
 CC downstream of this encoding a catalytic domain for the serine protease
 CC activity of Factor VIIa. The calcium binding domain comprises a gene
 CC encoding Factor VII, IX, X, Protein C, prothrombin or Protein S. The
 CC construct is used to transfect host cells to produce the protein which,
 CC on activation, yields Factor VIIa.
 XX
 SQ Sequence 466 AA;

Query Match 66.9%; Score 121; DB 7; Length 466;
 Best Local Similarity 52.3%; Pred. No. 7.2e-13;
 Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Oy 1 ANGFLXLRGSLRXRCXLCSEFXAXXIFPNXXRTQFWVSY 44
 ||||| ||||| | : ||| | ||: ||: ||: ||
 Db 61 anafllelrpslreckeegcsfeareilfkdaertklfwisy 104

RESULT 31

AAR52562
 ID AAR52562 standard; Protein: 466 AA.

AC AAR52562;

DT 27-MAY-1994 (first entry)

DE Factor VIII.

XX Truncated tissue factor; tTF; factor VIIa; FVIIa; activator;
 KW bleeding disorder; haemophilia; liver cirrhosis; coagulation;
 KW transmembrane domain; extracellular domain; soluble.

XX Homo sapiens.

OS

PN MO9323074-A.

PD 25-NOV-1993.

XX 12-MAY-1993; 93WO-US04493.

PR 13-MAY-1992; 92US-0882202.

PR 19-FEB-1993; 93US-0021615.

XX (OKLA-) OKLAHOMA MED RES FOUND.

PI Comp PC, Morrissey JH;

XX WPI; 1993-386218/48.

DR N-PSDB; AAO62229.

XX Compn. of truncated tissue factor and factor-VIIa or activator
 PT of VII - useful for treating bleeding disorders, e.g. haemophilia
 PT or liver cirrhosis

PS Disclosure: Page 26-28; 43pp; English.

CC A compn. for treatment of patients with prolonged or excessive
 CC bleeding disorders comprises truncated tissue factor (TF) (AA052439)
 CC and a substance effective to produce a plasma level of factor VIIa
 CC which in combination with tTF will control or stop the excessive
 CC bleeding. The substance may be factor VIIa itself or an activator
 CC which promotes the conversion of endogenous factor VII to factor VIIa.
 XX
 SQ Sequence 466 AA;

Query Match 66.9%; Score 121; DB 14; Length 466;
 Best Local Similarity 52.3%; Pred. No. 7.2e-13;
 Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Oy 1 ANGFLXLRGSLRXRCXLCSEFXAXXIFPNXXRTQFWVSY 44
 ||||| ||||| | : ||| | ||: ||: ||: ||

Db 61 anafllelrpslreckeegcsfeareilfkdaertklfwisy 104

RESULT 32

AAM69606
 ID AAM69606 standard; Protein: 466 AA.

AC AAM69606;

DT 16-OCT-1998 (first entry)

DE Human Factor VIIa.

XX Human; truncated; tissue factor; tTF; TF; tumour; coagulation;
 KW blood vessel; Factor VIIa; FVIIa; benign growth; vascularised;
 KW benign prostatic hypertrophy; malignant; necrosis; angiogenesis;
 KW diabetic retinopathy; restenosis; neovascular glaucoma; psoriasis;
 KW rheumatoid arthritis.

XX Homo sapiens.

OS

PN MO9831394-A2.

PD 23-JUL-1998.

XX 20-JAN-1998; 98WO-US01012.

PR 27-MAR-1997; 97US-0042427.

PR 22-JAN-1997; 97US-0035920.

PR 27-JAN-1997; 97US-0036205.

XX (TEXA) UNIV TEXAS SYSTEM.

PI Gao B, King SW, Thorpe PE;

XX WPI; 1998-413821/35.

DR N-PSDB; AAV40389.

XX Composition containing coagulation-defective tissue factor for
 PT treating, e.g. tumours - useful for, e.g. promoting coagulation in
 PT pro-thrombotic and tumour-associated vasculature, used with, e.g.
 PT factor 7 or anti-cancer agent

XX Claim 35; Page 196-197; 225pp; English.

XX A composition has been developed which comprises at least 1 coagulation-
 CC deficient tissue factor (TF) compound that is modified to increase its
 CC biological half-life, but excluding modification that involves attachment
 CC to an antibody (or its antigen-binding region) that binds to a component
 CC (cells, vasculature or stroma) of tumours. Also described in the present
 CC invention are compositions containing any coagulation-deficient TF for
 CC promoting coagulation. The coagulation-deficient TFs are used to promote
 CC coagulation preferentially in prothrombotic vessels, particularly those
 CC associated with: (i) benign growths (e.g. benign prostatic hypertrophy);
 CC (ii) vascularised, malignant tumours of medium or large size (where they
 CC also induce tumour necrosis), or (iii) other disorders that involve
 CC angiogenesis, e.g. diabetic retinopathy, restenosis, neovascular
 CC glaucoma, psoriasis and rheumatoid arthritis. The composition can be
 CC administered systemically, particularly intravenously, typically at
 CC 0.2-200 mg, given 3 times over 7 days. Truncated TF, and its variants,
 CC localise specifically in tumour-associated blood vessels after systemic
 CC administration, even though they contain no targeting agent. They cause
 CC little if any injury to normal tissue; may produce a synergistic response
 CC when used with other antitumour agents and they eliminate the multi-step,
 CC and expensive, preparation of antibody-based targeting constructs. The
 CC present sequence is human Factor VIIa, from the present invention.
 XX
 SQ Sequence 466 AA;

Query Match 66.9%; Score 121; DB 19; Length 466;
 Best Local Similarity 52.3%; Pred. No. 7.2e-13;
 Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

FT	Cleavage-site	290..291
FT	/note= "proteolytic site"	
FT	Disulfide-bond	310..329
FT	Cleavage-site	315..316
FT	/note= "proteolytic site"	
FT	Modified-site	322
FT	/note= "glycosylation site"	
FT	Disulfide-bond	340..368
FT	Cleavage-site	341..342
FT	/note= "proteolytic site"	
FT	Cleavage-site	392..393
FT	/note= "proteolytic site"	
FT	Cleavage-site	396..397
FT	/note= "proteolytic site"	
FT	Cleavage-site	402..403
FT	/note= "proteolytic site"	
XX		
PN	US5580560-A.	
XX		
PD	03-DEC-1996.	
XX		
PE	13-NOV-1989;	89US-0434149.
XX		
PR	09-AUG-1993;	93US-0104509.
PR	13-NOV-1989;	89US-0434149.
PR	12-JUN-1992;	92US-0898248.
PR	22-AUG-1994;	94US-0293778.
XX		
PA	(NOVO) NOVO-NORDISK AS.	
XX		
FI	Bjorn SE, Nicolaisen EM, Wilberg FC, Woodbury R;	
XX		
DR	WPI: 1997-033523/03.	
XX		
PT	Mutated human factor VII or VIIa proteins - With amino acid	
PT	substitutions to improve proteolytic stability	
XX		
PS	Claim 3; Page -: 28pp; English.	
XX		
CC	Modified human factor VII or VIIa proteins are stabilised against proteolytic cleavage by substitution of one of the residues Lys32, Lys38, Ile42, Tyr44, Phe278, Arg280, Arg304, Arg315, Tyr332 and Lys341 by an amino acid that provides a proteolytically more stable peptide bond, provided that Lys32 is replaced by Gln, Glu, His, Gly, Thr, Ala or Ser. The modified proteins are useful for treating bleeding disorders such as thrombocytopenia and von Willebrand's disease. They are also suitable for addition to plasma substitutes. The present sequence is a specific example of a modified factor VII protein.	
CC		
CC		
CC		
SC	Sequence	406 AA;
XX		
QY	Query Match	66.3%; Score 120; DB 18; Length 406; Best Local Similarity 52.3%; Pred. No. 9.4e-13; Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
DQ	1 ANGFLXLRxGLKRXCRXLCSFXXAXXIIFNNXXRTROFWFSY 44 : :: : : 1 anaifeelrpslereckeegcsfeaeailqdaerlkrlfwisy 44	
RESULT 35		
ID AAM14508		
AAM14508 standard; protein; 406 AA.		
AC AAM14508;		
DT 14-MAY-1997 (first entry)		
DE Modified blood coagulation Factor VII (K38T).		
FX Blood coagulation; factor 7; muten; mutation; modification;		

KW	thrombocytopenia: von Willebrand's disease, plasma substitute.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
FM	Key
FM	Modified-site
FM	6 location/Qualifiers
FM	/label= OTHER
FM	/note= "gamma-carboxyglutamic acid"
FM	7
FM	/label= OTHER
FM	/note= "gamma-carboxyglutamic acid"
FM	14
FM	/label= OTHER
FM	/note= "gamma-carboxyglutamic acid"
FM	16
FM	/label= OTHER
FM	/note= "gamma-carboxyglutamic acid"
FM	19
FM	/label= OTHER
FM	/note= "gamma-carboxyglutamic acid"
FM	20
FM	/label= OTHER
FM	/note= "gamma-carboxyglutamic acid"
FM	25
FM	/label= OTHER
FM	/note= "gamma-carboxyglutamic acid"
FM	26
FM	/label= OTHER
FM	/note= "gamma-carboxyglutamic acid"
FM	29
FM	/label= OTHER
FM	/note= "gamma-carboxyglutamic acid"
FM	32..33
FM	/note= "gamma-carboxyglutamic acid"
FM	35
FM	/label= OTHER
FM	/note= "gamma-carboxyglutamic acid"
FM	38..39
FM	/note= "proteolytic site in unmodified factor VII"
FM	38
FM	/note= "native Lys38 has been substituted by Thr to provide a proteolytically more stable peptidic bond"
FM	42..43
FM	/note= "proteolytic site"
FM	44..45
FM	/note= "proteolytic site"
FM	50..61
FM	/note= "proteolytic site"
FM	55..70
FM	63
FM	/label= OTHER
FM	/note= "beta-hydroxy-aspartic acid"
FM	72..81
FM	/note= "proteolytic site"
FM	91..102
FM	/note= "proteolytic site"
FM	98..112
FM	/note= "proteolytic site"
FM	114..127
FM	/note= "proteolytic site"
FM	135..162
FM	/note= "proteolytic site"
FM	143..144
FM	/note= "proteolytic site"
FM	145
FM	/note= "glycosylation site"
FM	159..164
FM	/note= "proteolytic site"
FM	178..194
FM	193
FM	242
FM	344
FM	290..291
FM	/note= "proteolytic site"
FM	310..329
FM	315..316
FM	/note= "proteolytic site"

```

FT Modified-site 322 /note= "glycosylation site"
FT Disulfide-bond 340..368
FT Cleavage-site 341..342 /note= "proteolytic site"
FT Cleavage-site 392..393 /note= "proteolytic site"
FT Cleavage-site 396..397 /note= "proteolytic site"
FT Cleavage-site 402..403 /note= "proteolytic site"
FT Cleavage-site /note= "proteolytic site"
PN USS580560-A.
PD 03-DEC-1996.
XX 13-NOV-1989; 89US-0434149.
XX 09-AUG-1993; 93US-0104509.
PR 13-NOV-1989; 89US-0434149.
PR 12-JUN-1992; 92US-0898248.
PR 22-AUG-1994; 94US-0293778.
XX
XX (NOVO ) NOVO-NORDISK AS.
XX
XX Bjorn SE, Nicolaisen EM, Wiberg FC, Woodbury R;
XX WPI; 1997-033523/03.
XX
XX Mutated human factor VII or VIIa proteins - with amino acid
XX substitutions to improve proteolytic stability
XX
XX Example 2; Page -; 28pp; English.
XX
XX Modified human factor VII or VIIa proteins are stabilised against
XX proteolytic cleavage by substitution of one of the residues Lys32,
XX Lys38, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and
XX Lys341 by an amino acid that provides a proteolytically more stable
XX peptide bond, provided that Lys32 is replaced by Gln, Glu, His,
XX Gly, Thr, Ala or Ser. The modified proteins are useful for treating
XX bleeding disorders such as thrombocytopenia and von Willebrand's
XX disease. They are also suitable for addition to plasma substitutes.
XX The present sequence is a specific example of a modified factor VII
XX
XX Sequence 406 AA;
SQ

```

Query Match 65.2%; Score 118; DB 18; Length 406;
 Best Local Similarity 52.3%; Pred. No. 2.1e-12;
 Matches 23; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

```

QY 1 ANGFLXLRXGSLRXCRXLCSPFXAXXIFRNXXRTQFWVSX 44
   ||||| ||||| ||| | ||| |||||
Db 1 anafleelrpgslereckeegsfearelfkdaertlfiwisy 44

```

RESULT 36
 AAY18313
 ID AAY18313 standard; peptide; 44 AA.
 XX
 AC AAY18313;
 XX
 DT 17-AUG-1999 (first entry)
 XX
 DE Modified GLA domain of vitamin K-dependent protein.
 XX
 KM GLA domain; muten; vitamin K-dependent protein; clotting disorder;
 KW therapy.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX

```

FH Key Location/Qualifiers
FT Misc-difference 1..44 /note= "Xaa" gamma-carboxyglutamic acid, or glutamic
FT /note= "acid"
FT
FT W09920767-A1.
XX
XX 29-APR-1999.
XX
XX 20-OCT-1998; 98WO-US22152.
XX
XX 23-OCT-1997; 97US-0955636.
XX
XX (MINU ) UNIV MINNESOTA.
XX
XX Nelsaetuen GL;
XX
XX WPI; 1999-288309/24.
XX
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
XX acid domain, useful for treating clotting disorders
XX
XX Disclosure; Page 81; 86pp; English.
XX
XX This sequence represents a modified GLA (gamma-carboxyglutamic acid)
XX domain. The invention relates to a vitamin K-dependent polypeptide
XX comprising a modified GLA domain containing an amino acid substitution
XX which enhances membrane binding of the modified polypeptide as compared
XX to the native polypeptide. The polypeptide is used to treat a clotting
XX disorder by decreasing or increasing clot formation. Modification of the
XX GLA domain results in a protein which has enhanced membrane binding
XX affinity as compared to the native protein.
XX
XX Sequence 44 AA;
SQ

```

Query Match 64.6%; Score 117; DB 20; Length 44;
 Best Local Similarity 75.0%; Pred. No. 3.7e-13;
 Matches 33; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

```

QY 1 ANGFLXLRXGSLRXCRXLCSPFXAXXIFRNXXRTQFWVSX 44
   ||||| ||||| ||||| ||| | ||| |||||
Db 1 anaflixlrpgslrxrcxxgcsfxaxrxfidaxrtlkfiwisy 44

```

RESULT 37
 AAM14511
 ID AAM14511 standard; protein; 406 AA.
 XX
 AC AAM14511;
 XX
 DT 14-MAY-1997 (first entry)
 XX
 DE Modified blood coagulation Factor VII (K32Q + K38T).
 XX
 KM Blood coagulation; factor 7; muten; mutation; modification;
 KW thrombocytopenia; von Willebrand's disease; plasma substitute.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 6 /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Modified-site 7 /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Modified-site 14 /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Modified-site 16 /label= OTHER
 FT


```

FT      Modified-site      /note= "gamma-carboxyglutamic acid"
FT      19
FT      /label= OTHER
FT      Modified-site      /note= "gamma-carboxyglutamic acid"
FT      20
FT      /label= OTHER
FT      Modified-site      /note= "gamma-carboxyglutamic acid"
FT      25
FT      /label= OTHER
FT      Modified-site      /label= "gamma-carboxyglutamic acid"
FT      26
FT      /note= OTHER
FT      Modified-site      /note= "gamma-carboxyglutamic acid"
FT      29
FT      /label= OTHER
FT      Modified-site      /note= "gamma-carboxyglutamic acid"
FT      35
FT      /label= OTHER
FT      /note= "gamma-carboxyglutamic acid"
XX
XX      CA2121927-A.
XX
XX      PD
XX      08-NOV-1994.
XX
XX      PE      22-APR-1994; 94CA-2121927.
XX
XX      PR      07-MAY-1993; 93JP-0130015.
XX      10-FEB-1994; 94JP-0016348.
XX
XX      PA      (EISA ) EISAI CO LTD.
XX
XX      PI      Iwasaki Y, Narakl T, Matanabe K;
XX
XX      DR      WPI; 1995-052669/08.
XX
XX      PT      Determination of protein induced by vitamin-K absence (PIVKA) - by
XX      using an anti-PIVKA antibody, useful as vitamin-K deficiency marker
XX
XX      PS      Disclosure; Page 10; 34pp: English.
XX
XX      CC      AAW11901-w11907 represent Gla regions of vitamin K dependent plasma
XX      proteins. This sequence is the Gla region of Factor VII. The Gla
XX      region is the N-terminal region of the protein, and contains 10 glutamic
XX      acid residues which are gamma-carboxylated. These 10 residues are
XX      uncarboxylated in the precursor form, and require the presence of
XX      vitamin K and a carboxylase to be converted into an active form. These
XX      proteins suffer incomplete carboxylation when a state of protein induced
XX      vitamin K absence (PIVKA) occurs. Various PIVKAs have been found to be
XX      produced in the blood as a result of hepatocellular carcinoma. These
XX      sequences are all epitopes for the anti-PIVKA-II monoclonal antibody.
XX      The anti-PIVKA-II antibody (such as WU-3) specifically recognises the
XX      prothrombin Gla region (see AAW11901), but has also been found to
XX      recognise the rest of these Gla regions. The antibody can be used in the
XX      method of the invention for the determination of PIVKA in a specimen.
XX      The determination of PIVKA is clinically useful, as PIVKA is produced in
XX      blood as a result of incomplete gamma-carboxylation in a state of
XX      vitamin K deficiency or suppression. The determination of PIVKA can
XX      therefore be used as a marker of the state of vitamin K deficiency or
XX      suppression.
XX
XX      SQ      Sequence 41 AA;

```

Query Match 59.1%; Score 107; DB 16; Length 41;
 Best Local Similarity 75.6%; Pred. No. 1.9e-11;
 Matches 31; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

```

QY      1 ANGFLXXLRKGSIXRCRXKLCSEFXAXXIFRNXRXRTPQFW 41
DB      1 anaflxxlfpsslxrckxxqsfxxaxrlfkdxartklfw 41

```

RESULT 39

```

AAU02959
ID      AAU02959 standard; Protein; 345 AA.
XX
XX      AC      AAU02959;
XX
XX      DT      12-SEP-2001 (first entry)
XX
XX      DE      Angiotensin converting enzyme (ACEV) splice variant protein #59.
XX
XX      KW      Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
XX      granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
XX      platelet-derived endothelial cell growth factor; cardiovascular disease;
XX      cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C;
XX      vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
XX      myocardial infarction; coronary arterial thrombosis; renal disease;
XX      diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
XX      multiple sclerosis; immune complex nephritis; deep vein thrombosis;
XX      noncardiotoxic pulmonary granulomatous disease; endothelial abnormality;
XX      vascular disorder; asbestosis.
XX
XX      OS      Mus sp..
XX
XX      PN      W0200136632-A2.
XX
XX      PD      25-MAY-2001.
XX
XX      PE      17-NOV-2000; 2000MO-IL00766.
XX
XX      PR      17-NOV-1999; 99IL-0132978.
XX      10-DEC-1999; 99IL-0133455.
XX
XX      PA      (COMP-) COMPUGEN LTD.
XX
XX      PI      Levine Z, David A, Azar I, Khosravi R, Bernstein J;
XX
XX      DR      WPI; 2001-336004/35.
XX      N-PSDB; AAS06059.
XX
XX      PT      Novel alternative splicing variants e.g. variant of angiotensin
XX      converting enzyme (ACEV), useful in identifying candidate compounds
XX      capable of binding to the variant and to detect anti-variant antibodies
XX
XX      PS      Claim 4; Fig 59; 519pp: English.
XX
XX      CC      The sequence represents an angiotensin converting enzyme splice variant
XX      (ACEV) polypeptide. The polypeptides of the invention include variants of
XX      granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
XX      platelet-derived endothelial cell growth factor, cyclin-dependent kinase
XX      inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal
XX      polypeptide receptor 2. The polypeptides and their associated nucleic
XX      acids are useful for identification of variant sequences and detection of
XX      candidate compounds capable of binding to the molecules. The sequences of
XX      the invention can be used in the treatment and diagnosis of various
XX      disorders including cardiovascular diseases such as arteriosclerosis,
XX      myocardial infarction and coronary arterial thrombosis, renal diseases
XX      such as diabetic nephropathy, muscular diseases such as hypertrophy,
XX      immune disorders such as immune complex nephritis, multiple sclerosis,
XX      cancer, sarcoidosis, noncardiotoxic pulmonary granulomatous diseases such
XX      as asbestosis and vascular pathologies involving an endothelial
XX      abnormality such as deep vein thrombosis.
XX
XX      SQ      Sequence 345 AA;

```

Query Match 57.5%; Score 104; DB 22; Length 345;
 Best Local Similarity 47.7%; Pred. No. 5e-10;
 Matches 21; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

```

QY      1 ANGFLXXLRKGSIXRCRXKLCSEFXAXXIFRNXRXRTPQFW 44
DB      42 anslllelwpsslereneeqsfearrelfkxpettkqfw 85

```

ID	AA	Label	Location/Qualifiers
RESULT 40			
AAW14506			
ID	AAW14506	standard: protein; 406 AA.	
XX			
AC	AAW14506;		
XX			
DT	14-MAY-1997	(first entry)	
XX			
DE	Modified blood coagulation Factor VII.		
XX			
KW	Blood coagulation; factor 7; mutein; mutation; modification;		
KW	thrombocytopenia; von Willebrand's disease; plasma substitute.		
XX			
OS	Homo sapiens.		
XX			
FH	Key		
FH	Modified-site	6	Location/Qualifiers
FT		/label= OTHER	
FT		/note= "gamma-carboxylutamic acid"	
FT	Modified-site	7	
FT		/label= OTHER	
FT		/note= "gamma-carboxylutamic acid"	
FT	Modified-site	14	
FT		/label= OTHER	
FT		/note= "gamma-carboxylutamic acid"	
FT	Modified-site	16	
FT		/label= OTHER	
FT		/note= "gamma-carboxylutamic acid"	
FT	Modified-site	19	
FT		/label= OTHER	
FT		/note= "gamma-carboxylutamic acid"	
FT	Modified-site	20	
FT		/label= OTHER	
FT		/note= "gamma-carboxylutamic acid"	
FT	Disulfide-bond	17..22	
FT	Modified-site	25	
FT		/label= OTHER	
FT		/note= "gamma-carboxylutamic acid"	
FT	Modified-site	26	
FT		/label= OTHER	
FT		/note= "gamma-carboxylutamic acid"	
FT	Modified-site	29	
FT		/label= OTHER	
FT		/note= "gamma-carboxylutamic acid"	
FT	Cleavage-site	32..33	
FT		/note= "proteolytic site in unmodified factor VII"	
FT	Misc-difference	32	
FT		/label= Lys, Gln, Glu, His, Gly, Thr, Ala, Ser	
FT		/note= "if native Lys32 is substituted by an amino acid which provides a proteolytically more stable peptide bond, then it must be substituted by one of the amino acids Gln, Glu, His, Gly, Thr, Ala or Ser"	
FT	Modified-site	35	
FT		/label= OTHER	
FT		/note= "gamma-carboxylutamic acid"	
FT	Cleavage-site	38..39	
FT		/note= "proteolytic site in unmodified factor VII"	
FT	Misc-difference	38	
FT		/note= "if native Lys38 is substituted by an amino acid which provides a proteolytically more stable peptide bond, then it is pref. substituted by one of the amino acids Thr, Asp, Leu, Gly, Ala, Ser, Asn or His"	
FT	Cleavage-site	42..43	
FT		/note= "proteolytic site in unmodified factor VII"	
FT	Misc-difference	42	
FT		/note= "native Ile42 may be substituted by an amino acid which provides a proteolytically more stable peptide bond"	
FT	Cleavage-site	44..45	
FT		/note= "proteolytic site in unmodified factor VII"	

FT	Misc-difference	44	/note=	"native Tyr44 may be substituted by an amino acid which provides a proteolytically more stable peptide bond"
FT				
FT	Disulfide-bond	50..61		
FT	Disulfide-bond	55..70		
FT	Modified-site	63	/label=	OTHER
FT			/note=	"beta-hydroxy-aspartic acid"
FT	Disulfide-bond	72..81		
FT	Disulfide-bond	91..102		
FT	Disulfide-bond	98..112		
FT	Disulfide-bond	114..127		
FT	Disulfide-bond	135..162		
FT	Cleavage-site	143..144		
FT			/note=	"proteolytic site"
FT	Modified-site	145		
FT			/note=	"glycosylation site"
FT	Disulfide-bond	159..164		
FT	Disulfide-bond	178..194		
FT	Active-site	193		
FT	Active-site	242		
FT	Active-site	344		
FT	Misc-difference	278	/note=	"native Phe278 may be substituted by an amino acid which provides a proteolytically more stable peptide bond"
FT				
FT	Cleavage-site	290..291	/note=	"proteolytic site in unmodified factor VII"
FT			/note=	"proteolytic site in unmodified factor VII"
FT	Misc-difference	290	/note=	"if native Arg290 is substituted by an amino acid which provides a proteolytically more stable peptide bond, then it is pref. substituted by one of the amino acids Gly, Thr, Ala, Ser or Lys"
FT				
FT	Misc-difference	304	/note=	"if native Arg304 is substituted by an amino acid which provides a proteolytically more stable peptide bond, then it is pref. substituted by one of the amino acids Gly, Thr, Ala, Ser or Gln"
FT				
FT	Disulfide-bond	310..329		
FT	Cleavage-site	315..316	/note=	"proteolytic site in unmodified factor VII"
FT			/note=	"proteolytic site in unmodified factor VII"
FT	Misc-difference	315	/note=	"if native Arg315 is substituted by an amino acid which provides a proteolytically more stable peptide bond, then it is pref. substituted by one of the amino acids Gly, Thr, Ala, Ser or Gln"
FT				
FT	Modified-site	322	/note=	"glycosylation site"
FT			/note=	"native Tyr332 may be substituted by an amino acid which provides a proteolytically more stable peptide bond"
FT	Misc-difference	332		
FT				
FT	Disulfide-bond	340..368		
FT	Cleavage-site	341..342	/note=	"proteolytic site in unmodified factor VII"
FT			/note=	"proteolytic site in unmodified factor VII"
FT	Misc-difference	341	/note=	"if native Lys341 is substituted by an amino acid which provides a proteolytically more stable peptide bond, then it is pref substituted by one of the amino acids Glu, Gln, Gly, Thr Ala or Ser"
FT				
FT	Cleavage-site	392..393	/note=	"proteolytic site"
FT			/note=	"proteolytic site"
FT	Cleavage-site	396..397	/note=	"proteolytic site"
FT			/note=	"proteolytic site"
FT	Cleavage-site	402..403	/note=	"proteolytic site"
FT				
PN	US5580560-A.			

XX 27-OCT-1995; 95WO-US13940.
 PF 28-OCT-1994; 94US-0330978.
 PR (CORT-) COR THERAPEUTICS INC.
 XX King RS;
 PI WPI: 1996-239270/24.
 DR
 XX Prepn. of an inhibited form of an activated blood factor, e.g.
 PT factor X - by treating partially purified blood factor preps. with
 PT an activating factor and an inhibiting factor
 PS Disclosure: Fig 1: 45pp; English.
 XX
 CC This sequence represents the light chain of human Factor X (the heavy
 CC chain is represented by AA05820). Factor X must be activated to Factor
 CC Xa before the protease is incorporated into the prothrombinase complex.
 CC In Factor Xa the light chain sequence is identical to the Factor X light
 CC chain, and the heavy chain is a truncated version of the Factor X heavy
 CC chain. An inhibited form of activated Factor X is prepared by the
 CC method of the invention. In this method, a partially purified
 CC preparation containing the blood factor is treated to convert the factor
 CC into an activated form (using an immobilised activating enzyme). The
 CC activated form is then converted into an inhibited form in a single step,
 CC and the inhibited factor is recovered. The inhibited blood factor is
 CC recovered by immunoaffinity chromatography using an antigen specific
 CC monoclonal antibody coupled to an activated resin (such as agarose), or
 CC an anion exchange column with an anion-exchange group linked to a
 CC naturally derived polysaccharide or a synthetically derived polymeric
 CC matrix. The activated resin used preferably uses activation chemistry
 CC selected from tressyl, azactone, aldehyde, hydrazide, N-hydroxy
 CC succinimide or triazine. This method produces a highly purified
 CC preparation of an inhibited form (either permanently or transiently
 CC inhibited) of an activated blood factor in high yield. The factors
 CC produced can be used in the treatment of coagulation disorders, or
 CC disorders of vasculature function.
 XX
 SQ Sequence 139 AA:
 (

Query Match 54.1%; Score 98; DB 17; Length 139;
 Best Local Similarity 36.4%; Pred. No. 2.3e-09;
 Matches 16; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

OY 1 ANGFLXLRXGSLRXRCRXXCFFXXAXXIFRNXXRTQFWVS 44
 II:::IIIIII:::IIIIII:::IIIIII:::IIIIII
 DB 1 ansfltmkghlrltcmlltcsytartarvfdsdktntfwnky 44

RESULT 43
 AAY18308
 ID AAY18308 standard; peptide; 44 AA.
 AC AAY18308;
 XX 17-AUG-1999 (first entry)
 DE Modified GLA domain of vitamin K-dependent protein.
 XX
 KW GLA domain; mutlein; vitamin K-dependent protein; clotting disorder;
 KW therapy.
 XX
 OS Bos taurus.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..44
 FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
 FT acid"
 XX

PN W09920767-A1.
 XX 29-APR-1999.
 PD 20-OCT-1998; 98WO-US22152.
 PF 23-OCT-1997; 97US-0955636.
 XX
 PR (MINU) UNIV MINNESOTA.
 PA
 XX Nelstuen GL;
 PI WPI: 1999-288309/24.
 DR
 XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
 PT acid domain, useful for treating clotting disorders
 PT
 PS Disclosure: Page 79; 86pp; English.
 XX
 CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)
 CC domain. The invention relates to a vitamin K-dependent polypeptide
 CC comprising a modified GLA domain containing an amino acid substitution
 CC which enhances membrane binding of the modified polypeptide as compared
 CC to the native polypeptide. The polypeptide is used to treat a clotting
 CC disorder by decreasing or increasing clot formation. Modification of the
 CC GLA domain results in a protein which has enhanced membrane binding
 CC affinity as compared to the native protein.
 XX
 SQ Sequence 44 AA:
 (

Query Match 53.0%; Score 96; DB 20; Length 44;
 Best Local Similarity 65.9%; Pred. No. 1.7e-09;
 Matches 29; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

OY 1 ANGFLXLRXGSLRXRCRXXCFFXXAXXIFRNXXRTQFWVS 44
 II:::IIIIII:::IIIIII:::IIIIII:::IIIIII
 DB 1 ansflxxlrlhgnvxxrcsxvxcffxxaxlfgntxdtnafwafy 44

RESULT 44
 AAY18304
 ID AAY18304 standard; peptide; 44 AA.
 AC AAY18304;
 XX 17-AUG-1999 (first entry)
 DE Bovine protein C GLA domain.
 XX
 KW GLA domain; vitamin K-dependent protein; clotting disorder;
 KW therapy.
 XX
 OS Bos taurus.
 OS
 FH Key Location/Qualifiers
 FT Misc-difference 1..44
 FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
 FT acid"
 XX
 PD W09920767-A1.
 XX 29-APR-1999.
 PD 20-OCT-1998; 98WO-US22152.
 PF 23-OCT-1997; 97US-0955636.
 XX
 PR (MINU) UNIV MINNESOTA.
 PA
 XX Nelstuen GL;
 PI WPI: 1999-288309/24.
 DR

XX	vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
PT	acid domain, useful for treating clotting disorders
XX	
PS	Disclosure: Page 14; 86pp; English.
XX	
CC	This sequence is the protein C GLA (gamma-carboxyglutamic acid)
CC	domain. The invention relates to a vitamin K-dependent polypeptide
CC	comprising a modified GLA domain containing an amino acid substitution
CC	which enhances membrane binding of the modified polypeptide as compared
CC	to the native polypeptide. The polypeptide is used to treat a clotting
CC	disorder by decreasing or increasing clot formation. Modification of the
CC	GLA domain results in a protein which has enhanced membrane binding
XX	affinity as compared to the native protein.
SQ	
Sequence	44 AA:
Query Match	52.5%; Score 95; DB 20; Length 44;
Best Local Similarity	65.9%; Pred. No. 2.6e-09;
Matches	29; Conservative 4; Mismatches 11; Indels 0; Gaps
Oy	1 ANGELXLRXGSLRXCRXXLCGFRXAXITRNXRRRQFVSY 44
Db	1 ansflxxlrpgnvxxrcsxvxcitxxarxtlfgntxdmawsfy 44
RESULT	45
AAB36403	
ID	AAB36403 standard; peptide: 44 AA.
XX	
AC	AAB36403:
XX	
DT	27-FEB-2001 (first entry)
XX	
DE	Bovine protein C gamma-carboxyglutamic acid domain SEQ ID NO:2.
XX	
KM	Vitamin K-dependent protein; factor VII; protein C; GLA domain;
KM	gamma-carboxyglutamic acid domain; factor IX; protein S; domain Z;
KM	factor X; prothrombin; enhanced membrane binding affinity;
KM	clot formation; thrombolytic; haemostatic; bleeding disorder;
KM	thrombosis; clotting disorder; haemophilia A; haemophilia B;
KM	liver disease.
XX	
OS	Bos taurus.
XX	
PN	WO200066753-A2.
XX	
PD	09-NOV-2000.
XX	
PF	28-APR-2000; 2000WO-US11416.
XX	
PR	29-APR-1999; 99US-0302239.
XX	
PA	(MINU) UNIV MINNESOTA.
XX	
PI	Nelstuen GL;
XX	
DR	WPI: 2001-007226/01.
XX	
PT	Novel vitamin K-dependent polypeptide useful for treating clotting
PT	disorders such as thrombosis and hemophilia, comprises modified
PT	gamma-carboxy glutamic acid domain that enhances membrane binding
XX	affinity
XX	
PS	Example 5; Page 42; 81pp; English.
XX	
CC	The present invention describes a vitamin K-dependent polypeptide (I)
CC	comprising a modified gamma-carboxy glutamic acid (GLA) domain having
CC	at least one amino acid substitution, that enhances membrane binding
CC	affinity and the activity of the polypeptide relative to a corresponding
CC	native vitamin K-dependent polypeptide and inhibits clot formation.
CC	(I) can have thrombolytic and haemostatic activities, and can be used

```
CC as an inhibitor of clot formation. (I) is useful for decreasing clot
CC formation in a mammal, a factor VII or factor IX containing a modified
CC GLA domain is useful for increasing clot formation and for treating a
CC bleeding disorder, including thrombosis and clotting disorders such as
CC haemophilia A, haemophilia B and liver disease. The present sequence
CC represents a bovine protein C GLA domain sequence, given in the
CC exemplification of the present invention.
```

```
SQ Sequence 44 AA:
```

```
Query Match 52.5%; Score 95; DB 22; Length 44;
Best Local Similarity 65.9%; Pred. No. 2.6e-09;
Matches 29; Conservative 4; Mismatches 11; Indels 0; Gaps 0
```

```
Oy 1 ANGFLXLLRPGSLKRCRRXXLCISFFAXXIIFRXXTROPFWSY 44
||| ||||| |::||| |::||| ||| |::| |
Db 1 ansflxxlirpgvxrxccvxfxxarxlfqntdumafwsfly 44
```

```
RESULT 46
AAP60057
ID AAP60057 standard; protein; 453 AA.
XX
AC AAP60057;
XX
DT 23-MAY-1991 (first entry)
XX
DE Factor IX/Factor VII fusion peptide.
XX
KW Factor VII; Factor IX; fusion peptide.
XX
PN EP200421-A.
XX
PD 10-DEC-1986.
XX
PF 16-APR-1986; 86EP-0302855.
XX
PR 16-DEC-1985; 85US-0810002.
PR 17-APR-1985; 85US-0724311.
PA (ZYMO-) ZYMOGENETICS INC.
XX
PI Hagen FS, Murry MJ, Berkner KL, Insley MY, Woodbury RG;
PI Gray CJ;
XX
DR WPT: 1986-326899/50.
DR N-PSDB: AAN60065.
XX
DNA construct used to transfect hosts - to produce protein which
activates to give factor VIIa
XX
Disclosure: Fig. 7; 55pp; English.
```

```
The peptide is encoded by a Factor IX/Factor VII fusion cDNA.
cDNA encoding Factor VIIcan be used in a DNA construct which contains
a nucleotide sequence encoding a protein which, on activation, has the
same biological activity for blood coagulation as Factor IIa. The
nucleotide codes at least partially for Factor VII and comprises sequence
encoding a calcium binding domain joined to second sequence downstream of
this encoding a catalytic domain for serine protease activity of Factor
VIIa. Calcium binding domain complises a gene encoding Factor VII, IX,
X, Protein C, prothombin or protein S. The construct is used to
transfect host cells to produce the protein which, on activation,
yields Factor VIIa.
```

```
SQ Sequence 453 AA:
```

```
Query Match 51.9%; Score 94; DB 7; Length 453;
Best Local Similarity 41.9%; Pred. No. 3.6e-08;
Matches 18; Conservative 5; Mismatches 20; Indels 0; Gaps 0;
```


ID	AA	Sequence	Score	DB	Length	Query Match
1D	AA	AAK35762 standard; proteoln; 448 AA.	51.4%	93	14	Best Local Similarity 36.4%; Pred. No. 5.4e-08;
XX	AA	AAK35762;	Matches 16;	Conservative 7;	Mismatches 21;	Indels 0;
XX	AA	24-SEP-1993 (first entry)				Gaps 0;
XX	AA	Factor X (X).				
XX	AA	PC; protein C; IX; Factor IX; X; Factor X; PT; prothrombin; VII;				
KW	AA	Factor VII; CT; chymotrypsinogen; SP; serine protease; binding;				
XX	AA	exosite; catalytic activity.				
OS	AA	Homo sapiens.				
XX	AA	Key	Location/Qualifiers			
FT	AA	Region	1..139			
FT	AA	Region	/note= "Factor X light chain"			
FT	AA	Region	140..142			
FT	AA	Region	/note= "Factor X activation"			
FT	AA	Region	143..448			
FT	AA	Peptide	/note= "Factor X heavy chain"			
FT	AA	Peptide	409..423			
FT	AA	Peptide	/note= "exosite 1"			
FT	AA	Peptide	330..350			
FT	AA	Peptide	/note= "exosite 2"			
FT	AA	Peptide	330..344			
FT	AA	Peptide	/note= "pref. PC polypeptide; claim 2, page 136"			
FT	AA	Peptide	404..418			
FT	AA	Peptide	/note= "pref. PC polypeptide; claim 2, page 136"			
FT	AA	Peptide	415..429			
FT	AA	Peptide	/note= "pref. PC polypeptide; claim 2, page 136"			
FT	AA	Peptide	285..306			
FT	AA	Peptide	/note= "claim 7, page 138 describes an antibody that reacts with Factor X; fragments 330-344, 404..418 and 415-429 but not with fragment 285-306"			
XX	AA	WO9309804-A.				
XX	AA	27-MAY-1993.				
XX	AA	18-NOV-1992; 92WO-US10242.				
XX	AA	18-NOV-1991; 91US-0793989.				
XX	AA	(SCRI) SCRIPPS RES INST.				
XX	AA	Griffin JH, Masters RM;				
XX	AA	WPI; 1993-182244/22.				
XX	AA	Serine protease derived-polypeptide(s) and anti-peptide antibodies - for inhibiting coagulation and assaying for the presence of serine protease in fluid samples				
XX	AA	Disclosure; Page 128-130; 149pp; English.				
XX	AA	The PC polypeptides indicated in the features table inhibit coagulation (they prevent binding of serine protease to natural substrates), esp. when admin. to give an intravascular blood concn. of 0.1-100 (pref. 0.5-10) microM.				
XX	AA	NB: Sequences corresp. to SEQ ID NO 6, 7, 8 and 9 are described in the specification but have not yet been added to the SEQUENCE LISTING.				
XX	AA	Sequence 448 AA;				

DB	1	ansfilemkgh1erecmeetsyeearevledsktnefwky	44
RESULT 50			
AAK37402	ID	AAK37402 standard; protein: 448 AA.	
AAK37402;	AC		
15-SEP-1993	DT	(first entry)	
Factor X.	DE		
Mac-1; macrophage-monocyte adhesive receptor; procoagulant; inflammation; thrombosis; atherosclerosis; septic shock; disseminated vascular coagulation; delayed hypersensitivity; haemostasis; angiogenesis; leucocyte recruitment; adhesion.	KM		
Homo sapiens.	OS		
Key	FT	Location/Qualifiers	
Region	FT	1..139	
Region	FT	/note= "Factor X light chain"	
Region	FT	140..142	
Region	FT	/note= "Factor X connecting tripeptide"	
Region	FT	143..448	
Region	FT	/note= "Factor X heavy chain"	
Region	FT	238..246	
Region	FT	/note= "recognition site for Mac-1 binding"	
Region	FT	366..373	
Region	FT	/note= "recognition site for Mac-1 binding"	
Region	FT	423..430	
Region	FT	/note= "recognition site for Mac-1 binding"	
W09309803-A.	PN		
27-MAY-1993.	PD		
20-NOV-1992;	PF	92WO-US10068.	
22-NOV-1991;	PR	91US-0798221.	
(SCHA/) SCHAEFER S C.	PA		
(SCRI) SCRIPPS RES INST.	PA		
Altieri DC, Edgington TS;	PI		
WPI; 1993-182243/22.	DR		
Factor X-derived polypeptide(s) inhibit binding of factor X to Mac-1 - useful for treating thrombosis, atherosclerosis, disseminated intravascular coagulation, septic shock etc.	PT		
Disclosure: Page 101-103; 122pp; English.	PS		
The sequence shown represents the complete amino acid sequence of human Factor X. Fragments of this sequence corresp. to the Mac-1 (macrophage-monocyte adhesive receptor) recognition sites (see features) of 10-25 amino acid residues may be used to inhibit Factor Xa monocyte procoagulant activity, specifically inflammation. The same effect may be achieved with antibodies raised to such fragments.	CC		
Typical applications include treatment of patients at risk of thrombosis or atherosclerosis before surgery, disseminated intravascular coagulation, septic shock, inflammation caused by infection (esp. by herpes simplex) or autoimmune diseases, delayed hypersensitivity, etc.	CC		
The fragments also inhibit leucocyte/endothelial cell interaction and thus regulate responses such as leucocyte recruitment, adhesion and extravasation, haematopoiesis, antigen presentation, angiogenesis, syncytial formation and haemostasis.	CC		
See also AAK37403-20.	CC		
Sequence 448 AA:	SQ		

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 3, 2002, 15:15:48 : Search time 20.6 Seconds
(without alignments)
52.171 Million cell updates/sec

Title: US-09-302-239-4-COPY
Perfect score: 181
Sequence: 1 ANGFLXXLRGSLXRCRXX.....XXAXXIFRNXXRTRQFWVS 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 10%
Listing first 50 summaries

Database : Issued Patents-AA:*
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6: /cgn2_6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	154	85.1	44	3	US-08-955-636-4 Sequence 4, Appl
2	122	67.4	44	3	US-08-955-636-26 Sequence 26, Appl
3	122	67.4	44	3	US-08-955-636-27 Sequence 27, Appl
4	121	66.9	44	3	US-08-955-636-3 Sequence 3, Appl
5	121	66.9	44	3	US-08-955-636-28 Sequence 28, Appl
6	121	66.9	406	1	US-08-293-778-24 Sequence 24, Appl
7	121	66.9	406	1	US-08-295-411-5 Sequence 5, Appl
8	121	66.9	406	2	US-08-955-471-5 Sequence 5, Appl
9	121	66.9	406	2	PCT-US92-10242-5 Sequence 5, Appl
10	121	66.9	444	1	US-08-475-845-2 Sequence 2, Appl
11	121	66.9	444	2	US-08-327-690-2 Sequence 2, Appl
12	121	66.9	444	2	US-08-660-289-2 Sequence 2, Appl
13	121	66.9	444	2	US-08-537-807-2 Sequence 2, Appl
14	121	66.9	444	2	US-08-871-003-2 Sequence 2, Appl
15	121	66.9	444	2	US-08-464-233-2 Sequence 2, Appl
16	121	66.9	444	4	US-09-189-607-2 Sequence 2, Appl
17	121	66.9	444	4	US-09-378-907-2 Sequence 2, Appl
18	121	66.9	444	5	PCT-US94-03779-2 Sequence 2, Appl
19	121	66.9	466	1	US-07-882-202A-4 Sequence 4, Appl
20	121	66.9	466	1	US-08-021-615A-4 Sequence 4, Appl
21	121	66.9	466	1	US-08-321-777-4 Sequence 4, Appl
22	121	66.9	466	1	US-09-009-217-14 Sequence 4, Appl
23	121	66.9	466	5	US-09-009-656-14 Sequence 14, Appl
24	121	66.9	466	5	PCT-US93-04493-4 Sequence 30, Appl
25	120	66.3	44	3	US-08-955-636-30 Sequence 29, Appl
26	117	64.6	44	3	US-08-955-636-29 Sequence 4, Appl
27	107	59.1	41	1	US-08-229-280-4

28	98	54.1	139	1	US-08-330-978-2 Sequence 2, Appl
29	98	54.1	139	1	US-08-474-042-2 Sequence 2, Appl
30	98	54.1	139	1	US-08-484-558-2 Sequence 2, Appl
31	98	54.1	139	1	US-08-774-592-2 Sequence 2, Appl
32	98	54.1	437	1	US-08-487-037-2 Sequence 2, Appl
33	98	54.1	437	1	US-08-487-037-2 Sequence 2, Appl
34	98	54.1	488	1	US-08-487-037-1 Sequence 23, Appl
35	96	53.0	44	3	US-08-955-636-23 Sequence 2, Appl
36	95	52.5	44	3	US-08-955-636-2 Sequence 2, Appl
37	93	51.4	448	1	US-08-295-411-3 Sequence 3, Appl
38	93	51.4	448	2	US-08-955-471-3 Sequence 3, Appl
39	93	51.4	448	5	PCT-US92-10242-3 Sequence 1, Appl
40	93	51.4	448	5	PCT-US92-10242-3 Sequence 3, Appl
41	90	49.7	41	1	US-08-229-280-5 Sequence 5, Appl
42	90	49.7	42	2	US-08-745-254A-2 Sequence 2, Appl
43	90	49.7	44	3	US-08-955-636-1 Sequence 1, Appl
44	90	49.7	44	3	US-08-955-636-24 Sequence 35, Appl
45	90	49.7	44	3	US-08-955-636-35 Sequence 2, Appl
46	90	49.7	45	2	US-08-965-832-2 Sequence 1, Appl
47	90	49.7	419	2	US-08-295-411-1 Sequence 1, Appl
48	90	49.7	419	2	US-08-955-471-1 Sequence 1, Appl
49	90	49.7	419	5	PCT-US92-10242-1 Sequence 1, Appl
50	90	49.7	460	2	US-08-756-506-2 Sequence 2, Appl

ALIGNMENTS

```
RESULT 1
US-08-955-636-4
: Sequence 4, Application US/08955636A
: Patent No. 6017882
: GENERAL INFORMATION:
: APPLICANT: Nelisestuen, Gary
: TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
: FILE REFERENCE: 09531/002001
: CURRENT APPLICATION NUMBER: US/08/955,636A
: CURRENT FILING DATE: 1997-10-23
: NUMBER OF SEQ ID NOS: 35
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 4
: LENGTH: 44
: TYPE: PRT
: ORGANISM: Bos taurus
: FEATURE:
: NAME/KEY: MOD_RES
: LOCATION: (0)...(0)
: OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-4

Query Match      85.1% Score 154; DB 3; Length 44;
Best local Similarity 95.5% Pred. No. 9.9e-21;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 ANGFLXXLRGSLXRCRXXLCSEYXAXXIFRNXXRTRQFWVS 44
DB      1 ANGFLXXLRGSLXRCRXXLCSEYXAXXIFRNXXRTRQFWVS 44

RESULT 2
US-08-955-636-26
: Sequence 26, Application US/08955636A
: Patent No. 6017882
: GENERAL INFORMATION:
: APPLICANT: Nelisestuen, Gary
: TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
: FILE REFERENCE: 09531/002001
: CURRENT APPLICATION NUMBER: US/08/955,636A
: CURRENT FILING DATE: 1997-10-23
: NUMBER OF SEQ ID NOS: 35
```

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (0)..(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-26

Query Match      67.4%; Score 122; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 5.1e-15;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY      1 ANGFLXLRXGSLXRCXKXLCSPFXAXXIFRNXXRTROFWVS 44
Db      1 ANAFLXLRGSLXRCXKXKXCSPFXAXXIFKDAKRTKLFWISY 44

RESULT      3
US-08-955-636-27
; Sequence 27, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
;   APPLICANT: Nelstuen, Gary
;   TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
;   FILE REFERENCE: 09531/002001
;   CURRENT APPLICATION NUMBER: US/08/955,636A
;   CURRENT FILING DATE: 1997-10-23
;   NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (0)..(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-27

Query Match      67.4%; Score 122; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 5.1e-15;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY      1 ANGFLXLRXGSLXRCXKXLCSPFXAXXIFRNXXRTROFWVS 44
Db      1 ANAFLXLRGSLXRCXKXKXCSPFXAXXIFKDAKRTKLFWISY 44

RESULT      4
US-08-955-636-3
; Sequence 3, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
;   APPLICANT: Nelstuen, Gary
;   TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
;   FILE REFERENCE: 09531/002001
;   CURRENT APPLICATION NUMBER: US/08/955,636A
;   CURRENT FILING DATE: 1997-10-23
;   NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
;   NAME/KEY: MOD_RES
```

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; LOCATION: (0)..(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-3

Query Match      66.9%; Score 121; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 7.7e-15;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY      1 ANGFLXLRXGSLXRCXKXLCSPFXAXXIFRNXXRTROFWVS 44
Db      1 ANAFLXLRPGSLXRCXKXKXCSPFXAXXIFKDAKRTKLFWISY 44

RESULT      5
US-08-955-636-28
; Sequence 28, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
;   APPLICANT: Nelstuen, Gary
;   TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
;   FILE REFERENCE: 09531/002001
;   CURRENT APPLICATION NUMBER: US/08/955,636A
;   CURRENT FILING DATE: 1997-10-23
;   NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (0)..(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-28

Query Match      66.9%; Score 121; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 7.7e-15;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY      1 ANGFLXLRXGSLXRCXKXLCSPFXAXXIFRNXXRTROFWVS 44
Db      1 ANAFLXLRPGSLXRCXKXKXCSPFXAXXIFKDAKRTKLFWISY 44

RESULT      6
US-08-293-778-24
; Sequence 24, Application US/08293778
; Patent No. 5580560
; GENERAL INFORMATION:
;   APPLICANT: Nicolaissen, Else M.
;   APPLICANT: Bjorn, Soren E.
;   APPLICANT: Wibergh, Finn C.
;   APPLICANT: Woodbury, Richard
;   TITLE OF INVENTION: MODIFIED FACTOR VII/VIIa
;   NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
;   ADDRESS: No. 55805600 No. 5580560disk of No. 5580560th America, Inc.
;   STREET: 405 Lexington Avenue, 62nd Floor
;   CITY: New York
;   STATE: New York
;   COUNTRY: United States of America
;   ZIP: 10174-6201
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/293,778
;   FILING DATE:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/104,509
FILING DATE:
APPLICATION NUMBER: DK 3235/87
FILING DATE: 25-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/434,149
FILING DATE: 13-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK88/00103
FILING DATE: 24-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/898,248
FILING DATE: 12-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Agis, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3129,224-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-293-778-24
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```
Query Match          66.9%; Score 121; DB 1; Length 406;
Best Local Similarity 52.3%; Pred. No. 7,2e-14;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
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```
Oy 1 ANGFLXLRXGSLRXRCXXLCSPYXXXXIFRNXXRTROFWVS 44
Db 1 ANAFLYLRPGSLYRCYKYGCSFYARYIFRDVARTKLFWISY 44
```

```
RESULT 7
US-08-295-411-5
Sequence 5, Application US/08295411
Patent No. 5679639
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Mesters, Rolf M.
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Office of Patent Counsel, The Scripps
ADDRESS: Research Institute
STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,411
FILING DATE: 22-AUG-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
CLASSIFICATION: 530
```

```
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI263.0C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..152
OTHER INFORMATION: /note="Factor VII Light Chain"
NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /note="Factor VII Heavy Chain"
US-08-295-411-5
```

```
Query Match          66.9%; Score 121; DB 1; Length 406;
Best Local Similarity 52.3%; Pred. No. 7,2e-14;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
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```
Oy 1 ANGFLXLRXGSLRXRCXXLCSPYXXXXIFRNXXRTROFWVS 44
Db 1 ANAFLELRPGSLERCKECCSFEPARETFDAERTKLFWISY 44
```

```
RESULT 8
US-08-955-471-5
Sequence 5, Application US/08955471
Patent No. 5968751
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Mesters, Rolf M.
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Office of Patent Counsel, The Scripps
ADDRESS: Research Institute
STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955,471
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/295,411
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI263.0C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
```

TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..152
OTHER INFORMATION: /note= "Factor VII Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
US-08-955-471-5

Query Match 66.9%; Score 121; DB 2; Length 406;
Best Local Similarity 52.3%; Pred. No. 7.2e-14;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Oy 1 ANGFLXXLRXGSLKRCRXKXCFXAXXIFRNXXRTROFWVSY 44
Db 1 ANAFLEELRPGSLERCKEEOCSFEAREIFKDAERTKLEWISY 44

RESULT 9
PCT-US92-10242-5
Sequence 5, Application PC/TUS9210242
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESSEE: Research Institute
STREET: 10666 North Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10242
FILING DATE: 19921118
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Filling, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRO472P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO

ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..152
OTHER INFORMATION: /note= "Factor VII Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
PCT-US92-10242-5

Query Match 66.9%; Score 121; DB 5; Length 406;
Best Local Similarity 52.3%; Pred. No. 7.2e-14;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Oy 1 ANGFLXXLRXGSLKRCRXKXCFXAXXIFRNXXRTROFWVSY 44
Db 1 ANAFLEELRPGSLERCKEEOCSFEAREIFKDAERTKLEWISY 44

RESULT 10
US-08-475-845-2
Sequence 2, Application US/08475845
Patent No. 5786965
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Brenggaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,845
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/327,690
FILING DATE: 24-OCT-1994
CLASSIFICATION: 435
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-475-845-2

Query Match 66.9%; Score 121; DB 1; Length 444;
Best Local Similarity 52.3%; Pred. No. 7.9e-14;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

OY 1 ANGFLXLRXGSLRXXCRXXLCSEFXAXXIFRNXXRTROFWVS 44
DB 39 ANAFLEELRPGSLERECKEEOCSFEAREIFKDAERTKLFWISY 82

RESULT 11

US-08-327-690-2
Sequence 2, Application US/08327690
Patent No. 5817788
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
FILING DATE: 21-MAY-1993
APPLICATION NUMBER: US/08/327,690
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-327-690-2

Query Match 66.9%; Score 121; DB 2; Length 444;
Best Local Similarity 52.3%; Pred. No. 7.9e-14;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

OY 1 ANGFLXLRXGSLRXXCRXXLCSEFXAXXIFRNXXRTROFWVS 44
DB 39 ANAFLEELRPGSLERECKEEOCSFEAREIFKDAERTKLFWISY 82

RESULT 12

US-08-660-289-2
Sequence 2, Application US/08660289
Patent No. 5833982
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
FILING DATE: 21-MAY-1993
APPLICATION NUMBER: US/08/660,289
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/475,845
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 08/327,690
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-660-289-2

Query Match 66.9%; Score 121; DB 2; Length 444;
Best Local Similarity 52.3%; Pred. No. 7.9e-14;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

OY 1 ANGFLXLRXGSLRXXCRXXLCSEFXAXXIFRNXXRTROFWVS 44
DB 39 ANAFLEELRPGSLERECKEEOCSFEAREIFKDAERTKLFWISY 82

RESULT 13
US-08-537-807-2
Sequence 2, Application US/08537807
Patent No. 5861374
GENERAL INFORMATION:
APPLICANT:

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-233-2

Query Match 66.9%; Score 121; DB 3; Length 444;
Best Local Similarity 52.3%; Pred. No. 7.9e-14;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRXGSLRXRCRXKCSFXXAXXIFRNXXRTROFWWSY 44
DB 39 ANAFLEELRPGSLERCKEEOCSFEAREIFDAERTKLFWSY 82

RESULT 16
US-09-189-607-2
Sequence 2, Application US/09189607
Patent No. 6168789
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/189,607
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,289
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/327,690
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Palmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-189-607-2
Query Match 66.9%; Score 121; DB 4; Length 444;

Best Local Similarity 52.3%; Pred. No. 7.9e-14;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRXGSLRXRCRXKCSFXXAXXIFRNXXRTROFWWSY 44
DB 39 ANAFLEELRPGSLERCKEEOCSFEAREIFDAERTKLFWSY 82

RESULT 17
US-09-378-907-2
Sequence 2, Application US/09378907
Patent No. 6183743
GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
APPLICANT: Petersen, Lars C.
APPLICANT: Hedner, Ulla
APPLICANT: Rasmussen, Mirella E.
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/378,907
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/871,003
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 90-0767
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-378-907-2
Query Match 66.9%; Score 121; DB 4; Length 444;
Best Local Similarity 52.3%; Pred. No. 7.9e-14;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRXGSLRXRCRXKCSFXXAXXIFRNXXRTROFWWSY 44
DB 39 ANAFLEELRPGSLERCKEEOCSFEAREIFDAERTKLFWSY 82

RESULT 18
PCT-US94-05779-2
Sequence 2, Application PC/TUS9405779
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US94/05779
;; FILING DATE: 23-MAY-1994
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/065,725
;; FILING DATE: 21-MAY-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/662,920
;; FILING DATE: 28-FEB-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Parmelee, Steven W.
;; REGISTRATION NUMBER: 31,990
;; REFERENCE/DOCKET NUMBER: 13952-8-1PC
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 206-467-9600
;; TELEFAX: 415-543-5043
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 444 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
PCT-US94-05779-2

Query Match 66.9%; Score 121; DB 5; Length 444;
Best Local Similarity 52.3%; Pred. No. 7.9e-14;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRGSLXRCRXKXLCSPFXAXXIFRNXXRTROFWVS 44
Db 39 ANAFLEELRPGSLERCKECCSFEAREIFKDAERTKLEWISY 82

RESULT 19
US-07-882-202A-4
; Sequence 4, Application US/07882202A
; Patent No. 5374617
; GENERAL INFORMATION:
; APPLICANT: Morrissey, James H.
; TITLE OF INVENTION: Treatment of bleeding with Modified
; TITLE OF INVENTION: Tissue Factor in Combination with FVIIa
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richards, Medlock & Andrews
; STREET: 1201 Elm Street, Suite 4500
; CITY: Dallas
; STATE: Texas
; COUNTRY: US
; ZIP: 75270-2197
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/882,202A
; FILING DATE: 13-MAY-1992
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hansen, Eugenia S.
; REGISTRATION NUMBER: 31,966
; REFERENCE/DOCKET NUMBER: OMRF B34290
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 214-939-4500
; TELEFAX: 214-939-4600
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 466 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

;; MOLECULE TYPE: protein
US-07-882-202A-4

Query Match 66.9%; Score 121; DB 1; Length 466;
Best Local Similarity 52.3%; Pred. No. 8.3e-14;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRGSLXRCRXKXLCSPFXAXXIFRNXXRTROFWVS 44
Db 61 ANAFLEELRPGSLERCKECCSFEAREIFKDAERTKLEWISY 104

RESULT 20
US-08-021-615A-4
; Sequence 4, Application US/08021615A
; Patent No. 5504064
; GENERAL INFORMATION:
; APPLICANT: Morrissey, James H.
; TITLE OF INVENTION: Treatment of bleeding with Modified
; TITLE OF INVENTION: Tissue Factor in Combination with an Activator of
; TITLE OF INVENTION: FVII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richards, Medlock & Andrews
; STREET: 1201 Elm Street, Suite 4500
; CITY: Dallas
; STATE: Texas
; COUNTRY: US
; ZIP: 75270-2197
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/021,615A
; FILING DATE: 19-FEB-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/882,202
; FILING DATE: 13-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hansen, Eugenia S.
; REGISTRATION NUMBER: 31,966
; REFERENCE/DOCKET NUMBER: OMRF B34290CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 214-939-4500
; TELEFAX: 214-939-4600
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 466 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-021-615A-4

Query Match 66.9%; Score 121; DB 1; Length 466;
Best Local Similarity 52.3%; Pred. No. 8.3e-14;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRGSLXRCRXKXLCSPFXAXXIFRNXXRTROFWVS 44
Db 61 ANAFLEELRPGSLERCKECCSFEAREIFKDAERTKLEWISY 104

RESULT 21
US-08-321-777-4
; Sequence 4, Application US/08321777
; Patent No. 5504067
; GENERAL INFORMATION:

APPLICANT: Morrissey, James H.
APPLICANT: Comp. Philip C.
TITLE OF INVENTION: Treatment of Bleeding with Modified
TITLE OF INVENTION: Tissue Factor In Combination with FVIIa
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richards, Medlock & Andrews
STREET: 1201 Elm Street, Suite 4500
CITY: Dallas
STATE: Texas
COUNTRY: US
ZIP: 75270-2197
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321,777
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/882202
FILING DATE: 13-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hansen, Eugenia S.
REGISTRATION NUMBER: 31,966
REFERENCE/DOCKET NUMBER: OMRF B34290C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4500
TELEFAX: 214-939-4600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 466 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-321-777-4

Query Match 66.9%; Score 121; DB 1; Length 466;
Best Local Similarity 52.3%; Pred. No. 8.3e-14;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXLRGSLRXRCXXLCSFXXAXXIFRNXXTRTFWWSY 44
DB 61 ANAFLELRPGSLRCKEKCQSFEEAREIFDAERTKLFWISY 104

RESULT 22
US-09-009-217-14
Sequence 14, Application US/09009217
Patent No. 6132729
GENERAL INFORMATION:
APPLICANT: Thorpe, Philip E.
APPLICANT: King, Steven W.
APPLICANT: Gao, Boning
TITLE OF INVENTION: COMBINED TISSUE FACTOR AND
TITLE OF INVENTION: CHEMOTHERAPEUTIC METHODS AND COMPOSITIONS FOR COAGULATION
TITLE OF INVENTION: AND TUMOR TREATMENT
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,217
FILING DATE: Concurrently Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/042,427
FILING DATE: 27-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,205
FILING DATE: 27-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,920
FILING DATE: 22-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: UTSD:536
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 466 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-009-217-14

Query Match 66.9%; Score 121; DB 4; Length 466;
Best Local Similarity 52.3%; Pred. No. 8.3e-14;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXLRGSLRXRCXXLCSFXXAXXIFRNXXTRTFWWSY 44
DB 61 ANAFLELRPGSLRCKEKCQSFEEAREIFDAERTKLFWISY 104

RESULT 23
US-09-009-656-14
Sequence 14, Application US/09009656
Patent No. 6132730
GENERAL INFORMATION:
APPLICANT: Thorpe, Philip E.
APPLICANT: King, Steven W.
APPLICANT: Gao, Boning
TITLE OF INVENTION: COMBINED TISSUE FACTOR AND FACTOR VIIa
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR COAGULATION AND TUMOR
TITLE OF INVENTION: TREATMENT
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,656
FILING DATE: Concurrently Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/042,427
FILING DATE: 27-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,205
FILING DATE: 27-JAN-1997
PRIOR APPLICATION DATA:

Db 1 ANAFLXLRPGSLXRXCKXKXCCSFXXARXIFDAXRTKLEWISY 44

RESULT 27

US-08-229-280-4

; Sequence 4, Application US/08229280

; Patent No. 5516640

; GENERAL INFORMATION:

APPLICANT: MATANABE, Kelsuke

APPLICANT: : NAKAKI, Toru

APPLICANT: : IWASAKI, Yoshihiro

TITLE OF INVENTION: METHOD OF DETERMINATION OF

TITLE OF INVENTION: PIKA OF EVERY KIND AND

TITLE OF INVENTION: REAGENT THEREFOR

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: FLYNN, THEL, BOUTELL & TANIS, P.C.

STREET: 2026 Rambling Road

CITY: Kalamazoo

STATE: Michigan

COUNTRY: USA

ZIP: 49008-1699

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage

COMPUTER: IBM PC/XT/AT Compatible

OPERATING SYSTEM: MS-DOS 5.0

SOFTWARE: WordPerfect 5.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/229, 280

FILING DATE:

CLASSIFICATION: 436

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 5-130015

FILING DATE: MAY 7, 1993

APPLICATION NUMBER: JP 6-16348

FILING DATE: FEBRUARY 10, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Terrence F. Chapman

REGISTRATION NUMBER: 32 549

REFERENCE/DOCKET NUMBER: Furuya Case 1312

TELECOMMUNICATION INFORMATION:

TELEPHONE: (616) 381-1156

TELEFAX: (616) 381-5465

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 41 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE:

ORGANISM: Homosapiens

FEATURE:

OTHER INFORMATION: Xaa in the sequence is

OTHER INFORMATION: -carboxylglutamic acid

US-08-229-280-4

Query Match 59.1%; Score 107; DB 1; Length 41;

Best Local Similarity 75.6%; Pred. No. 2.3e-12;

Matches 31; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 ANGFLXLRXGSLXRXCRXXICSFXXAXXIFRNXXRTROFW 41

Db 1 ANAFLXLRPGSLXRXCKXKXCCSFXXARXIFDAXRTKLEW 41

RESULT 28

US-08-330-978-2

; Sequence 2, Application US/08330978

; Patent No. 5589571

; GENERAL INFORMATION:

APPLICANT: King, Robert

TITLE OF INVENTION: PROCESS FOR PRODUCTION OF INHIBITED

TITLE OF INVENTION: FORMS OF ACTIVATED BLOOD FACTORS

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster

STREET: 2000 Pennsylvania Avenue, NW

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20006-1888

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/330, 978

FILING DATE: 28-OCT-1994

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/484,558

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Murashige, Kate H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 2803-0007.02

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)887-1500

TELEFAX: (202)822-0168

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 139 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: Disulfide-bond

LOCATION: 17..22

FEATURE:

NAME/KEY: Disulfide-bond

LOCATION: 50..61

FEATURE:

NAME/KEY: Disulfide-bond

LOCATION: 55..70

FEATURE:

NAME/KEY: Disulfide-bond

LOCATION: 72..81

FEATURE:

NAME/KEY: Disulfide-bond

LOCATION: 89..100

FEATURE:

NAME/KEY: Disulfide-bond

LOCATION: 96..109

FEATURE:

NAME/KEY: Disulfide-bond

LOCATION: 111..124

FEATURE:

NAME/KEY: Disulfide-bond

LOCATION: 132

OTHER INFORMATION: /note= "Disulfide linkage with

OTHER INFORMATION: residue 160 of SEQ ID NO:1, residue 108 of SEQ ID NO:3 or

OTHER INFORMATION: residue 108 of SEQ ID:4"

US-08-330-978-2

Query Match 54.1%; Score 98; DB 1; Length 139;

Best Local Similarity 36.4%; Pred. No. 3.1e-10;

Matches 16; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

OY 1 ANGFLXLRXGSLXRXCRXXICSFXXAXXIFRNXXRTROFWVS 44

Db 1 ANSFLTKMKGLTRCMTTCSYTTARTVFTDSDKTNFMWKY 44

```

RESULT 29
US-08-474-042-2
; Sequence 2, Application US/08474042
; Patent No. 5589572
; GENERAL INFORMATION:
; APPLICANT: King, Robert
; TITLE OF INVENTION: PROCESS FOR PRODUCTION OF INHIBITED
; TITLE OF INVENTION: FORMS OF ACTIVATED BLOOD FACTORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,042
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,558
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29, 959
; REFERENCE/DOCKET NUMBER: 2803-0007.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)887-1500
; TELEFAX: (202)822-0168
; TELEX: 90-4030 MRSNFOERSWSH
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 17..22
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 50..61
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 55..70
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 72..81
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 89..100
; NAME/KEY: Disulfide-bond
; LOCATION: 96..109
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 111..124
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 132
; OTHER INFORMATION: /note= "Disulfide linkage with
; OTHER INFORMATION: residue 160 of SEQ ID NO:1, residue 108 of SEQ ID NO:3 OR
; OTHER INFORMATION: residue 108 of SEQ ID:4"
US-08-474-042-2

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? LOCATION: -17
? OTHER INFORMATION: /note= "Location of Intron A"
?
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: (37/38)
? OTHER INFORMATION: /note= "Location of Intron B"
?
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: 46
? OTHER INFORMATION: /note= "Location of Intron C"
?
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: 63
? OTHER INFORMATION: /note= "An amino acid represented
? OTHER INFORMATION: by the greek letter Beta"
?
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: 84
? OTHER INFORMATION: /note= "Location of Intron D"
?
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: 128
? OTHER INFORMATION: /note= "Location of Intron E"
?
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: (158/159)
? OTHER INFORMATION: /note= "Location of Intron F"
?
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: 198
? OTHER INFORMATION: /note= "Location of Intron G"
?
? FEATURE:
? NAME/KEY: Disulfide-bond
? LOCATION: group(17..22, 50..61, 55..70, 72..81, 89..100, 96
? LOCATION: ..109, 111..124, 132..251, 150..155, 170..186,
? LOCATION: 299..313, 324..352)
?
US-08-487-037-2

Query Match 54.1%; Score 98; DB 1; Length 437;
Best Local Similarity 36.4%; Pred. No. 9.8e-10;
Matches 16; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

Oy 1 ANGFLXLRXGSLKRCXKXLCSEFXAXXIFRNXXRTROFWVS 44
Db 41 ANSFLTMKKGHLTRTCMTTCSTYTTARTVFTDSDKTMTFNK 84

RESULT 33
US-08-487-037-3
; Sequence 3, Application US/08487037
; Patent No. 5795863
;
; GENERAL INFORMATION:
; APPLICANT: Wolf, David L.
; TITLE OF INVENTION: RECOMBINANT AGENTS AFFECTING THROMBOSIS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW
; City: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,037
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
```

```

? NAME: Adler, Reid G.
? REGISTRATION NUMBER: 30,988
? REFERENCE/DOCKET NUMBER: 2803-0002.02
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (202) 887-1500
? TELEFAX: (202) 887-0763
? TELEX: 90-4030
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 437 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: both
?
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: -40..397
? OTHER INFORMATION: /note= "Same features apply from
? OTHER INFORMATION: SEQ ID NO:2"
?
? FEATURE:
? NAME/KEY: Protein
? LOCATION: 1..139
? OTHER INFORMATION: /note= "Factor Xa - Light Chain"
?
? FEATURE:
? NAME/KEY: Peptide
? LOCATION: -40..0
? OTHER INFORMATION: /note= "Pre-Pro leader sequence"
?
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: -17
? OTHER INFORMATION: /note= "Location of Intron A"
?
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: (37/38)
? OTHER INFORMATION: /note= "Location of Intron B"
?
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: 46
? OTHER INFORMATION: /note= "Location of Intron C"
?
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: 63
? OTHER INFORMATION: /note= "An amino acid represented
? OTHER INFORMATION: by the greek letter Beta"
?
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: 84
? OTHER INFORMATION: /note= "Location of Intron D"
?
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: 158/159
? OTHER INFORMATION: /note= "Location of Intron F"
?
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: 198
? OTHER INFORMATION: /note= "Location of Intron G"
?
? NAME/KEY: Disulfide-bond
? LOCATION: group(17..22, 50..61, 55..70, 72..81, 89..100, 96
? LOCATION: ..109, 111..124, 132..251, 150..155, 170..186,
? LOCATION: 299..313, 324..352)
?
US-08-487-037-3

Query Match 54.1%; Score 98; DB 1; Length 437;
Best Local Similarity 36.4%; Pred. No. 9.8e-10;
Matches 16; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

Oy 1 ANGFLXLRXGSLKRCXKXLCSEFXAXXIFRNXXRTROFWVS 44
Db 41 ANSFLTMKKGHLTRTCMTTCSTYTTARTVFTDSDKTMTFNK 84

RESULT 34
```



```

US-08-487-037-1
; Sequence 1, Application US/08487037
; Patent No. 5795863
; GENERAL INFORMATION:
; APPLICANT: Wolf, David L.
; TITLE OF INVENTION: RECOMBINANT AGENTS AFFECTING THROMBOSIS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,037
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 2803-0002.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: -17
; OTHER INFORMATION: /note= "Location of Intron A"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: (37~38)
; OTHER INFORMATION: /note= "Location of Intron B"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 46
; OTHER INFORMATION: /note= "Location of Intron C"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 63
; OTHER INFORMATION: /note= "Amino acid represented by
; OTHER INFORMATION: the greek letter Beta"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 84
; OTHER INFORMATION: /note= "Location of Intron D"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 128
; OTHER INFORMATION: /note= "Location of Intron E"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: (209~210)
; OTHER INFORMATION: /note= "Location of Intron F"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 249
; OTHER INFORMATION: /note= "Location of Intron G"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: -40..0

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```

; OTHER INFORMATION: /note= "Pre-Pro leader sequence"
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..139
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 143..194
; OTHER INFORMATION: /note= "Activation Peptide"
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 195..448
; OTHER INFORMATION: /note= "Factor Xa-Heavy Chain"
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: group(17..22, 50..61, 55..70, 72..81, 89..100, 96
; LOCATION: ..109, 111..124, 132..302, 201..206, 221..237,
; LOCATION: 350..364, 375..403)
US-08-487-037-1

Query Match 54.1%; Score 98; DB 1; Length 488;
Best Local Similarity 36.4%; Pred. No. 1.1e-09;
Matches 16; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

QY 1 ANGFLLXLRXGSLRXRCRXLLCSFXXAXXIFRXXXTROFWVSX 44
DB 41 ANSELTTRMKRGLTRTCMTTCSYTTARVFTDSDXTNFWNKY 84

RESULT 35
US-08-955-636-23
; Sequence 23, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelissen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-23

Query Match 53.0%; Score 96; DB 3; Length 44;
Best Local Similarity 65.9%; Pred. No. 2.2e-10;
Matches 29; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANGFLLXLRXGSLRXRCRXLLCSFXXAXXIFRXXXTROFWVSX 44
DB 1 ANSEFLXLRHGNVXRKCSXVCFFXXARXIFORTXDTMAFWSTY 44

RESULT 36
US-08-955-636-2
; Sequence 2, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelissen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A

```

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? CURRENT FILING DATE: 1997-10-23
? NUMBER OF SEQ ID NOS: 35
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 2
? LENGTH: 44
? TYPE: PRT
? ORGANISM: Bos taurus
? FEATURE:
? NAME/KEY: MOD_RES
? LOCATION: (0)..(0)
? OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid
US-08-955-636-2

```

Query Match	52.5%	Score	95	DB	3	Length	44
Best Local Similarity	65.9%	Pred	No.	3.4e-10			
Matches	29	Conservative	4	Mismatches	11	Indels	0
						Gaps	0

QY 1 ANGFLXLLRKGSLARXCRLXLCSEFXAXXIFRNXXRTQFWWSY 44
| | | | | : | | | | | : | | | | |
Db 1 ANSFLXLLRPGNVXRXCSXVXCXFXXARXIFQNTXDTMAFWWSFY 44

```

1      RESULT 37
2      US-08-295-411-3
3      : Sequence 3, Application US/08295411
4      : Patent No. 5679639
5      :
6      : GENERAL INFORMATION:
7      : APPLICANT: Griffin, John H.
8      : APPLICANT: Westers, Rolf M.
9      : TITLE OF INVENTION: Serine-Protease-Derived Polypeptides and
10     : TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
11     : TITLE OF INVENTION: for Inhibiting Coagulation
12     :
13     : NUMBER OF SEQUENCES: 10
14     :
15     : CORRESPONDENCE ADDRESSES:
16     : ADDRESSEE: Office of Patent Counsel, The Scripps
17     : ADDRESSEE: Research Institute
18     : STREET: ~10666 No. 5679639th Torrey Pines Road, TPC 8
19     : CITY: La Jolla
20     :
21     : STATE: CA
22     :
23     : COUNTRY: USA
24     :
25     : ZIP: 92037
26     :
27     : COMPUTER READABLE FORM:
28     : MEDIUM TYPE: Floppy disk
29     : COMPUTER: IBM PC compatible
30     : OPERATING SYSTEM: PC-DOS/MS-DOS
31     : SOFTWARE: Patent Release #1.0, Version #1.25
32     :
33     : CURRENT APPLICATION DATA:
34     : APPLICATION NUMBER: US/08/295,411
35     : FILING DATE: 22-AUG-1994
36     : CLASSIFICATION: 530
37     :
38     : PRIOR APPLICATION DATA:
39     : APPLICATION NUMBER: US 07/793,989
40     : FILING DATE: 18-NOV-1991
41     : CLASSIFICATION: 530
42     :
43     : ATTORNEY/AGENT INFORMATION:
44     : NAME: Fitting, Thomas
45     : REGISTRATION NUMBER: 34,163
46     : REFERENCE/DOCKET NUMBER: TSRI263.0C1
47     : TELECOMMUNICATION INFORMATION:
48     : TELEPHONE: 619-554-2937
49     : TELEFAX: 619-554-6312
50     : INFORMATION FOR SEQ ID NO: 3:
51     : SEQUENCE CHARACTERISTICS:
52     : LENGTH: 448 amino acids
53     : TYPE: amino acid
54     : TOPOLOGY: linear
55     : MOLECULE TYPE: protein
56     : HYPOTHETICAL: NO
57     : ANTI-SENSE: NO
58     : FEATURE:
59     : NAME/KEY: Region
60     : LOCATION: 1..139
61     :

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: OTHER INFORMATION: /note= "Factor X Light Chain"
:
: FEATURE:
:
: NAME/KEY: Region
: LOCATION: 140..142
: OTHER INFORMATION: /note= "Factor X Connecting
: OTHER INFORMATION: Tripeptide"
:
: FEATURE:
:
: NAME/KEY: Region
: LOCATION: 143..448
: OTHER INFORMATION: /note= "Factor X Heavy Chain"
:
US-08-295-411-3

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Query Match	51.48	Score 93	DB 1	Length 448
Best Local Similarity	36.48	Pred. No.	7.9e-09	
Matches 16	Conservative 7	Mismatches 21	Indels 0	Gaps 0

QY 1 ANGFLXXLRXGSLRXCRXXLCSFXXAXXIERNXXRTQFWVS Y 44
|||::| | | ||: | : |: || |
Db 1 ANSFLEEMKKGHLERECMEETCSYEAREVFEEDSDKTNEFNKY 44

```

1 RESULT 38
2 US-08-955-471-3
3 : Sequence 3, Application US/08955471
4 : Patent No. 5968751
5 :
6 : GENERAL INFORMATION:
7 : APPLICANT: Griffin, John H.
8 : APPLICANT: Westers, Rolf M.
9 : TITLE OF INVENTION: Serine-Protease-Derived Polypeptides and
10 : TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
11 : TITLE OF INVENTION: for Inhibiting Coagulation
12 : NUMBER OF SEQUENCES: 10
13 :
14 : CORRESPONDENCE ADDRESS:
15 : ADDRESSEE: Office of Patent Counsel, The Scripps
16 : ADDRESSEE: Research Institute
17 : STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
18 : CITY: La Jolla
19 :
20 : STATE: CA
21 :
22 : COUNTRY: USA
23 : ZIP: 92037
24 :
25 : COMPUTER READABLE FORM:
26 : MEDIUM TYPE: Floppy disk
27 : COMPUTER: IBM PC compatible
28 : OPERATING SYSTEM: PC-DOS/MS-DOS
29 : SOFTWARE: PatentIn Release #1.0, Version #1.25
30 :
31 : CURRENT APPLICATION DATA:
32 : APPLICATION NUMBER: US/08/955,471
33 : FILING DATE:
34 :
35 : CLASSIFICATION:
36 : PRIOR APPLICATION DATA:
37 : APPLICATION NUMBER: 08/295,411
38 : FILING DATE:
39 :
40 : CLASSIFICATION:
41 : ATTORNEY/AGENT INFORMATION:
42 : NAME: Filling, Thomas
43 : REGISTRATION NUMBER: 34,163
44 : REFERENCE/DOCKET NUMBER: TSRI263.0C1
45 : TELECOMMUNICATION INFORMATION:
46 : TELEPHONE: 619-554-2937
47 : TELEFAX: 619-554-6312
48 :
49 : INFORMATION FOR SEQ ID NO: 3:
50 : SEQUENCE CHARACTERISTICS:
51 : LENGTH: 448 amino acids
52 : TYPE: amino acid
53 :
54 : TOPOLOGY: linear
55 : MOLECULE TYPE: protein
56 : HYPOTHETICAL: NO
57 : ANTI-SENSE: NO
58 : FEATURE:
59 :
60 : NAME/KEY: Region
61 : LOCATION: 1..139
62 :
63 : OTHER INFORMATION: /note= "Factor X Light Chain"
64 :
65 :
66 :
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99 :

```

FEATURE:
NAME/KEY: Region
LOCATION: 140..142 /note="Factor X Connecting"
OTHER INFORMATION: tripeptide"
FEATURE:
NAME/KEY: Region
LOCATION: 143..448
OTHER INFORMATION: /note="Factor X Heavy Chain"
US-08-955-471-3

Query Match
Best Local Similarity 51.4%; Score 93; DB 2; Length 448;
Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

QY 1 ANGFLXLRXGSLXRCXKXLCFXXAXIIFNXXKTRQFWYSY 44
DB 1 ANSFLEMKKGLHRECMETCTSYEARVFEEDSDKTNEFWNKY 44

RESULT 39
PCT-US92-10068-1
Sequence 1, Application PC/TUS9210068
GENERAL INFORMATION:
APPLICANT: Allieri, Dario C
APPLICANT: Edgington, Thomas S
APPLICANT: Fair, Daryl S
TITLE OF INVENTION: Factor X-Derived Polypeptides and
TITLE OF INVENTION: Anti-peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Inflammation
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESSEE: Research Institute
STREET: 10666 North Torrey Pines Road
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10068
FILING DATE: 19921120
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/798,221
FILING DATE: 22-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: SCR1221P
REFERENCE/DOCKET NUMBER: 34,163
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..139
OTHER INFORMATION: /note="Factor X Light Chain"
FEATURE:
NAME/KEY: Region

LOCATION: 140..142 /note="Factor X Connecting"
OTHER INFORMATION: tripeptide"
FEATURE:
NAME/KEY: Region
LOCATION: 143..448
OTHER INFORMATION: /note="Factor X Heavy Chain"
PCT-US92-10068-1

Query Match
Best Local Similarity 51.4%; Score 93; DB 5; Length 448;
Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

QY 1 ANGFLXLRXGSLXRCXKXLCFXXAXIIFNXXKTRQFWYSY 44
DB 1 ANSFLEMKKGLHRECMETCTSYEARVFEEDSDKTNEFWNKY 44

RESULT 40
PCT-US92-10242-3
Sequence 3, Application PC/TUS9210242
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Masters, Rolf
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESSEE: Research Institute
STREET: 10666 North Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10242
FILING DATE: 19921118
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRO472P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..139
OTHER INFORMATION: /note="Factor X Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 140..142
OTHER INFORMATION: /note="Factor X Connecting"
FEATURE:
NAME/KEY: Region

FEATURE:
NAME/KEY: Region
LOCATION: 143..448
OTHER INFORMATION: /note= "Factor X Heavy Chain"
PCT-US92-10242-3

Query Match 51.4%; Score 93; DB 5; Length 448;
Best Local Similarity 36.4%; Pred. No. 7.9e-09;
Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

QY 1 ANGFLXXLRXGSLXRCRXSLCSPFXAXXIFRNXXRTROFVSY 44
Db 1 ANSFLEEMKRGHLEECMEETCSYEAREVEFEDSDKTNEFWNKY 44

RESULT 41
US-08-229-280-5
Sequence 5, Application US/08229280
Patent No. 5516640
GENERAL INFORMATION:
APPLICANT: MATANABE, Katsuke
APPLICANT: NAKAKI, Toru
APPLICANT: IMASAKI, Yoshihiro
TITLE OF INVENTION: METHOD OF DETERMINATION OF
TITLE OF INVENTION: PIVKA OF EVERY KIND AND
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THIEL, BOUWELL & TANIS, P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 MB storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/229,280
FILING DATE:
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-130015
FILING DATE: MAY 7, 1993
APPLICATION NUMBER: JP 6-16348
FILING DATE: FEBRUARY 10, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Terryence F. Chapman
REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Furuya Case 1312
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homosapiens
FEATURE:
OTHER INFORMATION: Xaa in the sequence is
OTHER INFORMATION: -carboxyglutamic acid
US-08-229-280-5

Query Match 49.7%; Score 90; DB 1; Length 41;
Best Local Similarity 68.3%; Pred. No. 2.4e-09;
Matches 28; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANGFLXXLRXGSLXRCRXSLCSPFXAXXIFRNXXRTROFW 41
Db 1 ANSFLLXLRHSSSLXRCXCIXXICDFXAXKXIFQNVDTLAFW 41

RESULT 42
US-08-745-254A-2
Sequence 2, Application US/08745254A
Patent No. 5837843
GENERAL INFORMATION:
APPLICANT: Smirnov, Mikhail, D.
APPLICANT: Esmen, Charles, T.
TITLE OF INVENTION: Modified Protein C
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1201 West Peachtree Street
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/745,254A
FILING DATE: 8-NOV-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF 165
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8795
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29
OTHER INFORMATION: /note= "where Xaa means gamma
FEATURE:
NAME/KEY:
LOCATION:
OTHER INFORMATION: /note= "partial sequence of human protein C"
US-08-745-254A-2

Query Match 49.7%; Score 90; DB 2; Length 42;
Best Local Similarity 68.3%; Pred. No. 2.5e-09;
Matches 28; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANGFLXXLRXGSLXRCRXSLCSPFXAXXIFRNXXRTROFW 41
Db 1 ANSFLLXLRHSSSLXRCXCIXXICDFXAXKXIFQNVDTLAFW 41

RESULT 43
US-08-955-636-1
Sequence 1, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Neilsen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
TITLE OF INVENTION: POLYPEPTIDES

FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid
US-08-955-636-1

Query Match 49.7%; Score 90; DB 3; Length 44;
Best Local Similarity 68.3%; Pred. No. 2.6e-09;
Matches 28; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANGFLXLLRSGSLXRXCRXXLCSPXXAXIFRNXXKTRQFW 41
DB 1 ANSFLXLLRHSSLLXRXCLXXICDFXXAKXIFQNVDDTLAFW 41

RESULT 44
US-08-955-636-24
Sequence 24, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Nelstuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 24
LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid
US-08-955-636-24

Query Match 49.7%; Score 90; DB 3; Length 44;
Best Local Similarity 68.3%; Pred. No. 2.6e-09;
Matches 28; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANGFLXLLRSGSLXRXCRXXLCSPXXAXIFRNXXKTRQFW 41
DB 1 ANSFLXLLRHSSLLXRXCLXXICDFXXAKXIFQNVDDTLAFW 41

RESULT 45
US-08-955-636-35
Sequence 35, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Nelstuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 35
LENGTH: 44

TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid
US-08-955-636-35

Query Match 49.7%; Score 90; DB 3; Length 44;
Best Local Similarity 68.3%; Pred. No. 2.6e-09;
Matches 28; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANGFLXLLRSGSLXRXCRXXLCSPXXAXIFRNXXKTRQFW 41
DB 1 ANSFLXLLRHSSLLXRXCLXXICDFXXAKXIFQNVDDTLAFW 41

RESULT 46
US-08-965-832-2
Sequence 2, Application US/08965832
Patent No. 5847085
GENERAL INFORMATION:
APPLICANT: CHARLES T. ESMON AND MIKHAIL D. SMIRNOV
TITLE OF INVENTION: Modified Protein C
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1201 West
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,832
FILING DATE: 7-NOV-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/745,254
FILING DATE: 8-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/053,768
FILING DATE: 25-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMR# 165/167
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29
OTHER INFORMATION: /note="where Xaa means gamma
OTHER INFORMATION: carboxyglutamic acid"
FEATURE:
NAME/KEY:
LOCATION:
OTHER INFORMATION: /note="partial sequence of human protein C"
US-08-965-832-2

GenCore version 4.5
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OW protein - protein search, using sw model

Run on: September 3, 2002, 15:15:22 ; Search time 25.1 Seconds
(without alignments)
168.443 Million cell updates/sec

Title: US-09-302-239-4-COPY
Perfect score: 181
Sequence: 1 ANGFLXXLRGSLXRCRX.....XXAXXIFRNXXRTRQFWVS 44

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 50 summaries

Database :
1: PIR_71: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	147	81.2	407	1 KFB07	coagulation factor
2	129	71.3	443	2 I16932	coagulation factor
3	121	66.9	466	1 KFH07	coagulation factor
4	106	58.6	461	1 S18994	protein C (activat
5	105	58.0	461	1 JX0210	protein C (activat
6	95	52.5	456	1 KXBO	protein C (activat
7	93	51.4	482	1 EXRT	coagulation factor
8	93	51.4	488	1 EXHU	coagulation factor
9	90	49.7	461	1 KXHU	protein C (activat
10	88	48.6	492	1 EXBO	coagulation factor
11	86	47.5	416	1 KFHU	coagulation factor
12	86	47.5	461	1 KFHU	coagulation factor
13	81	44.8	452	1 A30351	coagulation factor
14	81	44.8	459	2 U00419	coagulation factor
15	80	44.2	475	1 EXCH	coagulation factor
16	78	43.1	622	1 TBNH	coagulation factor
17	75	41.4	617	2 S10511	thrombin (EC 3.4.2
18	75	41.4	618	2 A35827	thrombin (EC 3.4.2
19	73	40.3	642	2 S53433	thrombin (EC 3.4.2
20	69	38.1	625	1 TBBO	thrombin (EC 3.4.2
21	69	38.1	675	1 KXBO	plasma protein S p
22	68	37.6	642	2 S53434	plasma protein S p
23	68	37.6	646	2 S38819	plasma protein S p
24	68	37.6	676	1 KXHU	plasma protein S p
25	65	36.5	675	1 KXRT	plasma protein S p
26	65	35.9	422	1 KXHU	plasma protein Z p
27	61	33.7	396	1 KXBO	plasma protein Z -
28	59	32.6	675	1 KXMS	plasma protein S p
29	57	31.5	678	2 B48089	growth arrest-spec

30	56	30.9	673	2 A48089	growth arrest-spec
31	54	29.8	605	1 W1WLB	E1 protein - bovin
32	54	29.8	620	1 W1WLB2	E1 protein - bovin
33	54	29.8	674	2 I55476	growth potentiatin
34	50	27.6	413	1 VHVNH	nucleoprotein - in
35	48.5	26.8	594	2 D84859	probable MAP kinase
36	48.5	26.8	603	2 C96575	probable MAP kinase
37	47.5	26.2	576	2 G96763	probable MAP kinase
38	45	24.9	687	2 T08528	probable DNA topoi
39	44	24.3	219	2 A62449	hypothetical prote
40	44	23.2	320	2 G84993	glutathione syntha
41	42	23.2	440	2 C83368	probable MFS trans
42	42	23.2	892	2 D69393	large helicase-rel
43	42	23.2	1217	2 T21403	hypothetical prote
44	42	23.2	1275	2 T18556	hypothetical prote
45	41	22.7	484	2 S43737	O-antigen biosynth
46	40.5	22.4	907	2 T15792	protein kinase SLR
47	40	22.1	402	2 C72226	hypothetical prote
48	40	22.1	629	2 T37255	acetylcholinestera
49	40	22.1	1101	2 T26919	hypothetical prote
50	39.5	21.8	355	2 F86328	FlpI.7 protein -

ALIGNMENTS

RESULT 1
KFB07
coagulation factor VIIa (EC 3.4.21.21) - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 21-May-1990 #sequence_revision 23-Mar-1995 #text_change 16-Jul-1999
C:Accession: A31979; C20274
R:Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, S.
J. Biol. Chem. 263, 14868-14877, 1988
A>Title: Bovine Factor VII. Its purification and complete amino acid sequence.
A:Reference number: A31979; MUID:89008362
A:Accession: A31979
A:Molecule type: protein
A:Residues: 1-407 <TRAK>
R:McMullen, B.A.; Fujikawa, K.; Kistel, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A>Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood
A:Reference number: A20274; MUID:83308813
A:Accession: C20274
A:Molecule type: protein
A:Residues: 58-62, 'X', 64-68 <MCK>
A>Note: the residue designated 'X' was determined to be hydroxyaspartic acid
R:Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga
J. Biochem. 104, 867-868, 1988
A>Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood c
A:Reference number: A44556; MUID:89213999
A:Contents: annotation
A>Note: structure and location of covalently bound carbohydrate
C:Function:
A:Description: catalyzes the proteolytic activation of coagulation factor X in the pr
gulation factor IX in the presence of calcium and tissue factor
A:Pathway: blood coagulation extrinsic pathway
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglu
F:1-152/Product: coagulation factor VIIa light chain #status experimental <MA1>
F:1-14/Domains: Gla domain homology (fragment) <GLA>
F:50-81/Domains: EGF homology <EG2>
F:91-127/Domains: EGF homology <EG2>
F:153-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
F:153-387/Domains: trypsin homology <TR>
F:6,7,14,16,19,20,25,26,29,34,35/Modified site: gamma-carboxyglutamic acid (Glu) #sta
F:17-22,50-61,55-70,72-81,91-102,98-112,114-127,135-262,159-164,178-194,310-329,340-3
F:52/Binding site: carbohydrate (Ser) (covalent) #status experimental
F:63/Modified site: erythro-beta-hydroxyaspartic acid (Asp) (partial) #status experim
F:145/203/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:152-153/Cleavage site: Arg-Ile (coagulation factor Xla) #status experimental
F:193,242,344/Active site: His, Asp, Ser #status predicted
F:290-291/Cleavage site: Arg-Gly (coagulation factor Xa) #status experimental

Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

QY 1 ANGFLXXLRKSLXRCXKXLCSEFXKXIXFRNXXRTRQFWVSY 44
 Db 40 ANSFLEELRPGNVRECESEVCEFEAREIFQNTEDTMAFMSFY 83

RESULT 7

EXRT
 coagulation factor Xa (EC 3.4.21.6) precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 31-Jan-1995 #sequence_revision 07-Feb-1997 #text_change 08-Dec-2000
 C:Accession: S49075; J04670; PS0191; PS0190; 162745
 R:Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.
 Thromb. Res. 80, 63-73, 1995
 A:Title: Evidence for competition between vitamin K-dependent clotting factors for intr
 A:Reference number: A58498; MUID:96093366
 A:Accession: S49075
 A:Molecule type: mRNA
 A:Residues: 1-482 <STAL>
 A:Cross-references: EMBL:X79807; NID:9506600; PIDN:CAAS6202.1; PID:9506601
 A:Note: submitted to the EMBL Data Library, June 1994
 A:Note: neither the complete nucleic acid sequence nor the complete translation are show
 R:Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.
 Gene 169, 269-273, 1996
 A:Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.
 A:Reference number: J04670; MUID:96194815
 A:Accession: J04670
 A:Molecule type: mRNA
 A:Residues: 1-482 <STAA>
 A:Cross-references: EMBL:X79807; NID:9506600; PIDN:CAAS6202.1; PID:9506601
 A:Experimental source: Cos-1 cell
 R:Enjyoji, K.; Miyazaki, K.; Kato, H.
 J. Biochem. 109, 890-898, 1991
 A:Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat pla
 A:Reference number: PS0190; MUID:92041742
 A:Accession: PS0191
 A:Molecule type: protein
 A:Residues: 41-58, 'X', 60-65 <ENJ1>
 A:Accession: PS0190
 A:Molecule type: protein
 A:Residues: 183-186, 'X', 188-207 <ENJ2>
 R:Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.
 Eur. J. Haematol. 52, 162-168, 1994
 A:Title: Analysis of the partial nucleotide sequences and deduced primary structures of
 A:Reference number: I46196; MUID:94222160
 A:Accession: I62745
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 295-383, 'G', 385-455 <MUR>
 A:Cross-references: GB:D21215; NID:9415309; PIDN:BA04756.1; PID:9455396
 C:Function:
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
 C:Pathway: blood coagulation
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutan
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-40/Domain: propeptide #status predicted <PRO>
 F:41-119/Domain: Gla domain homology <GLA>
 F:90-121/Domain: coagulation factor X light chain #status predicted <LCH>
 F:129-164/Domain: EGF homology <EGF>
 F:183-482/Product: coagulation factor X heavy chain #status predicted <HCH>
 F:183-231/Domain: activation peptide #status predicted <APT>
 F:232-482/Product: coagulation factor Xa heavy chain #status predicted <ACH>
 F:232-460/Domain: trypsin homology <TRY>
 F:46-47, 54-56, 59-60, 65-66, 69-72, 75/Modified site: gamma-carboxylglutamic acid (Glu) #stat
 F:57-62, 90-101, 95-110, 112-121, 129-140, 136-149, 151-164, 172-340, 238-243, 259-275, 389-402, 41
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
 F:187/Binding site: carboxylate (Asn) (covalent) #status experimental
 F:208/Binding site: carboxylate (Thr) (covalent) #status predicted
 F:218/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:231-232/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #stat

F:274,320,417/Active site: His, Asp, Ser #status predicted

Query Match 51.4%; Score 93; DB 1; Length 482;
 Best Local Similarity 36.4%; Pred. No. 9.5e-09;
 Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLXXLRKSLXRCXKXLCSEFXKXIXFRNXXRTRQFWVSY 44
 Db 41 ANSFEEIKKGNLRECEVEICSEFEAREVEDNEKTEFWNKY 84

RESULT 8

EXHU
 coagulation factor Xa (EC 3.4.21.6) precursor [validated] - human
 N:Alternate names: Stuart factor
 C:Species: Homo sapiens (man)
 C>Date: 15-Nov-1984 #sequence_revision 02-May-1994 #text_change 08-Dec-2000
 C:Accession: A24478; J00917; A42485; A23853; A22208; A21284; A20362; S39415; I54051;
 R:Leytus, S.P.; Foster, D.C.; Kirsch, K.; Davie, E.W.
 Biochemistry 25, 5098-5102, 1986
 A:Title: Gene for human Factor X: a blood coagulation factor whose gene organization
 A:Reference number: A24478; MUID:87026600
 A:Accession: A24478
 A:Molecule type: DNA
 A:Residues: 1-488 <LEY>
 A:Cross-references: GB:L29433; GB:M4327; NID:9459809; PIDN:AAA52764.1; PID:9182831
 R:Messier, T.L.; Pittman, D.D.; Long, G.L.; Kaufman, R.J.; Church, W.R.
 Gene 99, 291-294, 1991
 A:Title: Cloning and expression in COS-1 cells of a full-length cDNA encoding human c
 A:Reference number: J00917; MUID:91216473
 A:Accession: J00917
 A:Molecule type: mRNA
 A:Residues: 1-488 <MES>
 A:Cross-references: GB:M57285; NID:9182389; PIDN:AAA52421.1; PID:9182390
 R:Miao, C.H.; Leytus, S.P.; Chung, D.W.; Davie, E.W.
 J. Biol. Chem. 267, 7395-7401, 1992
 A:Title: Liver-specific expression of the gene coding for human factor X, a blood coa
 A:Reference number: A42485; MUID:92218390
 A:Accession: A42485
 A:Molecule type: DNA
 A:Residues: 1-15 <MIA>
 A:Experimental source: liver
 A:Note: sequence extracted from NCBI backbone (NCBIN:93780, NCBI:93787)
 R:Kaul, R.K.; Hildebrand, B.; Roberts, S.; Jagadeeswaran, P.
 Gene 41, 311-314, 1986
 A:Title: Isolation and characterization of human blood-coagulation factor X cDNA.
 A:Reference number: A25853; MUID:86221713
 A:Accession: A25853
 A:Molecule type: mRNA
 A:Residues: 19-284, 'E', 289-488 <KAU>
 A:Cross-references: GB:M22613; NID:9180335; PIDN:AAA51984.1; PID:9180336
 R:Fung, M.R.; Hay, C.W.; MacGillivray, R.T.A.
 Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985
 A:Title: Characterization of an almost full-length cDNA coding for human blood coagul
 A:Reference number: A22208; MUID:85216545
 A:Accession: A22208
 A:Molecule type: mRNA
 A:Residues: 13-441, 'S', 443-488 <FUN>
 A:Cross-references: GB:R03194; NID:9182840; PIDN:AAA52490.1; PID:9182841
 R:Leytus, S.P.; Chung, D.W.; Kistiel, W.; Kirsch, K.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 81, 3699-3702, 1984
 A:Title: Characterization of a cDNA coding for human factor X.
 A:Reference number: A21284; MUID:84222026
 A:Accession: A21284
 A:Molecule type: mRNA
 A:Residues: 15-284, 'E', 289-488 <LE2>
 A:Cross-references: GB:R01886
 R:McMullen, B.A.; Fujikawa, K.; Kistiel, W.; Sasagawa, T.; Howald, W.N.; Kwa, E.Y.; We
 Biochemistry 22, 2875-2884, 1983
 A:Title: Complete amino acid sequence of the light chain of human blood coagulation f
 A:Reference number: A20362; MUID:83257207
 A:Accession: A20362

A:Molecule type: protein
 A:Residues: 41-179 <MCM>
 R:Inoue, K.; Morita, T.
 Eur. J. Biochem. 218, 153-163, 1993
 A>Title: Identification of O-linked oligosaccharide chains in the activation peptides of
 A:Reference number: S39414; MUID:94062825
 A:Accession: S39415
 A:Molecule type: Protein
 A:Residues: 183-234 <INO>
 A>Note: glycosylation sites
 A>Note: Identification and characterization of beta-hydroxyaspartic acid
 R:Jadadeswaran, P.; Reddy, S.V.; Rao, K.J.; Hamsabhusanham, K.; Lyman, G.
 Gene 84, 517-519, 1989
 A>Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human
 A:Reference number: 154051; MUID:90128299
 A:Accession: 154051
 A>Status: translation not shown; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-23 <RES>
 A:Cross-references: GB:M33297; NID:9183860; PIDN:AAA52636.1; PID:9553330
 R:Padmanabhan, K.; Padmanabhan, K.P.; Tulinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Bie
 J. Mol. Biol. 232, 947-966, 1993
 A>Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.
 A:Reference number: A49458; MUID:93360277
 A:Contents: annotation: X-ray crystallography, 2.2 angstroms
 C:Comment: The two chains held together by one disulfide bond are formed from a single-C
 C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or
 C:Genetics:
 A:Gene: GDB:F10
 A:Cross-references: GDB:119890; OMIM:227600
 A:Map position: 13q34-13q34
 A:Introns: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1
 A>Note: deficiency of this factor causes Stuart disease
 C:Function:
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
 A:Pathway: blood coagulation
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglut
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-40/Domain: propeptide #status predicted <PRO>
 F:25-84/Domain: Gla domain homology <GUA>
 F:41-179/Product: coagulation factor X light chain #status experimental <LCH>
 F:90-121/Domain: EGF homology <EG1>
 F:129-164/Domain: EGF homology <EG2>
 F:183-488/Product: coagulation factor X heavy chain #status experimental <HCH>
 F:235-488/Product: activation peptide #status experimental <APT>
 F:235-488/Product: coagulation factor Xa heavy chain #status experimental <ACT>
 F:235-468/Domain: trypsin homology <TRY>
 F:46-47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #stat
 F:57-62/Disulfide bonds: #status predicted
 F:90-101,95-110,112-121,129-140,136-149,151-164,172-342,241-246,261-277,390-404,415-443/
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:199,211/Binding site: carboxylate (Thr) (covalent) #status experimental
 F:221,231/Binding site: carboxylate (Asn) (covalent) #status experimental
 F:234-235/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #stat
 F:276,322,419/Active site: His, Asp, Ser #status experimental

Query Match 51.4%; Score 93; DB 1; Length 488;
 Best Local Similarity 36.4%; Pred. No. 9.6e-09;
 Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

OY 1 ANGFLXLRGSLRXRCXICSFXXAXXIFRNXXRTQFWWSY 44
 DB 41 ANSFLPKMKKGLHRECKMETCTSYEDAREVFEDSKTNEFWNKY 84

RESULT 9
 KKHU
 protein C (activated) (EC 3.4.21.69) precursor - human
 M:Alternate names: autoproteohombin IIA; plasma protein C
 C:Species: Homo sapiens (man)
 C:Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999

C:Accession: A22331; A25426; A21781; A23789; A00927
 R:Foster, D.C.; Yoshitake, S.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985
 A>Title: The nucleotide sequence of the gene for human protein C.
 A:Reference number: A22331; MUID:85270390
 A:Accession: A22331
 A:Molecule type: DNA
 A:Residues: 1-461 <FOS1>
 A:Cross-references: GB:M11226; NID:9190333; PIDN:AAA60166.1; PID:9190334
 R:Plutsky, J.; Hoskins, J.A.; Long, G.L.; Crabtree, G.R.
 Proc. Natl. Acad. Sci. U.S.A. 83, 546-550, 1986
 A>Title: Evolution and organization of the human protein C gene.
 A:Reference number: A25426; MUID:86120978
 A:Accession: A25426
 A:Molecule type: DNA
 A:Residues: 1-445, 1-446-461 <PLU>
 A:Cross-references: GB:M12712; NID:9190330; PIDN:AAA60165.1; PID:9190332
 R:Foster, D.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 81, 4766-4770, 1984
 A>Title: Characterization of a cDNA coding for human protein C.
 A:Reference number: A21781; MUID:84272714
 A:Accession: A21781
 A:Molecule type: mRNA
 A:Residues: 1-107-461 <FOS2>
 A:Cross-references: GB:X02750; NID:9190322; PIDN:AAA60164.1; PID:9190323
 R:Beckmann, R.J.; Schmidt, R.J.; Santerre, R.F.; Plutsky, J.; Crabtree, G.R.; Long, G
 Nucleic Acids Res. 13, 5233-5241, 1985
 A>Title: The structure and evolution of a 461 amino acid human protein C precursor an
 A:Reference number: A23789; MUID:85269639
 A:Accession: A23789
 A:Molecule type: mRNA
 A:Residues: 1-461 <BRC>
 A:Cross-references: GB:X02750; NID:935689; PIDN:CAA26528.1; PID:9763120
 R:Millett, J.P.; Broze Jr., G.J.
 J. Biol. Chem. 265, 11397-11404, 1990
 A>Title: Beta protein C is not glycosylated at asparagine 329. The rate of translatio
 A:Reference number: A44605; MUID:90293094
 A:Contents: annotation: carbohydrate binding sites; activation peptide
 A>Note: The alpha form of protein C is glycosylated at Asn-329, and the beta form is
 R:Harris, R.J.; Ling, V.T.; Spellman, M.W.
 J. Biol. Chem. 267, 5102-5107, 1992
 A>Title: O-linked fucose is present in the first epidermal growth factor domain of fa
 A:Reference number: A44606; MUID:92184750
 A:Contents: annotation: beta-hydroxyaspartic acid
 C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that
 lation of factor Va is strongly enhanced by complexing with protein S. Protein C als
 C:Comment: Protein C is synthesized in the liver as a single chain precursor, which i
 bin, which cleaves a dodecapeptide from the amino end of the heavy chain; this react
 C:Genetics:
 A:Gene: GDB:PROC
 A:Cross-references: GDB:120317; OMIM:176860
 A:Map position: 2q13-2q21
 A:Introns: 24/1; 88/1; 134/1; 179/1; 226/3; 266/1
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol
 C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium bind
 F:1-32/Domain: signal sequence #status predicted <SIG>
 F:27-86/Domain: Gla domain homology <GUA>
 F:33-42/Domain: propeptide #status predicted <PRO>
 F:43-197/Product: protein C light chain #status predicted <LCH>
 F:92-131/Domain: EGF homology <EG1>
 F:140-175/Domain: EGF homology <EG2>
 F:200-461/Product: protein C heavy chain #status predicted <HCH>
 F:200-211/Domain: activation peptide #status experimental <APT>
 F:212-445/Domain: trypsin homology <TRY>
 F:48,49,56,58,61,62,67,68,71/Modified site: gamma-carboxyglutamic acid (Glu) #status
 F:59-64,92-105,101-120,122-131,140-151,147-160,162-175,183-319,238-254,373-387,398-42
 F:106-111/Disulfide bonds: #status predicted
 F:110/Binding site: carboxylate (Thr) (covalent) #status absent
 F:113/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:139,290,355/Binding site: carboxylate (Asn) (covalent) #status experimental
 F:211-212/Cleavage site: Arg-Ileu (thrombin) #status experimental
 F:253,299,402/Active site: His, Asp, Ser #status predicted
 F:371/Binding site: carboxylate (Asn) (covalent) (partial) #status atypical

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Query Match      49.7%; Score 90; DB 1; Length 461;
Best Local Similarity 46.3%; Pred. No. 3.2e-08;
Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

OY      1  ANGFLXXLRXGSLRXCXKCSFXKXAXIFRNXXRTQEFV 41
Db      43  ANSFLEELRHSSLERECLEECDEFEAKEIFQNVDDTLAFW 83

RESULT 10
EXBO
coagulation factor Xa (EC 3.4.21.6) precursor - bovine
N:Alternate names: Stuart factor
C:Species: Bos primigenius taurus (cattle)
C:Date: 24-Apr-1984 #sequence.revision 17-Mar-1987 #text.change 16-Jul-1999
C:Accession: A22867; A14997; A12030; A34412; S39414; A00925
R:Func, M.R.; Campbell, R.M.; Macgillivray, T.A.
Nucleic Acids Res. 12, 4481-4492, 1984
A:Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a
A:Reference number: A22867; MUID:84247315
A:Accession: A22867
A:Molecule type: mRNA
A:Residues: 1-487 <FUN>
A:Cross-references: GB:X00673; NID:g192; PIDN:CAA25286.1; PID:g193
R:Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K.
Biochemistry 19, 659-667, 1980
A:Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).
A:Reference number: A14997; MUID:80130563
A:Accession: A14997
A:Molecule type: protein
A:Residues: 41-102, 'N', 104-180 <ENF>
R:McMullen, B.A.; Fujikawa, K.; Kistiel, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co
A:Reference number: A20274; MUID:83308813
A:Contents: annotation; revision to residue 103
R:Titani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.
Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975
A:Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.
A:Reference number: A12030; MUID:76053069
A:Accession: A12030
A:Molecule type: protein
A:Residues: 183-292, 294-295, 'GDE', 299-334, 336-348, 'AE', 351-354, 356-441, 'GRFG', 446-492 <T
A:Note: carboxydrate binding sites and disulfide bonds were determined
R:Persson, E.; Selander, M.; Linse, S.; Drakenberg, T.; Oehlin, A.K.; Stenflo, J.
J. Biol. Chem. 264, 16897-16904, 1989
A:Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal
A:Reference number: A34412; MUID:89380326
A:Accession: A34412
A:Molecule type: protein
A:Residues: 85-126 <PER>
A:Note: beta-hydroxyaspartic acid site
R:Inoue, K.; Morita, T.
Eur. J. Biochem. 218, 153-163, 1993
A:Title: Identification of O-linked oligosaccharide chains in the activation peptides of
A:Reference number: S39414; MUID:94062825
A:Accession: S39414
A:Molecule type: protein
A:Residues: 183-196, 199-209, 216-233 <INO>
A:Note: carboxydrate binding sites
R:Titani, K.; Hermanson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.; D
Biochemistry 11, 4899-4903, 1972
A:Title: Bovine factor X-1a (activated Stuart factor). Evidence of homology with mammal
A:Reference number: A12453; MUID:73055314
A:Contents: annotation; active site
R:Fujikawa, K.; Titani, K.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975
A:Title: Activation of bovine factor X (Stuart factor): conversion of factor Xalpha to
A:Contents: annotation; activation
R:Stigo, T.; Bjork, I.; Holmgren, A.; Stenflo, J.

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J. Biol. Chem. 259, 5705-5710, 1984
A:Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxygluta
A:Reference number: A38024; MUID:84185716
A:Contents: annotation; calcium binding
R:Morita, T.; Jackson, C.M.
J. Biol. Chem. 261, 4008-4014, 1986
A:Reference number: A38025; MUID:86140210
A:Contents: annotation; sulfate binding
C:Comment: Factor Xa converts prothrombin to thrombin during blood clotting.
C:Comment: The two chains are formed from a single-chain precursor by the excision of
C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway)
activation.
C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with s
C:Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vita
C:Genetics:
A:Gene: F10
A:Map position: 13q34
C:Function:
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the
A:Pathway: blood coagulation
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglu
E:1-15/Domain: signal sequence #status predicted <SIG>
E:16-40/Domain: propeptide #status predicted <PRO>
E:25-84/Domain: Gla domain homology <GLA>
E:41-180/Product: coagulation factor X light chain #status experimental <LCH>
E:90-121/Domain: EGF homology <EGF>
E:129-164/Domain: EGF homology <EG2>
E:183-492/Product: coagulation factor X heavy chain #status experimental <HC>
E:183-223/Domain: activation peptide #status experimental <APT>
E:234-492/Product: coagulation factor Xa heavy chain #status experimental <AHC>
E:234-461/Domain: trypsin homology <TRY>
E:46-47, 54, 55, 59, 60, 65, 66, 69, 72, 75, 79/Modified site: gamma-carboxyglutamic acid (Glu)
E:57-62, 90-101, 95-110, 112-121, 129-140, 136-149, 151-164, 172-341/Disulfide bonds: #statu
E:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
E:200/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental
E:208, 485/Binding site: carboxydrate (Thr) (covalent) #status experimental
F:218/Binding site: carboxydrate (Asn) (covalent) #status experimental
F:233-234/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #s
F:240-245, 260-276, 389-403, 414-442/Disulfide bonds: #status experimental
F:275, 321, 418/Active site: His, Asp, Ser #status predicted

Query Match      48.6%; Score 88; DB 1; Length 492;
Best Local Similarity 36.4%; Pred. No. 7.7e-08;
Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

OY      1  ANGFLXXLRXGSLRXCXKCSFXKXAXIFRNXXRTQEFVSV 44
Db      41  ANSFLEEVKQGNLERECLEACSLAEAREVEFEDAQTDPEWSKY 84

RESULT 11
EXBO
coagulation factor IXa (EC 3.4.21.22) precursor - bovine
N:Alternate names: Christmas factor
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Nov-1980 #sequence.revision 03-Aug-1984 #text.change 16-Jul-1999
C:Accession: A14757; B20274; I45891; A00923
R:Katayama, K.; Ericsson, L.H.; Enfield, D.L.; Walsh, K.A.; Neurath, H.; Davie, E.W.;
Proc. Natl. Acad. Sci. U.S.A. 76, 4990-4994, 1979
A:Title: Comparison of amino acid sequence of bovine coagulation factor IX (Christmas
A:Reference number: A14757; MUID:80056619
A:Accession: A14757
A:Molecule type: protein
A:Residues: 1-63, 'T', 65-416 <KAT>
R:McMullen, B.A.; Fujikawa, K.; Kistiel, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood
A:Reference number: A20274; MUID:83308813
A:Accession: B20274
A:Molecule type: protein
A:Residues: 59-63, 'X', 65-69 <MCW>

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A:Accession: S12058
 A:Molecule type: mRNA; protein
 A:Residues: 1-68 <JAL>
 A:Note: processed forms expressed in recombinant system
 R:Handford, P.A.; Baron, M.; Mayhew, M.; Willis, A.; Beesley, T.; Brownlee, G.G.; Campden
 EMO J. 9, 475-480, 1990
 A:Title: The first EGF-like domain from human factor IX contains a high-affinity calcium
 A:Reference number: S12377; MUID:90151623
 A:Accession: S12377
 A:Molecule type: protein
 A:Residues: 92-130 <HAN>
 A:Note: NMR detection of calcium binding by domain expressed in recombinant system
 R:de la Salle, C.; Charmanier, J.L.; Baas, M.J.; Schwartz, A.; Wiesel, M.L.; Grunbaum,
 Thromb. Haemost. 70, 370-371, 1993
 A:Title: A deletion located in the 3' non translated part of the factor IX gene respons
 A:Reference number: I59612; MUID:94054330
 A:Accession: I59612
 A:Molecule type: DNA
 A:Status: translated from GB/EMBL/DBJ
 A:Residues: 444-461 <RES>
 A:Cross-references: GB:S66752; NID:q439773; PIDN:AA828588.1; PID:q439774
 R:Stoffel, E.S.; Koebel, D.D.; Sarkar, G.; Sommer, S.S.
 Science 239, 491-494, 1988
 A:Title: Genomic amplification with transcript sequencing.
 A:Reference number: I59529; MUID:88127096
 A:Accession: I59529
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 290-359 <RE2>
 A:Cross-references: GB:M19063; NID:q182622; PIDN:AA52456.1; PID:q182623
 R:Agarwal, K.L.; Kawabata, S.; Takao, T.; Murata, H.; Shimonishi, Y.; Nishimura, H.; I
 Biochemistry 33, 5167-5171, 1994
 A:Title: Activation peptide of human factor IX has oligosaccharides O-glycosidically lin
 A:Reference number: A54255; MUID:94227047
 A:Accession: A54255
 A:Molecule type: protein
 A:Residues: 'D', 204, 'X', 206-211; 212, 'D', 214, 'X', 216-221, 'D', <AGA>
 A:Note: the residues designated 'X' were determined to be threonine bound to carbohydrat
 R:Di Sciopio, R.G.; Kurachi, K.; Davie, E.W.
 J. Clin. Invest. 61, 1528-1538, 1978
 A:Title: Activation of human factor IX (Christmas factor).
 A:Reference number: A18483; MUID:78194509
 A:Contents: annotation: activation; active site: carbohydrate binding
 R:McGrath, R.A.; Davys, L.M.; Noyes, C.M.; Graham, J.B.; Roberts, H.R.; Stafford, D.W.
 Am. Soc. Hematol. Abstr. 64(Suppl.1), 262a, 1984
 A:Reference number: A37569
 A:Accession: A37569
 A:Contents: annotation
 A:Note: 194-Thr was also found
 R:Morita, T.; Isaacs, B.S.; Esmon, C.T.; Johnson, A.E.
 J. Biol. Chem. 259, 5698-5704, 1984
 A:Title: Derivatives of blood coagulation factor IX contain a high affinity Ca2+-binding
 A:Reference number: A37543; MUID:84185715
 A:Contents: annotation: calcium binding
 R:Morita, T.; Isaacs, B.S.; Esmon, C.T.; Johnson, A.E.
 J. Biol. Chem. 260, 2583, 1985
 A:Reference number: A37544
 A:Contents: annotation: calcium binding; correction
 R:Bentley, A.K.; Rees, D.J.G.; Rizza, C.; Brownlee, G.G.
 Cell 45, 343-348, 1986
 A:Title: Defective propeptide processing of blood clotting factor IX caused by mutation
 A:Reference number: A37545; MUID:86189947
 A:Contents: annotation; signal sequence cleavage site
 R:Sehltro, K.; Kawabata, S.I.; Miyata, T.; Takeya, H.; Takamatsu, J.; Ogata, K.; Kamiya,
 J. Biol. Chem. 264, 21257-21265, 1989
 A:Title: Blood clotting factor IX B(M) Nagoya: substitution of arginine 180 by tryptoph
 A:Reference number: A30622; MUID:90078229
 A:Contents: annotation: sequence of mutant B(M) Nagoya
 A:Note: carboxylation, glycosylation, and cleavage sites
 R:Baron, M.; Norman, D.G.; Harvey, T.S.; Hanford, P.A.; Mayhew, M.; Tse, A.G.D.; Brownl
 submitted to the Brookhaven Protein Data Bank, November 1991
 A:Reference number: A51252; PDB:1IXA
 A:Contents: annotation: conformation by (1)H-NMR, residues 92-130
 A:Note: recombinant form expressed in yeast

C:Comment: Factor IX is activated by factor XIa, which excises the activation peptide
 C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitam
 C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with s
 C:Genetics:
 A:Gene: GDB:F9
 A:Cross-references: GDB:119900; OMIM:306900
 A:Map position: Xq27.1-Xq27.2
 A:Introns: 30/1; 84/2; 93/1; 131/1; 174/1; 241/3; 280/1
 A:Function:
 C:Description: catalyzes the proteolytic activation of coagulation factor X in the pr
 A:Pathway: blood coagulation intrinsic pathway
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglu
 F:1-28/Domain: signal sequence #status predicted <SIG>
 F:29-46/Domain: propeptide #status predicted <PPT>
 F:31-91/Domain: Gla domain homology <Gla>
 F:47-191/Product: coagulation factor IXa light chain #status experimental <ALC>
 F:97-128/Domain: EGF homology <EGF>
 F:134-170/Domain: EGF homology <EG2>
 F:182-226/Domain: activation peptide #status experimental <ACT>
 F:227-461/Product: coagulation factor IXa heavy chain #status experimental <AHC>
 F:227-454/Domain: trypsin homology <TRY>
 F:53-54,61,63,66,67,72,73,76,79,82,86/Modified site: gamma-carboxyglutamic acid (Glu)
 F:64-69,97-108,102-117,119-128,134-145,141-155,157-170,178-335,252-268,382-396,407-43
 F:99/Binding site: carbohydrate (Ser) (covalent) #status experimental
 F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:191-192/Cleavage site: Arg-Ala (coagulation factor XIa) #status experimental
 F:203,213/Binding site: carboxylate (Asn) (covalent) #status experimental
 F:205,215/Binding site: carboxylate (Thr) (covalent) #status experimental
 F:226-227/Cleavage site: Arg-Val (coagulation factor XIa) #status experimental

Query Match 47.5%; Score 86; DB 1; Length 461;
 Best Local Similarity 39.5%; Pred. No. 1,7e-07;
 Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

QY 2 NGELXLRGSLRXCRXXLCSEFXAXXIFRNXXRTQFVWSY 44
 Db 49 SGKLEEVQGLRECEMEKCFEAREVEFNTERTTFWQY 91

RESULT 13
 A30351
 coagulation factor IXa (EC 3.4.21.22) precursor - dog
 C:Species: Canis lupus familiaris (dog)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A30351; MUID:146201
 R:Evans, J.P.; Matzke, H.H.; Ware, J.L.; Stafford, D.W.; High, K.A.
 Blood 74, 207-212, 1989
 A:Title: Molecular cloning of a cDNA encoding canine factor IX.
 A:Reference number: A30351; MUID:89323338
 A:Accession: A30351
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-452 <EVA>
 A:Cross-references: GB:M21757; NID:q972719; PIDN:AA75006.1; PID:q163948
 R:Axelrod, J.H.; Read, M.S.; Brinkhaus, K.W.; Yerna, I.M.
 Proc. Natl. Acad. Sci. U.S.A. 87, 5173-5177, 1990
 A:Title: Phenotypic correction of factor IX deficiency in skin fibroblasts of hemophi
 A:Reference number: I46201; MUID:90311364
 A:Accession: I46201
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-452 <XNE>
 A:Cross-references: GB:M33826; NID:q163949; PIDN:AA30844.1; PID:q163950
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglu
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-40/Domain: propeptide #status predicted <PPT>
 F:24-80/Domain: Gla domain homology <Gla>
 F:41-452/Product: coagulation factor IX #status predicted <MAT>
 F:90-121/Domain: EGF homology <EG1>
 F:127-163/Domain: EGF homology <EG2>
 F:218-445/Domain: trypsin homology <TRY>

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 384-618 'E' <BAN>
A:Cross-references: GB:M01394
C:Superfamily: Thrombin; Gla domain homology; kringle homology; trypsin homology
C:Keywords: blood coagulation; calcium binding; carboxylutamic acid; glycoprotein; hyd
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-43/Domain: propeptide #status predicted <PRO>
F:28-88/Domain: Gla domain homology <GLA>
F:44-618/Product: prothrombin B #status predicted <MAT>
F:109-187/Domain: kringle homology <KR1>
F:215-293/Domain: kringle homology <KR2>
F:361-610/Domain: trypsin homology <TRY>
F:501-515,58,60,63,64,69,70,73,76/Modified site: gamma-carboxylutamic acid (Glu) #statu
F:61-66,91-104,109-187,130-170,158-182,215-293,236-276,264-288,333-479,388-404,533-547,5
F:403,459,565/Active site: His, Asp, Ser #status predicted

Query Match 41.4%; Score 75; DB 2; Length 618;
Best Local Similarity 37.2%; Pred. No. 2,1e-05;
Matches 16; Conservative 4; Mismatches 23; Indels 0; Gaps 0;

Oy 2 NGFLXLRXGSLRXCRXXLCSEFXAXXIFRNXXRTQFWVS 44
Db 46 SGFLELRKGNLEKCEQSYEAFPALESPQDTDFWMAKY 88

RESULT 19

S53433
Plasma protein S precursor, vitamin K dependent - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 01-Aug-1995 #sequence_revision 18-Jul-1997 #text_change 16-Jul-1999
C:Accession: S53433
R:Greengard, J.S.; Fernandez, J.A.; Radtke, K.P.; Griffin, J.H.
Biochem. J. 305, 397-403, 1995
A:Title: Identification of candidate residues for interaction of protein S with C4b bind
A:Reference number: S53433; MUID:95134217
A:Accession: S53433
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-642 <GRE>
A:Cross-references: EMBL:L31379
A:Experimental source: tissue type liver
C:Genetics:
A:Gene: PROS
C:Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom
F:1-51/Domain: Gla domain homology (fragment) <GLA>
F:1-7/Domain: signal sequence (fragment) #status predicted <SIG>
F:8-642/Product: plasma protein S #status predicted <MAT>
F:87-120/Domain: EGF homology <EG1>
F:127-165/Domain: EGF homology <EG2>
F:171-207/Domain: EGF homology <EG3>
F:213-248/Domain: EGF homology <EG4>
F:281-633/Domain: sex hormone-binding globulin homology <SHB>
F:291-444/Domain: laminin G repeat homology <LGR>

Query Match 40.3%; Score 73; DB 2; Length 642;
Best Local Similarity 36.4%; Pred. No. 4,9e-05;
Matches 16; Conservative 5; Mismatches 23; Indels 0; Gaps 0;

Oy 1 ANGFLXLRXGSLRXCRXXLCSEFXAXXIFRNXXRTQFWVS 44
Db 8 ANSMLEKRGKGNLEKCEQSYEAFPALESPQDTDFWMAKY 51

RESULT 20

TBBO
Thrombin (EC 3.4.21.5) precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 24-Apr-1994 #sequence_revision 14-Jul-1994 #text_change 18-Jun-1999
C:Accession: S02537; A00915; A37552; I46045; S67518
R:Irwin, D.M.; Robertson, K.A.; Macgillivray, R.T.A.

J. Mol. Biol. 200, 31-45, 1988
A:Title: Structure and evolution of the bovine prothrombin gene.
A:Reference number: S02537; MUID:88245190
A:Accession: S02537
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-625 <IRM>
R:Macgillivray, R.T.A.; Davie, E.W.
Biochemistry 23, 1626-1634, 1984
A:Title: Characterization of bovine prothrombin mRNA and its translation product.
A:Reference number: A00915; MUID:84203525
A:Accession: A00915
A:Molecule type: mRNA
A:Residues: 1-230, 'H', 232-625 <MAC>
A:Note: 600-Asn was also found
R:Magnusson, S.; Soltup-Jensen, L.; Petersen, T.E.; Claess, H.
In Boehrhaave Symposium on Prothrombin and Related Coagulation Factors, Hemker, H.C.,
A:Reference number: A37552
A:Accession: A37552
A:Molecule type: protein
A:Residues: 44-287, 'N', 289-352, 'E', 354, 'Q', 356-548, 'ND', 551-599, 'N', 601-625 <MAG>
A:Note: the evidence for 231-Ser is strong
A:Note: disulfide bonds and carbohydrate binding sites were determined
R:Park, C.H.; Tulinsky, A.
Biochemistry 25, 3977-3982, 1986
A:Title: Three-dimensional structure of the kringle sequence: structure of prothrombi
A:Reference number: A37553; MUID:86296631
A:Contents: annotation; residues 44-317, X-ray crystallography, 2.8 angstroms
R:Irwin, D.M.; Ahern, K.G.; Pearson, G.D.; Macgillivray, R.T.A.
Biochemistry 24, 6854-6861, 1985
A:Title: Characterization of the bovine prothrombin gene.
A:Reference number: A37554; MUID:86077733
A:Contents: annotation; gene structure
R:Macgillivray, R.T.; Deegen, S.J.; Chandra, T.; Woo, S.L.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 77, 5153-5157, 1980
A:Title: Cloning and analysis of a cDNA coding for bovine prothrombin.
A:Reference number: I46045; MUID:81054926
A:Accession: I46045
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 466-599, 'N', 601-625 <MA2>
A:Cross-references: EMBL:V00135; NID:q772; PIDN:CAA23451.1; PID:9808945
R:Pejler, G.; Karlstroem, A.R.; Berg, L.
Eur. J. Biochem. 227, 102-107, 1995
A:Title: Identification of the proteolytic thrombin fragments formed after cleavage w
A:Reference number: S67518; MUID:95154277
A:Accession: S67518
A:Status: preliminary
A:Molecule type: protein
A:Residues: 318-325,333-338, 'X', 340:367-374,481-484, 'X', 486-488,515-522 <PEJ>
C:Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fi
C:Comment: Prothrombin is activated on the surface of a phospholipid membrane that bi
tivation peptide and cleaves the remaining part into light and heavy chains. The acti

C:Comment: Thrombin can cleave the amino-terminal activation peptide 1 from prothromb
C:Comment: The gamma-carboxylutamic acid residues bind calcium ions, result from the carb
ent interaction with the negatively charged phospholipid membrane surface.
C:Comment: The prothrombin precursor is synthesized in the liver.
C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C:Keywords: blood coagulation; calcium binding; carboxylutamic acid; duplication; gl
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-43/Domain: propeptide #status predicted <PRO>
F:28-88/Domain: Gla domain homology <GLA>
F:44-625/Product: prothrombin #status experimental <MP1>
F:109-187/Domain: kringle homology <KR1>
F:200-317/Domain: activation peptide 2 #status experimental <PR2>
F:214-292/Domain: kringle homology <KR2>
F:318-366/Product: thrombin light chain #status experimental <LC1>
F:367-625/Product: thrombin heavy chain #status experimental <HC1>
F:367-616/Domain: trypsin homology <TRY>
F:501-515,58,60,63,64,69,70,73,76/Modified site: gamma-carboxylutamic acid (Glu) #stat
F:61-66,91-104,109-187,130-170,158-182,214-292,235-275,263-287,339-485,394-410,539-555

F:120-144/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:409,465,571/Active site: His, Asp, Ser #status experimental

Query Match 38.1%; Score 69; DB 1; Length 625;
Best Local Similarity 35.7%; Pred. No. 0.00025;
Matches 15; Conservative 3; Mismatches 24; Indels 0; Gaps 0;

Qy 3 GFLXLRKXSLKRXCRXXLCSPFXAXXIFRNXXRTROFWVS 44
Db 47 GFLEEVKKNLERECLEPCSRREAFALBSLSTADFAWKY 88

RESULT 21

KXBOS

N:plasma protein S precursor - bovine

N:Alternate names: vitamin K-dependent protein S

C:Species: Bos primigenius taurus (cattle)

C>Date: 08-Aug-1987 #sequence_revision 26-Jan-1996 #text_change 16-Jul-1999

C:Accession: A24759; A23888

R:Dahlback, B.; Lundwall, A.; Stenflo, J.
Proc. Natl. Acad. Sci. U.S.A. 83, 4199-4203, 1986A:Title: Primary structure of bovine vitamin K-dependent protein S.
A:Reference number: A24759; PMID:86233400

A:Accession: A24759

A:Molecule type: mRNA

A:Residues: 1-675 <DAH>

A:Cross-references: GB:M13044; NID:g163697; PIDN:AAA30757.1; PID:g163698

A:Note: parts of this sequence, including the amino end of the mature protein, were detected

R:Dahlback, B.; Lundwall, A.; Stenflo, J.
J. Biol. Chem. 261, 5111-5115, 1986

A:Title: Localization of thrombin cleavage sites in the amino-terminal region of bovine

A:Reference number: A23888; PMID:86168236

A:Accession: A23888

A:Molecule type: protein

A:Residues: 42-141 <DA2>

C:Complex: in plasma forms a complex with C4b binding protein

C:Function:

A:Description: a cofactor for activated protein C (EC 3.4.21.69); thrombin cleavage deest

C:Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom

C:Keywords: beta-hydroxyasparagine; beta-hydroxyaspartic acid; blood coagulation; carbox

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-41/Domain: propeptide #status predicted <PRO>

F:26-85/Domain: Gla domain homology <GLA>

F:42-675/Product: plasma protein S #status experimental <MAT>

F:121-154/Domain: EGF homology <EG1>

F:161-199/Domain: EGF homology <EG2>

F:205-241/Domain: EGF homology <EG3>

F:247-282/Domain: EGF homology <EG4>

F:315-666/Domain: sex hormone-binding globulin homology <SHB>

F:325-478/Domain: laminin G repeat homology <LGR>

F:47,48,55,57,60,61,66,67,70,73,77/Modified site: gamma-carboxyglutamic acid (Glu) #stat

F:58-63,88-113,121-134,126-143,145-154,161-175,171-184,186-199,205-217,212-226,228-241,2

F:93-94/Cleavage site: Arg-Ala (thrombin) #status experimental

F:111-112/Cleavage site: Arg-Ser (thrombin) #status experimental

F:136/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

F:177,219,255/Modified site: erythro-beta-hydroxyasparagine (Asn) #status experimental

F:288-567,449-475,638-665/Disulfide bonds: #status experimental

F:499/Binding site: carbohydrate (Asn) (covalent) #status experimental

F:509/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 38.1%; Score 69; DB 1; Length 675;
Best Local Similarity 36.4%; Pred. No. 0.00027;

Matches 16; Conservative 4; Mismatches 24; Indels 0; Gaps 0;

Qy 1 ANGFLXLRKXSLKRXCRXXLCSPFXAXXIFRNXXRTROFWVS 44

Db 42 ANTLLEETKKNLERECLEPCSRREAFALBSLSTADFAWKY 85

RESULT 22

S53434

plasma protein S precursor, vitamin K dependent - rhesus macaque (fragment)
C:Species: Macaca mulatta (rhesus macaque)

C>Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 16-Jul-1999

C:Accession: S53434

R:Greenard, J.S.; Fernandez, J.A.; Radtke, K.P.; Griffiin, J.H.
Biochem. J. 305, 397-403, 1995

A:Title: Identification of candidate residues for interaction of protein S with C4b b

A:Reference number: S53433; PMID:95134217

A:Accession: S53434

A>Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-642 <GRE>

A:Cross-references: EMBL:L31380

A:Experimental source: tissue type liver

A:Note: the source is designated as rhesus monkey

C:Genetics:

A:Gene: PROS

C:Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat

F:1-51/Domain: Gla domain homology (fragment) <GLA>

F:1-7/Domain: signal sequence (fragment) #status predicted <SIG>

F:8-642/Product: plasma protein S #status predicted <MAT>

F:87-120/Domain: EGF homology <EG1>

F:127-165/Domain: EGF homology <EG2>

F:171-207/Domain: EGF homology <EG3>

F:213-248/Domain: EGF homology <EG4>

F:261-633/Domain: sex hormone-binding globulin homology <SHB>

F:291-444/Domain: laminin G repeat homology <LGR>

Query Match 37.6%; Score 68; DB 2; Length 642;
Best Local Similarity 34.1%; Pred. No. 0.00039;

Matches 15; Conservative 5; Mismatches 24; Indels 0; Gaps 0;

Qy 1 ANGFLXLRKXSLKRXCRXXLCSPFXAXXIFRNXXRTROFWVS 44

Db 8 ANSMLEETKKNLERECLEPCSRREAFALBSLSTADFAWKY 51

RESULT 23

S38819

N:plasma protein S - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 18-Feb-1994 #sequence_revision 21-Jul-1995 #text_change 16-Jul-1999

C:Accession: S38819; S37238

R:He, X.; Dahlback, B.
Eur. J. Biochem. 217, 857-865, 1993

A:Title: Molecular cloning, expression and functional characterization of rabbit anti

A:Reference number: S38819; PMID:94039141

A:Accession: S38819

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-646 <HEX>

A:Cross-references: EMBL:226485

R:He, X.; Dahlback, B.
Submitted to the EMBL Data Library, September 1993

A:Description: Molecular Cloning and Expression of Rabbit Anticoagulant Vitamin K-dep

A:Reference number: S37238

A:Accession: S37238

A:Molecule type: mRNA

A:Residues: 1502,1504-646 <HE2>

A:Cross-references: EMBL:226485; NID:g403306; PIDN:CA81259.1; PID:g403307

C:Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat

F:1-56/Domain: Gla domain homology (fragment) <GLA>

F:92-125/Domain: EGF homology <EG1>

F:132-170/Domain: EGF homology <EG2>

F:176-212/Domain: EGF homology <EG3>

F:218-253/Domain: EGF homology <EG4>

F:286-637/Domain: sex hormone-binding globulin homology <SHB>

F:296-449/Domain: laminin G repeat homology <LGR>

Query Match 37.6%; Score 68; DB 2; Length 646;
Best Local Similarity 34.1%; Pred. No. 0.00039;

F:136/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
E:117.219.258/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F:499.509/Binding site: carbonylrate (Asn) (covalent) #status predicted

Query Match	32.6%	Score 59	DB 1	Length 675
Best Local Similarity	31.8%	Pred. No. 0.017		
Matches 11, Conservative	4	Mismatches 26	Indels 0	Gaps 0

OY	1	A	N	G	E	L	A	L	R	G	S	L	R	K	C	R	X	A	L	C	S	F	F	A	X	I	R	N	X	R	T	Q	E	V	S	Y	44
Db	42	A	N	T	L	F	E	E	T	M	K	G	N	L	E	R	E	C	I	E	L	C	N	K	E	A	E	V	E	N	N	E	D	E	T	Y	85

RESULT 29
B48089 growth arrest-specific protein gas6 - human
C:Species: Homo sapiens (man)
C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 05-Nov-1999
R:Accession: B48089
R:Manfioletti, G.; Brancolini, C.; Avanzi, G.; Schneider, C.
Mol. Cell. Biol. 13, 4976-4985, 1993
A:Title: The protein encoded by a growth arrest-specific gene (gas6) is a new member of
A:Reference number: A48089; MUID:9330291

Query Match	31.5%	Score 57	DB 2	Length 678
Best Local Similarity	36.1%	Pred. NO	0.039	
Matches 13; Conservative		3; Mismatches	20; Indels	0; Gaps

```

0y      9 RKGSLRACRXXLLCSFFXXAXIIFRNXXRTRQFWSY 44
      : | | | | | | | | | | | | | | | | | |
Db     57 KQGHLENECVEEELCSREAREFFENDPETDYFPRY 92

```

```

RESULT      30
A48089      growth arrest-specific protein gas6 - mouse
C:Species:  Mus musculus (house mouse)
C:Date:      26-May-1994 #sequence_revision 26-May-1994 #text_change 05-Nov-1999
C:Accession: A48089; S37437
R:Manfioletti, G.; Brancolini, C.; Avanzi, G.; Schneider, C.
Mol. Cell. Biol. 13, 4976-4985, 1993
A:Title:     The protein encoded by a growth arrest-specific gene (gas6) is a new member of
A:Reference number: A48089, MUID:93330291

```

F:239-274/Domain: EGF homology <EG4>
F:308-666/Domain: sex hormone-binding globulin homology <SHB>
F:318-470/Domain: laminin G repeat homology <LGR>

	Query Match	30.9%	Score 56;	DB 2;	Length 673;
	Best Local Similarity	33.3%	Pred. NO.	0.058;	
	Matches	12;	Conservative	4;	Mismatches 20; Indels 0; Gaps 0;
OY	9	RXGSLRXRCRXXLCSFXAXXTFRNXXXTROFWASY	44	:	: : : : : :
Db	54	KQGHLEKRECVCEVCKSEAREVEFENDPEFYFPY	89	:	: : : : : :

```

RESULT 31
M1MLEB
E1 protein - bovine papillomavirus type 1
C:Species: bovine papillomavirus type 1
C:Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 28-Jul-2000
C:Accession: A03663
R:Chen, E.Y.; Howley, P.M.; Levinson, A.D.; Seeburg, P.H.
Nature 299, 529-534, 1982
A:Title: The primary structure and genetic organization of the bovine papillomavirus
A:Reference number: A93289; MUID:83012974
A:Accession: A03663
A:Molecule type: DNA
A:Residues: 1-605 <CHED>
A:Cross-references: GB:X02346; GB:J02044; GB:M24622; GB:X00473; NID:g60965; PIDN:CAB4
C:Superfamily: papillomavirus E1 protein
C:Keywords: early protein

```

Query Match	29.8%	Score 54;	DB 1;	Length 605;
Best Local Similarity	45.5%	Pred. No. 0.12;		
Matches 10; Conservative	2;	Mismatches 10;	Indels 0;	Gaps 0;
Oy	21	LCSEFXAXXIFRNXXRTQFWY	42	
db	172	LCSEFDITRLKNDKXTNOQWV	193	

```

RESULT      32
M1M1B2
E1 protein - bovine papillomavirus type 2
C1:Species: bovine papillomavirus type 2
C1:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 12-Jun-1998
C1:Accession: C311169
R1:Groff, D.E.; Mitra, R.; Lancaster, W.D.
submitted to GenBank, May 1988
A1:Reference number: A94519
A1:Accession: C311169
A1:Molecule type: DNA
A1:Residues: 1-620 <GRO>
A1:Cross-references: GB:M20219; GB:M19551; NID:g332996
C1:Superfamily: papillomavirus E1 protein
C1:Keywords: early protein; glycoprotein
F:72,109,173/Binding site: carbohydrate (Asn) (covalent) #status predicted

```

Query Match	29.8%	Score 54;	DB 1;	Length 620;
Best Local Similarity	45.5%	Pred. No. 0.12;		
Matches 10; Conservative	2;	Mismatches 10;	Indels 0;	Gaps 0;
OY	21	LCSEFXAXXIFRNXXRTROFVY	42	
db	187	LCSEFHLTRLEKNDKRTINQOAV	208	

RESULT 33
155476
growth potentiating factor - rat
C:Species: Rattus sp. (rat)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Apr-2001

C:Accession: I55476
R:Nakano, T.; Higashino, K.; Kikuchi, N.; Kishino, J.; Nomura, K.; Fujita, H.; Ohara, O.
J. Biol. Chem. 270, 5702-5705, 1995
A:Title: Vascular smooth muscle cell-derived, Glu-containing growth-potentiating factor
A:Reference number: I55476; MUID:95197586
A:Accession: I55476
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-674 <RES>
A:Cross-references: GB:D42148; NID:g1526567; PIDN:BAA07719.1; PID:g893402
C:Superfamily: plasma protein S; EGF homology; Glu domain homology; laminin G repeat hom
F:117-150/Domain: Glu domain homology <Glu>
F:117-150/Domain: EGF homology <EG1>
F:157-192/Domain: EGF homology <EG2>
F:198-233/Domain: EGF homology <EG3>
F:239-274/Domain: EGF homology <EG4>
F:308-667/Domain: sex hormone-binding globulin homology <SHB>
F:318-470/Domain: laminin G repeat homology <LGR>

Query Match

Best Local Similarity 29.8%; Score 54; DB 2; Length 674;
Matches 12; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

Oy 9 RCGSLRXCRRXXLCSEFYXXAXIFRNXXRTRQFWVS 44
Db 54 KQHLRECEVEVCSKEAREVEFNDPTTFYFPRY 89

RESULT 34

VHVNIIH
nucleoprotein - infectious hematopoietic necrosis virus
N:Alternate names: nucleocapsid protein
C:Species: Infectious hematopoietic necrosis virus
C:Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 16-Jul-1999
C:Accession: A31834
R:Gilmore Jr., R.D.; Leong, J.C.
Virology 167, 644-648, 1988
A:Title: The nucleocapsid gene of infectious hematopoietic necrosis virus, a fish rhabd
A:Reference number: A31834; MUID:89073771
A:Accession: A31834
A:Molecule type: mRNA
A:Residues: 1-413 <GTL>
A:Cross-references: GB:U04321; NID:g331304; PIDN:AAA6240.1; PID:g331305
C:Superfamily: Infectious hematopoietic necrosis virus nucleoprotein
C:Keywords: nucleocapsid; nucleoprotein

Query Match

Best Local Similarity 27.6%; Score 50; DB 1; Length 413;
Matches 10; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

Oy 11 GSLRXCRRXXLCSEFYXXAXIFRNXXRTRQFW 41
Db 57 GEGTRALGLCAFTVETVHRGKSPNFM 87

RESULT 35

Probable MAP kinase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: D84859
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentol, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: D84859
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-594 <STO>

A:Cross-references: GB:AE002093; NID:g4512667; PIDN:AAD21721.1; GSPDB:GN00139
C:Genetics:
A:Gene: Atg242880
A:Map position: 2

Query Match

Best Local Similarity 26.8%; Score 48.5; DB 2; Length 594;
Matches 10; Conservative 2; Mismatches 15; Indels 1; Gaps 1;

Oy 17 CRXXLCSEFYXXAXIFRNXXRTRQFWVS 44
Db 151 CKLKICDFGLARVAF-NDPTTFWTDY 177

RESULT 36

Probable MAP kinase ATM9K, 96271-101224 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: C96575
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitl, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: C96575
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-603 <STO>
A:Cross-references: GB:AE005173; NID:g10645353; PIDN:AAG21473.1; GSPDB:GN00141
C:Genetics:
A:Gene: F22G10.12
A:Map position: 1

Query Match

Best Local Similarity 26.8%; Score 48.5; DB 2; Length 603;
Matches 10; Conservative 2; Mismatches 15; Indels 1; Gaps 1;

Oy 17 CRXXLCSEFYXXAXIFRNXXRTRQFWVS 44
Db 151 CKLKICDFGLARVAF-NDPTTFWTDY 177

RESULT 37

Probable MAP kinase F25P22.9 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: G96763
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitl, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: G96763
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-576 <STO>
A:Cross-references: GB:AE005173; NID:g6692731; PIDN:AAF24837.1; GSPDB:GN00141

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
 A:Authors: Overbeek, T.; Cotton, M.D.; Spriggs, T.; Artlach, P.; Kaine, B.P.; Sykes, S.; Smith, H.O.; Woese, C.R.; Venter, J.C.
 A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon
 A:Reference number: A69250; MWID:98049343
 A:Accession: D69393
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-892 <LIE>
 A:Cross-references: GB:AE001024; GB:AE000782; NID:g2689347; PID:AA090094.1; PID:g264943
 C:Keywords: ATP; nucleotide binding; P-loop
 F:39-46/Region: nucleotide-binding motif A (P-loop)
 F:144-149/Region: nucleotide-binding motif B
 F:148-151/Region: DEXH motif

Query Match 23.2%; Score 42; DB 2; Length 892;
 Best Local Similarity 70.0%; Pred. No. 25;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 32 RNXXRTQFW 41
 || |||:|
 Db 882 RNVIRTRFW 891

RESULT 43
 T21403
 hypothetical protein F26D2.10 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
 C:Accession: T21403
 R:McMurray, A.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: 219418
 A:Accession: T21403
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1217 <MID>
 A:Cross-references: EMBL:281513; PIDN:CAB04180.1; GSPDB:GN00023; CESP:F26D2.10
 A:Experimental source: clone F26D2
 C:Genetics:
 A:Gene: CESP:F26D2.10
 A:Map position: 5
 A:Insertions: 29/1; 568/2; 608/3; 746/1; 871/3; 910/1; 985/1; 1018/3; 1124/1; 1170/3
 C:Superfamily: Caenorhabditis elegans hypothetical protein F36D3.5

Query Match 23.2%; Score 42; DB 2; Length 1217;
 Best Local Similarity 52.9%; Pred. No. 33;
 Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 NGFLXLRXGSLRXRCR 18
 ||| ||| |
 Db 707 NGFAGSLRNGSLREMAR 723

RESULT 44
 T18556
 O-antigen biosynthesis protein homolog rfbC - Myxococcus xanthus
 C:Species: Myxococcus xanthus
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T18556
 R:Guo, D.; Bowden, M.G.; Pershad, R.; Kaplan, H.B.
 J. Bacteriol. 178, 1631-1639, 1996
 A:Title: The Myxococcus xanthus rfbC operon encodes an ATP-binding cassette transport
 A:Reference number: Z18970; MWID:96198166
 A:Accession: T18556
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1275 <GUO>
 A:Cross-references: EMBL:U06795; NID:g1235659; PID:g1235662; PIDN:AA05019.1
 C:Genetics:

A:Note: rfbC

Query Match 23.2%; Score 42; DB 2; Length 1275;
 Best Local Similarity 45.0%; Pred. No. 34;
 Matches 9; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 3 GFLXLRXGSLRXRCXXLC 22
 || | | | | |
 Db 1144 GMLPAERTGALYRCDVGLC 1163

RESULT 45
 S43737
 protein kinase SLT2 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein H8179.16; protein YHR030C
 C:Species: Saccharomyces cerevisiae
 C:Date: 30-Sep-1993 #sequence_revision 27-Jan-1995 #text_change 23-Mar-2001
 C:Accession: S43737; S46743; S19051
 R:Nombela, C.
 submitted to the EMBL Data Library, January 1994
 A:Reference number: S43737
 A:Accession: S43737
 A:Molecule type: DNA
 A:Residues: 1-484 <NOM>
 A:Cross-references: EMBL:X59262; NID:g455518; PIDN:CAA41954.1; PID:g455519
 A:Note: this is a revision to the sequence from reference S19051
 R:Du, Z.
 submitted to the EMBL Data Library, May 1994
 A:Description: The sequence of S. cerevisiae cosmid 8179.
 A:Reference number: S46732
 A:Accession: S46743
 A:Molecule type: DNA
 A:Residues: 1-484 <DUZ>
 A:Cross-references: EMBL:U00062; NID:g488162; PIDN:AA068912.1; PID:g488177; MIPS:YHR0
 R:Torres, L.; Martin, H.; Garcia-Saez, M.I.; Arroyo, J.; Molina, M.; Sanchez, M.; Nom
 Mol. Microbiol. 5, 2845-2854, 1991
 A:Title: A protein kinase gene complements the lytic phenotype of Saccharomyces cerev
 A:Reference number: S19051; MWID:92140049
 A:Accession: S19051
 A:Molecule type: DNA
 A:Residues: 1-55, 'L', '57-466', 'S', '468-484' <TOR>
 A:Cross-references: EMBL:X59262
 A:Note: this sequence has been revised in reference S43737
 C:Genetics:
 A:Gene: SGD:SLT2
 A:Cross-references: SGD:S0001072; MIPS:YHR030C
 A:Map position: 8R
 C:Function:
 A:Description: phosphotransferase; serine/threonine-specific protein kinase
 C:Superfamily: unassigned ser/Thr or Tyr-specific protein kinases; protein kinase hom
 C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
 F:21-287/Domain: protein kinase homology <RIN>
 F:29-37/Region: protein kinase ATP-binding motif
 F:153/Active site: Asp #status predicted

Query Match 22.7%; Score 41; DB 2; Length 484;
 Best Local Similarity 28.2%; Pred. No. 22;
 Matches 11; Conservative 4; Mismatches 22; Indels 2; Gaps 1;

Qy 8 LRKGSLL--XRXCRXXLCSEFYXXAXIIFNXXRTQFWVS 44
 || | | | | | | | | | | |
 Db 154 LRPNLLVNVADQLKICDFGLRGSNPVENSQFLREY 192

RESULT 46
 T15792
 hypothetical protein CA2D8.5 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
 C:Accession: T15792
 R:Hallsworth, K.

submitted to the EMBL Data Library, April 1996
A:Description: The sequence of C. elegans cosmid C42D8.
A:Reference number: 218405
A:Accession: U15792

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-907 <HAL>

A:Cross-references: EMBL:U56966; NID:g1293844; PID:g1293847; PIDN:AAA9719.1; GSPDB:GN00
A:Experimental source: strain Bristol N2; clone C42D8
C:Genetics:

A:Gene: CESP:C42D8.5
A:Map position: X
A:Introns: 140/3; 170/3; 194/3; 300/2; 467/3; 551/2; 600/2; 697/3; 774/2; 851/3

Query Match 22.4%; Score 40.5; DB 2; Length 907;
Best Local Similarity 50.0%; Pred. No. 47;

Matches 9; Conservative 1; Mismatches 5; Indels 3; Gaps 1;

Oy 30 IFRN---XXRTQFWVS 44
||| | : |||
Db 307 IFRNEKASRLQHLWVS 324

RESULT 47
C72226
hypothetical protein TM1677 - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: C72226

R:Neelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999

A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316
A:Accession: C72226

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-402 <ARN>

A:Cross-references: GB:AE001808; GB:AE000512; NID:g4982233; PIDN:AAD36744.1; PID:g498225
A:Experimental source: strain MSB8
C:Genetics:

A:Gene: TM1677
C:Superfamily: hypothetical protein b1432

Query Match 22.1%; Score 40; DB 2; Length 402;
Best Local Similarity 26.3%; Pred. No. 28;

Matches 10; Conservative 5; Mismatches 19; Indels 4; Gaps 1;

Oy 11 GSLXKX---RXKCSFXKXKXIFRNXXRTQFWVS 44
| | | | | : | | | | |
Db 15 GHLSTCEELNRTAARIYNTKMTSVIRKIRKGFMLSW 52

RESULT 48
T37255

acetylcholinesterase (EC 3.1.1.7) 2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C:Accession: T37255
R:Grauso, M.; Culetto, E.; Combes, D.; Fedon, Y.; Toutant, J.P.; Arpagaus, M.
FEBS Lett. 424, 279-284, 1998

A:Title: Existence of four acetylcholinesterase genes in the nematodes Caenorhabditis el
A:Reference number: Z21648; MUID:98198570
A:Accession: T37255

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-629 <GRA>

A:Cross-references: EMBL:AF025378; NID:g5148937; PIDN:AAC14016.2; PID:g5091489
A:Experimental source: strain N2
C:Genetics:

A:Gene: ace-2
A:Map position: I
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase

Query Match 22.1%; Score 40; DB 2; Length 629;
Best Local Similarity 50.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 31 FRNXXRTQFWVS 44
| | | | | : | | | | |
Db 531 FANTGRTDFEMPQY 544

RESULT 49
T26919
hypothetical protein Y45F10B.10 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T26919

R:McMurray, A.
submitted to the EMBL Data Library, January 1998
A:Reference number: 220286
A:Accession: T26919

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1101 <WIL>

A:Cross-references: EMBL:AL021487; PIDN:CAA16357.1; GSPDB:GN00022; CESP:Y45F10B.10
A:Experimental source: clone Y45F10B
C:Genetics:

A:Gene: CESP:Y45F10B.10
A:Map position: 4
A:Introns: 217/3; 292/1; 451/3; 556/2; 637/3; 755/3; 823/2; 946/1; 1078/3

Query Match 22.1%; Score 40; DB 2; Length 1101;
Best Local Similarity 29.7%; Pred. No. 68;

Matches 11; Conservative 4; Mismatches 16; Indels 6; Gaps 1;

Oy 8 LRXGSLXRCRXKXLCSPXKXKXIFRNXXRTQFWVS 44
| | | | | : | | | | |
Db 243 LHSGLNDRKELSLCHFVYDV-----TRFYGISH 273

RESULT 50
F86328

F14P1.7 protein - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
C:Accession: F86328

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Deward,
ansen, N.F.; Hughes, B.; Huizler, L.
Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: F86328

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-355 <STO>

A:Cross-references: GB:AE005172; NID:g9795587; PIDN:AAF98405.1; GSPDB:GN00141
C:Genetics:

A:Map position: 1

Query Match 21.8%; Score 39.5; DB 2; Length 355;
Best Local Similarity 45.8%; Pred. No. 31;

	Matches	11;	Conservative	2;	Mismatches	10;	Indels	1;	Gaps	1;
Qy	1	ANGFLXXLRK6-SLXRCRXXLCS	23							
		:								
Db	296	ASGFLYGLIKGLSLLECCKVGSCS	319							

Search completed: September 3, 2002, 15:15:23
Job time: 811 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 3, 2002, 15:21:35 : Search time 15.9 Seconds
(without alignments)
107.148 Million cell updates/sec

Title: US-09-302-239-4-COPY
Perfect score: 181
Sequence: 1 ANGFLXLLKRGSLKRCRXX.....XXAXXIFRNXXRTQFVWSY 44

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 50 summaries

Database : SWISSPROT_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	147	81.2	407	1	FA7_BOVIN
2	129	71.3	444	1	FA7_RABIT
3	121	66.9	466	1	FA7_HUMAN
4	106	58.6	218	1	TMG1_HUMAN
5	106	58.6	461	1	PRTC_RAT
6	105	58.0	461	1	PRTC_MOUSE
7	104	57.5	446	1	FA7_MOUSE
8	100	55.2	459	1	PRTC_PIG
9	99	54.7	231	1	TMG3_HUMAN
10	95	52.5	456	1	PRTC_BOVIN
11	94	51.9	490	1	FA10_RABIT
12	93	51.4	488	1	FA10_HUMAN
13	90	49.7	461	1	PRTC_HUMAN
14	88	48.6	492	1	FA10_BOVIN
15	86	47.5	416	1	FA9_BOVIN
16	86	47.5	461	1	FA9_HUMAN
17	83	45.9	458	1	PRTC_RABIT
18	81	44.8	452	1	FA9_CANFA
19	81	44.8	459	1	FA9_MOUSE
20	80	44.2	475	1	FA10_CHICK
21	78	43.1	622	1	THRB_HUMAN
22	75	41.4	617	1	THRB_RAT
23	75	41.4	618	1	THRB_MOUSE
24	69	38.1	202	1	TMG2_HUMAN
25	69	38.1	226	1	TMG4_HUMAN
26	69	38.1	625	1	THRB_BOVIN
27	69	38.1	675	1	PRTC_BOVIN
28	68	37.6	646	1	PRTC_RABIT
29	68	37.6	649	1	PRTC_MACMU
30	68	37.6	676	1	PRTC_HUMAN
31	67	37.0	376	1	FA10_TROCA
32	66	36.5	675	1	PRTC_RAT
33	65	35.9	400	1	PRTC_HUMAN

34	61	33.7	396	1	PRTC_BOVIN	P00744 bos taurus
35	59	32.6	675	1	PRTC_MOUSE	O08761 mus musculus
36	54	29.8	604	1	VEL_BPV2	P11298 bovine papilloma virus
37	54	29.8	605	1	VEL_BPV1	P03116 bovine papilloma virus
38	50	27.6	413	1	NCAP_THNV	P19691 infectious bovine rhinotracheitis virus
39	42	23.2	320	1	GSIB_BUCAL	P57612 bucheira ap
40	42	23.2	1275	1	RPRC_MYXSA	O05086 myxococcus
41	41	22.7	484	1	SILT2_YEAST	O00772 saccharomyces cerevisiae
42	39.5	21.8	503	1	ATPA_ODOST	O00820 odontella
43	39	21.5	2476	1	ZAN_PIG	O28983 sus scrofa
44	38	21.0	818	1	CDBI_HUMAN	O28983 sus scrofa
45	38	21.0	912	1	ICAF_RABIT	O28730 oryctolagus
46	37.5	20.7	1536	1	GLSF_ANTSP	O06434 antithrombin
47	37.5	20.7	2116	1	RRLI_SYNV	P31332 sorbus yel
48	37	20.4	273	1	Y152_HALHA	P04137 halobacterium
49	37	20.4	278	1	Y152_HALHA	O03285 escherichia coli
50	37	20.4	538	1	BUD5_YEAST	P25300 saccharomyces cerevisiae

ALIGNMENTS

RESULT 1	
FA7_BOVIN	
ID	FA7_BOVIN
AC	P22457; STANDARD; PRT; 407 AA.
DT	01-AUG-1991 (Rel. 19, Created)
DT	01-AUG-1991 (Rel. 19, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	Coagulation factor VII (EC 3.4.21.21) (Serum prothrombin conversion accelerator).
GN	F7.
OS	Bos taurus (Bovine).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC	Bovidae; Bovinae; Bos.
OX	NCBI_TaxID=9913;
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=89008362; PubMed=3049594;
RA	Takeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T.,
RA	Iwanaga S.;
RT	"Bovine factor VII. Its purification and complete amino acid
RT	sequence.";
RL	J. Biol. Chem. 263:14868-14877(1988).
RN	[2]
RP	STRUCTURE OF CARBOHYDRATE ON SER-52.
RX	MEDLINE=89213999; PubMed=3149637;
RA	Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T.,
RA	Miyata T., Iwanaga S., Takeo T., Shimomishi Y., Ikenaka T.;
RT	"A new trisaccharide sugar chain linked to a serine residue in bovine
RT	blood coagulation factors VII and IX.";
RL	J. Biochem. 104:867-868(1988).
RN	[3]
RP	STRUCTURE OF CARBOHYDRATE ON SER-52.
RX	MEDLINE=91344709; PubMed=2129367;
RA	Iwanaga S., Nishimura H., Kawabata S., Kishi W., Hase S., Ikenaka T.;
RT	"A new trisaccharide sugar chain linked to a serine residue in the
RT	first EGF-like domain of clotting factors VII and IX and protein Z.";
RL	Adv. Exp. Med. Biol. 281:121-131(1990).
CC	- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
CC	CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR
CC	THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
CC	AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA
CC	BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO
CC	FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.
CC	- CATALYTIC ACTIVITY: Hydrolyses one Arg-Ile bond in factor X to
CC	form factor Xa.
CC	- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
CC	BY A DISULFIDE BOND.
CC	- TISSUE SPECIFICITY: PLASMA.
CC	- PTM: THE VITAMIN K-DEPENDENT, ENZYMIC CARBOXYLATION OF SOME
CC	GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND

CC CALCIUM.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 CC PIR: A31979; A31979.
 CC HSSP: P08709; 1BF9.
 CC MEROPS: S01.215; -.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000742; EGF-2.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR001438; EGF_II.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Trypsin.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam: PF00008; EGF_2.
 DR Pfam: PF00594; gla_1.
 DR Pfam: PF00089; trypsin_1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00010; EGFBLOOD.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00179; EGF_CA_1.
 DR SMART: SM00001; EGF_Like_1.
 DR SMART: SM00069; GLA_1.
 DR SMART: SM00020; tryp_Spec_1.
 DR PROSITE: PS00010; ASX_HYDROXYL_1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF_CA_1.
 DR PROSITE: PS00011; GLU-CARBOXYLATION; 1.
 DR PROSITE: PS50240; TRYPsin_DOM; 1.
 DR PROSITE: PS00134; TRYPsin_HIS; 1.
 DR PROSITE: PS00135; TRYPsin_SER; 1.
 KM Hydrolyase: Serine protease; Blood coagulation; Zymogen; Glycoprotein;
 KM Liver: Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
 KM EGF-like domain; Repeat.
 FT CHAIN 1 152 FACTOR VII LIGHT CHAIN.
 FT CHAIN 153 407 FACTOR VII HEAVY CHAIN.
 FT DOMAIN 6 35 GLA-RICH.
 FT DOMAIN 46 82 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 87 128 EGF-LIKE 2.
 FT DOMAIN 153 407 SERINE PROTEASE.
 FT SITE 152 153 CLEAVAGE (BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR THROMBIN).
 FT ACT_SITE 193 193 BY SIMILARITY.
 FT ACT_SITE 242 242 BY SIMILARITY.
 FT ACT_SITE 344 344 BY SIMILARITY.
 FT BINDING 338 338 SUBSTRATE (BY SIMILARITY).
 FT DISULFID 17 22 BY SIMILARITY.
 FT DISULFID 50 61 BY SIMILARITY.
 FT DISULFID 55 70 BY SIMILARITY.
 FT DISULFID 72 81 BY SIMILARITY.
 FT DISULFID 91 102 BY SIMILARITY.
 FT DISULFID 98 112 BY SIMILARITY.
 FT DISULFID 114 127 BY SIMILARITY.
 FT DISULFID 135 262 BY SIMILARITY.
 FT DISULFID 159 164 BY SIMILARITY.
 FT DISULFID 178 194 BY SIMILARITY.
 FT DISULFID 310 329 BY SIMILARITY.
 FT DISULFID 340 368 BY SIMILARITY.
 FT MOD_RES 6 6 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 7 7 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 14 14 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 16 16 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 19 19 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 20 20 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 25 25 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 26 26 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 29 29 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 35 35 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 52 52 O-LINKED (GLC...').
 FT CARBOHYD 145 145 N-LINKED (GLCNAC...').

FT CARBOHYD 203 203 N-LINKED (GLCNAC...').
 SQ SEQUENCE 407 AA; 44431 MW; 703ELFE0636E7F10 CRC64;
 Query Match 81.2%; Score 147; DB 1; Length 407;
 Best Local Similarity 68.2%; Pred. No. 5,9e-20;
 Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
 QY 1 ANGELXXLRXGSLXRCXKXLCSEFXKXKXIFRNXXRRQFVWSY 44
 Db 1 ANGFEELLPSLRRECHREELCSFEAEHIFRNEERTQFVWSY 44
 RESULT 2
 FA7_RABIT STANDARD; PRT; 444 AA.
 ID FA7_RABIT
 AC P98139; P79224;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
 conversion accelerator).
 GN F7.
 OS Oryctolagus cuniculus (Rabbit).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eulheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE:93190306; Pubmed-8383365.
 RA Brothers A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;
 RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation
 factor VII.";
 RL Thromb. Res. Suppl. 69:231-238(1993).
 RN [2]
 RP REVISION TO 395.
 RC TISSUE=Liver;
 RA Ruiz S.R., Blajchman M.A., Clarke B.J.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
 CC CONVERTED TO FACTOR VIIa BY FACTOR Xa, FACTOR XIa, FACTOR IXa, OR
 CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR Xa
 CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
 CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
 CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
 CC SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Hydrolyses one Arg-|-Ile bond in factor X to
 CC form factor Xa.
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
 CC BY A DISULFIDE BOND (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 CC -----
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 CC -----
 DR EMBL: U77477; AAB37326.1; -.
 DR HSSP: P08709; 1BF9.
 DR MEROPS: S01.215; -.
 DR InterPro: IPR002086; Aldehyde dehydr.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.


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ID   TMG1_HUMAN          STANDARD;          PRT;          218 AA.
AC   O14668;
DT   01-MAR-2002 (Rel. 41, Created)
DT   01-MAR-2002 (Rel. 41, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Transmembrane gamma-carboxyglutamic acid protein 1 precursor (Proline-
DE   rich gla protein 1) (Proline-rich gamma-carboxyglutamic acid protein
DE   1).
GN   PRG1 OR TMG1 OR PRG1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97404347; PubMed=9256434;
RA   Kulman J.D., Harris J.E., Haldeman B.A., Davie E.W.;
RT   "Primary structure and tissue distribution of two novel proline-rich
RT   gamma-carboxyglutamic acid proteins.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997).
CC   -1- TISSUE SPECIFICITY: Highly expressed in the spinal cord.
CC   -1- PTM: Gla residues are produced after subsequent posttranslational
CC   modifications of glutamic acid by a vitamin K-dependent gamma-
CC   carboxylase.
CC   -----
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@sib-sib.ch).
CC   -----
DR   EMBL; AF009242; AAB67070.1; -
DR   MIM; 604428; -
DR   HSSP; P00740; ICFH.
DR   InterPro: IPR000294; VitK_dep_GLA.
DR   InterPro: IPR002383; GLA_blood.
DR   Pfam; PF00594; gla; 1.
DR   PRINTS; PR00001; GLABLOOD.
DR   SMART; SM00069; GLA; 1.
DR   PROSITE; PS00011; GLU_CARBOXYLATION; 1.
KW   Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
FT   PROPEP          1..20
FT   CHAIN           1..218
FT   DOMAIN          21..83
FT   TRANSMEM       84..106
FT   DOMAIN          107..218
FT   DOMAIN          24..61
FT   DOMAIN          131..135
SO   SEQUENCE        218 AA; 24947 MW; 26538A61AB0AEB98 CRC64;

Query Match          58.6%; Score 106; DB 1; Length 218;
Best Local Similarity 38.6%; Pred. No. 1.6e-12;
Matches 17; Conservative 9; Mismatches 18; Indels 0; Gaps 0;
Qy 1 ANGFLXLRKXGSLKRXCRXXLCSFYXAXXIFRNXXRTQFWVSY 44
    |||  :|::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 21 ANGFEELRQGNIEREKEFEFTFEARERAFENNEKTEKFWSTY 64

RESULT 5
PRTC_RAT          STANDARD;          PRT;          461 AA.
AC   P31394;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Vitamin-K dependent protein C precursor (EC 3.4.21.69)
DE   (Antopthrombin IIA) (Anticoagulant protein C) (blood coagulation
DE   factor XIV).

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GN   PROC.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MISPAR; TISSUE=Liver;
RX   MEDLINE=92329550; PubMed=1627650;
RA   Okafuji T., Maekawa K., Nawa K., Marumoto Y.;
RT   "The cDNA cloning and mRNA expression of rat protein C.";
RL   Biochim. Biophys. Acta 1131:329-332(1992).
CC   -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC   REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VILLA
CC   IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC   -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC   and Villi.
CC   -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC   INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC   BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC   TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
CC   REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC   STRONGLY PROMOTED BY THROMBOMODULIN.
CC   -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC   -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC   GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC   -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC   ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC   SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC   THROMBIN-THROMBOMODULIN COMPLEX.
CC   -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC   -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC   TRYPsin FAMILY.
CC   -----
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@sib-sib.ch).
CC   -----
DR   EMBL; X64336; CAA45617.1; -
DR   PIR; S18994; S18994.
DR   PIR; S24312; S24312.
DR   HSSP; P04070; IPCU.
DR   MEROPS; S01.218; -.
DR   InterPro: IPR000152; Asx_hydroxyl.
DR   InterPro: IPR001314; Chymotrypsin.
DR   InterPro: IPR000561; EGF-like.
DR   InterPro: IPR001881; EGF_Ca.
DR   InterPro: IPR002383; GLA_blood.
DR   InterPro: IPR001254; Trypsin.
DR   InterPro: IPR000294; VitK_dep_GLA.
DR   Pfam; PF00008; EGF; 2.
DR   Pfam; PF00594; gla; 1.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00001; GLABLOOD.
DR   SMART; SM00179; EGF_CA; 1.
DR   SMART; SM00001; EGF_like; 1.
DR   SMART; SM00069; GLA; 1.
DR   SMART; SM00020; TRYP_SPC; 1.
DR   PROSITE; PS00010; ASX_HYDROXYL; 1.
DR   PROSITE; PS00022; EGF_1; 1.
DR   PROSITE; PS01186; EGF_2; 2.
DR   PROSITE; PS01187; EGF_CA; 1.
DR   PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR   PROSITE; PS00240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Blood coagulation; Glycoprotein; Serine protease;
Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;

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KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
FT SIGNAL 1 32
FT PROPEP 33 41
FT CHAIN 42 196
FT CHAIN 199 461
FT PEPTIDE 199 212
FT SITE 212 213
FT DOMAIN 96 131
FT DOMAIN 135 175
FT DOMAIN 213 461
FT MOD_RES 47 47
FT MOD_RES 48 48
FT MOD_RES 55 55
FT MOD_RES 57 57
FT MOD_RES 60 60
FT MOD_RES 61 61
FT MOD_RES 66 66
FT MOD_RES 67 67
FT MOD_RES 70 70
FT MOD_RES 112 112
FT ACT_SITE 254 254
FT ACT_SITE 300 300
FT ACT_SITE 402 402
FT DISULFID 58 63
FT DISULFID 91 110
FT DISULFID 100 105
FT DISULFID 104 119
FT DISULFID 121 130
FT DISULFID 139 150
FT DISULFID 146 159
FT DISULFID 161 174
FT DISULFID 182 320
FT DISULFID 239 255
FT DISULFID 373 387
FT DISULFID 398 426
FT CARBOHYD 215 215
FT CARBOHYD 291 291
FT CARBOHYD 355 355
SO SEQUENCE 461 AA; 51912 MW; 8A4CF93664EDACD5 CRC64;

Query Match 58.6%; Score 106; DB 1; Length 461;
Best Local Similarity 45.5%; Pred. No. 3..je-12;
Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFVXLRKGSIXKRCXALCSFXAXXIFRXNXXRTGRWVS 44
DB 42 ANSFLEEVRAGSLEIRECMEDICDEEAEQELFQVVEDTLAFWIKY 85

RESULT 6
PRIC_MOUSE STANDARD; PRT; 461 AA.
AC P33587; O35498;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Vitamin-K dependent protein C precursor (BC 3.4.21.69)
DE (Autoprotechombin IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV).
GN PROC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92318697; PubMed=1618739;
RA Tada N., Sato M., Tsujimura A., Iwase R., Hashimoto-Gotoh T.;
RT "Isolation and characterization of a mouse protein C cDNA.";
RL J. Biochem. 111:491-495(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=98152576; PubMed=9493582;
RA Jaldert L.R., Rosen E.D., Lissens A., Carmeliet P., Collen D.,
RA Castellino F.J.;
RT "Nucleotide structure and characterization of the murine gene encoding
RT anticoagulant protein C.";
RL Thromb. Haemost. 79:310-316(1998).
RN [3]
RP SEQUENCE OF 274-434 FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=94318474; PubMed=8043441;
RA Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Nihio Y.;
RT "A comparative study of partial primary structures of the catalytic
RT region of mammalian protein C.";
RL Bc. J. Haematol. 86:590-600(1994).
CC -I- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -I- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIIA.
CC -I- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC STRONGLY PROMOTED BY THROMBOMODULIN.
CC -I- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -I- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -I- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC THROMBIN-THROMBOMODULIN COMPLEX.
CC -I- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
CC -----
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CC -----
DR EMBL: D10445; BAA01235.1; -
DR EMBL: AF034569; AAC3795.1; -
DR EMBL: DA3755; BAA07812.1; -
DR PIR: JX0210; JX0210.
DR HSSP: P04070; 1PCU.
DR MEROPS: S01.218; -.
DR MGD: MGI:97771; Proc.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF-Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Trypsin.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; gla_1.
DR Pfam: PF00089; trypsin_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.

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DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00001; EGF_Like; 1.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; TRYP_Spc; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Blood coagulation; Glycoprotein; Serine protease;
KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
FT SIGNAL 1 33
FT PROPEP 34 41
FT CHAIN 42 196
FT CHAIN 199 461
FT PEPTIDE 199 212
FT SITE 212 213
FT DOMAIN 96 131
FT DOMAIN 135 175
FT DOMAIN 213 461
FT MOD_RES 47 47
FT MOD_RES 48 48
FT MOD_RES 55 55
FT MOD_RES 57 57
FT MOD_RES 60 60
FT MOD_RES 61 61
FT MOD_RES 66 66
FT MOD_RES 67 67
FT MOD_RES 70 70
FT MOD_RES 112 112
FT ACT_SITE 253 253
FT ACT_SITE 299 299
FT ACT_SITE 402 402
FT DISULFID 58 63
FT DISULFID 91 110
FT DISULFID 100 105
FT DISULFID 104 119
FT DISULFID 121 130
FT DISULFID 139 150
FT DISULFID 146 159
FT DISULFID 161 174
FT DISULFID 182 319
FT DISULFID 238 254
FT DISULFID 373 387
FT DISULFID 398 426
FT CARBOHYD 214 214
FT CARBOHYD 290 290
FT CARBOHYD 355 355
FT CONFLICT 328 328
FT CONFLICT 393 393
SQ SEQUENCE 461 AA; 51945 MM; 53FAAD085B194D6E CRC64;

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Query Match 58.0%; Score 105; DB 1; Length 461;
Best Local Similarity 45.5%; Pred. No. 5.2e-12;
Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;
1 ANGFLXLRXGSLRXRCXRLCSFXAXXIFRNXXRTQFWWSY 44
| | | : | | | | : | | | | | : | | :

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DB 42 ANSFLEMRPGSLERECMEICDFEADRIQNVEDTIAFWIKY 85
RESULT 7
ID FA7_MOUSE STANDARD; PRT; 446 AA.
AC P70375;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator).
GN F7 OR CF7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
[1]
RP MEDLINE=97127167; PubMed=8972017;
RX Idusogie E., Rosen E.D., Carmeliet P., Collen D., Castellino F.J.;
RT "Nucleotide structure and characterization of the murine blood
RT coagulation factor VII gene.";
RL Thromb. Haemost. 76:957-964(1996).
CC -!- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR
CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
CC AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA
CC BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO
CC FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
CC SIMILARITY).
CC -!- CATALYTIC ACTIVITY: Hydrolyses one Arg-1-Ile bond in factor X to
CC form factor xa.
CC -!- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
CC BY A DISULFIDE BOND (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: PLASMA.
CC -!- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM (BY SIMILARITY).
CC -!- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
CC -----
CC EMBL: U66079; AAC3796.1; -.
CC HSSP: P08709; 1BF9.
CC MEROPS: S01.215; -.
CC MGD, MGI:109325; F7.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF_Like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_CA.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Trypsin.
DR InterPro: IPR000294; Vitk_dep_GLA.
DR Pfam: PF00008; EGF; 2.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00001; EGF_Like; 1.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; TRYP_Spc; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.

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FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 48 48 SIMILARITY).
FT MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 112 112 HYDROXYLATION (BY SIMILARITY).
FT ACT_SITE 255 255 CHARGE RELAY SYSTEM.
FT ACT_SITE 301 301 CHARGE RELAY SYSTEM.
FT ACT_SITE 400 400 CHARGE RELAY SYSTEM.
FT DISULFID 58 63 BY SIMILARITY.
FT DISULFID 91 110 BY SIMILARITY.
FT DISULFID 100 105 BY SIMILARITY.
FT DISULFID 104 119 BY SIMILARITY.
FT DISULFID 121 130 BY SIMILARITY.
FT DISULFID 139 150 BY SIMILARITY.
FT DISULFID 146 159 BY SIMILARITY.
FT DISULFID 161 174 BY SIMILARITY.
FT DISULFID 182 321 INTERCHAIN (BY SIMILARITY).
FT DISULFID 240 256 BY SIMILARITY.
FT DISULFID 371 385 BY SIMILARITY.
FT DISULFID 396 424 BY SIMILARITY.
FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 459 AA; 51866 MW; 8541AAC14C16D09 CRC64;
```

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Query Match 55.2%; Score 100; DB 1; Length 459;
Best Local Similarity 45.5%; Pred. No. 4.5e-11;
Matches 20; Conservative 2; Mismatches 22; Indels 0; Gaps 0;

Oy 1 ANGFLXLRXGSLXRCXRXLCSEFXAXXIFRNXXRTQFWVSY 44
Db 42 ANSFLELRPSSLERECKEETCDFEAREIFONTENTMAFWSKY 85

RESULT 9
TMG3_HUMAN STANDARD; PRT; 231 AA.
AC Q9B2D7;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Transmembrane gamma-carboxyglutamic acid protein 3 precursor.
GN TMG3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=spinal cord; PubMed=11171957;
RX MEDLINE=21117044; PubMed=11171957;
RA Kulman J.D., Harris J.E., Xie L., Davie E.W.;
RT "Identification of two novel transmembrane gamma-carboxyglutamic acid
RT proteins expressed broadly in fetal and adult tissues.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:1370-1375(2001).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in brain, lung, kidney and heart.
CC -1- PTM: Gla residues are produced after subsequent posttranslational
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CC modifications of glutamic acid by a vitamin K-dependent gamma-
CC carboxylase.
CC -----
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CC -----
CC EMBL: AF326350; IACB.
CC HSSP: P00740; ICFH.
CC InterPro: IPR002383; GLA_blood.
CC InterPro: IPR00294; VltK_dep_GLA.
CC PRINTS: PR00001; GLABLOOD.
CC SMART: SM00069; GLA; 1.
CC PROSITE: PS00011; GLU_CARBOXYLATION; 1.
CC Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
CC PROPEP 1 19 POTENTIAL.
CC CHAIN 20 231 TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
CC FT DOMAIN 20 78 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 79 101 POTENTIAL.
CC FT DOMAIN 102 231 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 23 60 GLA-RICH.
CC SEQUENCE 231 AA; 25848 MW; 8A373E4848490D81 CRC64;
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Query Match 54.7%; Score 99; DB 1; Length 231;
Best Local Similarity 38.6%; Pred. No. 3.4e-11;
Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;
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Oy 1 ANGFLXLRXGSLXRCXRXLCSEFXAXXIFRNXXRTQFWVSY 44
Db 20 ANSFLELRQGTIERECHEICSYEVEVFNKKTMEFWMGY 63
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RESULT 10
PRTC_BOVIN STANDARD; PRT; 456 AA.
ID PRTC_BOVIN
AC P00745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
DE (Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV) (Fragment).
GN PROC.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecorida; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014826; PubMed=60911100;
RA Long G.L., Balagaje R.M., McGillivray R.T.A.;
RT "Cloning and sequencing of liver cDNA coding for bovine protein C.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).
RN [2]
RP SEQUENCE OF 40-194.
RX MEDLINE=83007325; PubMed=6896876;
RA Fernlund P., Stenflo J.;
RT "Amino acid sequence of the light chain of bovine protein C.";
RL J. Biol. Chem. 257:12170-12179(1982).
RN [3]
RP REVISION TO 110.
RX MEDLINE=83169769; PubMed=6572939;
RA Drakenberg T., Fernlund P., Roepstorff P., Stenflo J.;
RT "Beta-hydroxyaspartic acid in vitamin K-dependent protein C.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).
RN [4]
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RA	Penduth U.R., Anderson K.D., James H.L.;
RT	"Characterization of a full-length cDNA for rabbit factor X";
RL	Thromb. Res. 85:503-514(1997).
CC	-1- FUNCTION: FACTOR XA IS A VITAMIN K-DEPENDENT GLYCOPROTEIN THAT
CC	CONVERTS PROTHROMBIN TO THROMBIN IN THE PRESENCE OF FACTOR VA,
CC	C++ AND PHOSPHOLIPID DURING BLOOD CLOTTING.
CC	-1- CATALYTIC ACTIVITY: Preferential cleavage: Arg- -Thr and then
CC	Arg- -Ile bonds in prothombin to form thrombin.
CC	-1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
CC	BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
CC	MORE DISULFIDE BONDS.
CC	-1- PTM: THE VITAMIN K-DEPENDENT, ENZYMTIC CARBOXYLATION OF SOME
CC	GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC	CALCIUM (BY SIMILARITY).
CC	-1- PTM: N- AND O-GLYCOSYLATED (BY SIMILARITY).
CC	-1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
CC	INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY)
CC	(BY SIMILARITY).
CC	-1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC	ANOTHER SITE, BEYOND THE GLA DOMAIN.
CC	-1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC	TRYPSIN FAMILY.
CC	-----
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CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL: AF003200; AAB62542.1; -.
DR	HSSP: P00742; IHCG.
DR	InterPro: IPR000152; Asx_hydroxyl.
DR	InterPro: IPR001314; Chymotrypsin.
DR	InterPro: IPR000561; EGF-like.
DR	InterPro: IPR000742; EGF_2.
DR	InterPro: IPR001881; EGF_Ca.
DR	InterPro: IPR002383; GLA_blood.
DR	InterPro: IPR001254; Trypsin.
DR	InterPro: IPR000294; Vitk_dep_GLA.
DR	Pfam: PF00008; EGF_2.
DR	Pfam: PF00594; gla; 1.
DR	Pfam: PF00089; trypsin; 1.
DR	PRINTS: PR00722; CHYMOTRYPSIN.
DR	PRINTS: PR00001; GLABLOOD.
DR	SMART: SM00179; EGF_CA; 1.
DR	SMART: SM00001; EGF_like; 1.
DR	SMART: SM00069; GLA; 1.
DR	PROSITE: PS00010; ASX_HYDROXYL; 1.
DR	PROSITE: PS00022; EGF_1; 1.
DR	PROSITE: PS01186; EGF_2; 2.
DR	PROSITE: PS01187; EGF_CA; 1.
DR	PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR	PROSITE: PS50240; TRYPSIN_DOM; 1.
DR	PROSITE: PS00134; TRYPSIN_HIS; 1.
DR	PROSITE: PS00135; TRYPSIN_SER; 1.
KW	Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
KW	Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
KW	Signal; Zymogen; EGF-like domain; Repeat.
FT	SIGNAL 1 20 POTENTIAL.
FT	PROPEP 21 40 BY SIMILARITY.
FT	CHAIN 41 180 FACTOR X LIGHT CHAIN.
FT	CHAIN 184 490 FACTOR X HEAVY CHAIN.
FT	PROPEP 184 232 ACTIVATION PEPTIDE.
FT	CHAIN 233 490 ACTIVATED FACTOR XA, HEAVY CHAIN.
FT	DOMAIN 86 122 EGF-like 1.
FT	DOMAIN 125 165 EGF-like 2.
FT	DOMAIN 233 490 SERINE PROTEASE.
FT	MOD_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT	SIMILARITY).

FT	MOD_RES	47		47	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	54		54	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	56		56	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	59		59	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	60		60	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	65		65	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	66		66	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	69		69	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	72		72	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	75		75	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	79		79	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	103		103	HYDROXYLATION (BY SIMILARITY).
FT	ACT_SITE	274		274	CHARGE RELAY SYSTEM.
FT	ACT_SITE	320		320	CHARGE RELAY SYSTEM.
FT	ACT_SITE	417		417	CHARGE RELAY SYSTEM.
FT	DISULFID	90		101	BY SIMILARITY.
FT	DISULFID	95		110	BY SIMILARITY.
FT	DISULFID	112		121	BY SIMILARITY.
FT	DISULFID	129		140	BY SIMILARITY.
FT	DISULFID	136		149	BY SIMILARITY.
FT	DISULFID	151		164	BY SIMILARITY.
FT	DISULFID	172		340	INTERCHAIN (BY SIMILARITY).
FT	DISULFID	239		244	BY SIMILARITY.
FT	DISULFID	259		275	BY SIMILARITY.
FT	DISULFID	388		402	BY SIMILARITY.
FT	DISULFID	413		441	BY SIMILARITY.
FT	CARBOHYD	61		61	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	187		187	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	205		205	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	450 AA;	53965 MW;	3A39FA85AF2A6D11 CnC64;	

Query Match 51.9%; Score 94; DB 1; Length 490;
 Best Local Similarity 38.6%; Pred. No. 6,4e-10;
 Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

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OY      1 ANGFLXLRKSGSLAKRXCRRXXLCSPFYXAXIFENNXRTFRQFWVSY 44
          |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
DB       41 ANSFLEELKKGNLBERECMEHCNSYEALAEVFEDREKTNEFWNKY 84

RESULT  12
ID       FA10_HUMAN                STANDARD;             PRT;   488 AA.
AC       P00742; O14340;
DT       21-JUL-1986 (Rel. 01, Created)
DT       01-OCT-1989 (Rel. 12, Last sequence update)
DT       16-OCT-2001 (Rel. 40, Last annotation update)
DE       Coagulation factor X precursor (BC 3.4.21.6) (Stuart factor).
GN       F10.
OS       Homo sapiens (Human).
OC       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC       Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX       NCBI_TaxId=9606;
RN       [1]
RP       SEQUENCE FROM N.A.
RX       MEDLINE=91216473; PubMed=1902434;
RA       Messier T.L., Pittman D.D., Long G.L., Kaufman R.J., Church W.R.;
RT       "Cloning and expression in COS-1 cells of a full-length cDNA encoding
RL       human coagulation factor X.";
RN       Gene 99:291-294(1991).
RN       [2]
```

RP SEQUENCE FROM N.A.
 RA MEDLINE=67026600; PubMed=3768336;
 RX Leytus S.P., Foster D.C., Kurachi K., Davie E.W.;
 RT "Gene for human factor X: a blood coagulation factor whose gene
 RT organization is essentially identical with that of factor IX and
 RT protein C.";
 RL Biochemistry 25:5098-5102(1986).
 RN [3]
 RP SEQUENCE OF 13-488 FROM N.A.
 RX MEDLINE=85216545; PubMed=2582420;
 RA Fung M.R., Hay C.W., McGillivray R.T.A.;
 RT "Characterization of an almost full-length cDNA coding for human
 RT blood coagulation factor X.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).
 RN [4]
 RP SEQUENCE OF 19-488 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=86221713; PubMed=3011603;
 RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;
 RT "Isolation and characterization of human blood-coagulation factor X
 RT cDNA.";
 RL Gene 41:311-314(1986).
 RN [5]
 RP SEQUENCE OF 41-179.
 RX MEDLINE=83257207; PubMed=6871167;
 RA McMullen B.A., Fujikawa K., Kistiel W., Sasagawa T., Howard W.N.,
 RA Kwa E.Y., Weinstein B.;
 RT "Complete amino acid sequence of the light chain of human blood
 RT coagulation factor X: evidence for identification of residue 63 as
 RT beta-hydroxyaspartic acid.";
 RL Biochemistry 22:2875-2884(1983).
 RN [6]
 RP SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY.
 RC TISSUE=Liver;
 RX MEDLINE=84222026; PubMed=6587384;
 RA Leytus S.P., Chung D.W., Kistiel W., Kurachi K., Davie E.W.;
 RT "Characterization of a cDNA coding for human factor X.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702(1984).
 RN [7]
 RP SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=94062825; PubMed=8243461;
 RA Inoue K., Morita T.;
 RT "Identification of O-linked oligosaccharide chains in the activation
 RT peptides of blood coagulation factor X. The role of the carbohydrate
 RT moieties in the activation of factor X.";
 RL Eur. J. Biochem. 218:153-163(1993).
 RN [8]
 RP SEQUENCE OF 1-23 FROM N.A.
 RX MEDLINE=90128299; PubMed=2612918;
 RA Jagadeeswaran P., Reddy S.V., Rao K.J., Hamsabhusanam K., Lyman G.;
 RT "Cloning and characterization of the 5' end (exon 1) of the gene
 RT encoding human factor X.";
 RL Gene 84:517-519(1989).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.
 RX MEDLINE=93360277; PubMed=8355279;
 RA Padmanabhan K., Padmanabhan K.P., Tulinsky A., Park C.H., Bode W.,
 RA Huber R., Blankenship D.T., Cardin A.D., Kistiel W.;
 RT "Structure of human des(1-45) factor Xa at 2.2-A resolution.";
 RL J. Mol. Biol. 232:947-966(1993).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.
 RX MEDLINE=98283982; PubMed=9618463;
 RA Kanata K., Kawamoto H., Honma T., Iwama T., Kim S.H.;
 RT "Structural basis for chemical inhibition of human blood coagulation
 RT factor Xa.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).
 CC -1- FUNCTION: FACTOR XA IS A VITAMIN K-DEPENDENT GLYCOPROTEIN THAT
 CC CONVERTS PROTHROMBIN TO THROMBIN IN THE PRESENCE OF FACTOR VA,
 CC CA++ AND PHOSPHOLIPID DURING BLOOD CLOTTING.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-1-Thr and then
 CC Arg-1-Ile bonds in prothrombin to form thrombin.
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR

CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 CC MORE DISULFIDE BONDS.
 CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC -1- PTM: N- AND O-GLYCOSYLATED.
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 CC -----
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 CC -----
 CC EMBL; K03194; AAA52490.1; -;
 CC EMBL; M57285; AAA52421.1; -;
 CC EMBL; L29433; AAA52764.1; -;
 CC EMBL; L00390; AAA52764.1; JOINED.
 CC EMBL; L00391; AAA52764.1; JOINED.
 CC EMBL; L00392; AAA52764.1; JOINED.
 CC EMBL; L00393; AAA52764.1; JOINED.
 CC EMBL; L00394; AAA52764.1; JOINED.
 CC EMBL; L00395; AAA52764.1; JOINED.
 CC EMBL; L00396; AAA52764.1; JOINED.
 CC EMBL; M22613; AAA51984.1; -;
 CC EMBL; K01886; AAA52486.1; -;
 CC EMBL; M33297; AAA52636.1; -;
 CC PIR; A00924; EXHU.
 CC PIR; A25853; A25853.
 CC PIR; A24478; A24478.
 CC PDB; 1HCG; 08-MAY-95.
 CC PDB; 1FAX; 29-OCT-97.
 CC PDB; 1EXX; 17-JUN-98.
 CC PDB; 1XKA; 23-MAR-99.
 CC PDB; 1XKB; 23-MAR-99.
 CC MEROPS; S01.216; -;
 CC Carbank; CCSD:29393; -;
 CC GlycoSiteDB; P00742; -;
 CC MIM; 134530; -;
 CC MIM; 227600; -;
 CC InterPro; IPR000152; Asx_hydroxyl.
 CC InterPro; IPR001314; Chymotrypsin.
 CC InterPro; IPR000561; EGF-like.
 CC InterPro; IPR000742; EGF_2.
 CC InterPro; IPR001881; EGF_CA.
 CC InterPro; IPR002383; GLA_blood.
 CC InterPro; IPR001254; trypsin.
 CC InterPro; IPR00294; vitK_dep_GLA.
 CC Pfam; PF00008; EGF_2.
 CC Pfam; PF00054; gla; 1.
 CC Pfam; PF00089; trypsin; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC PRINTS; PR00001; GLABLOOD.
 CC SMART; SM00179; EGF_CA; 1.
 CC SMART; SM00001; EGF_like; 1.
 CC SMART; SM00069; GLA; 1.
 CC SMART; SM00020; TRYP_SPC; 1.
 CC PROSITE; PS00010; ASX_HYDROXYL; 1.
 CC PROSITE; PS00022; EGF_1; 1.
 CC PROSITE; PS01186; EGF_2; 2.
 CC PROSITE; PS01187; EGF_CA; 1.
 CC PROSITE; PS00011; GLU CARBOXYLATION; 1.
 CC PROSITE; PS05240; TRYPSIN_DOM; 1.
 CC PROSITE; PS00134; TRYPSIN_HIS; 1.
 CC PROSITE; PS00135; TRYPSIN_SER; 1.
 CC GlycoProtein; Hydrolase; Serine protease; Plasma; Blood coagulation;

KM Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 KW Signal; Zymogen; EGF-like domain; Repeat; 3D-structure.
 FT SIGNAL 1 31 POTENTIAL.
 FT PROPEP 32 40
 FT CHAIN 41 179 FACTOR X LIGHT CHAIN.
 FT CHAIN 183 488 FACTOR X HEAVY CHAIN.
 FT PROPEP 183 234 ACTIVATION PEPTIDE.
 FT CHAIN 235 488 ACTIVATED FACTOR XA, HEAVY CHAIN.
 FT DOMAIN 86 122 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 125 165 EGF-LIKE 2.
 FT DOMAIN 235 488 SERINE PROTEASE.
 FT MOD_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 72 72 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 79 79 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 103 103 HYDROXYLATION.
 FT CARBOHYD 199 199 O-LINKED (GALNAC. . .).
 FT CARBOHYD 211 211 O-LINKED (GALNAC. . .).
 FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 221 221 /FTIG-CAR-000012.
 FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 231 231 /FTIG-CAR-000013.
 FT ACT_SITE 276 276 CHARGE RELAY SYSTEM.
 FT ACT_SITE 322 322 CHARGE RELAY SYSTEM.
 FT ACT_SITE 419 419 CHARGE RELAY SYSTEM.
 FT DISULFID 90 101 CHARGE RELAY SYSTEM.
 FT DISULFID 95 110
 FT DISULFID 112 121

Query Match 51.4%; Score 93; DB 1; Length 488;
 Best Local Similarity 36.4%; Pred. No. 9, 8e-10;
 Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

OY 1 ANGFLXXLRXGSLRXRCXXLCSEFXAXXIFRNXXRTQFWVSX 44
 DB 41 ANSFLEMKKHLEHRECMETCSYEAREVFEEDSKTNEFWKX 84

RESULT 13
 PRTG_HUMAN STANDARD; PRT; 461 AA.
 ID P04070; Q16001; Q15190; Q15189;
 DT 01-NOV-1986 (Rel. 03, Created)
 DT 01-NOV-1986 (Rel. 03, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
 DE (Autoproteolytic cleavage of protein C) (Blood coagulation factor XIV).
 GN PROC.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85270390; PubMed=2991887;
 RA Foster D.C., Yoshitake S., Davie E.W.;
 RT "The nucleotide sequence of the gene for human protein C.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:4673-4677(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85269639; PubMed=2991859;
 RA Beckmann R.J., Schmidt R.J., Santner R.F., Plutsky J., Crabtree G.R.,
 RA Long G.L.;
 RT "The structure and evolution of a 461 amino acid human protein C
 RT precursor and its messenger RNA, based upon the DNA sequence of

RT Cloned human liver cDNAs.";
 RL Nucleic Acids Res. 13:5233-5247(1985).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86120978; PubMed=3511471;
 RA Plutsky J., Hoskins J.A., Long G.L., Crabtree G.R.;
 RT "Evolution and organization of the human protein C gene";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986).
 RN [4]
 RP SEQUENCE OF 106-461 FROM N.A.
 RX MEDLINE=84272714; PubMed=6589623;
 RA Foster D.C., Davie E.W.;
 RT "Characterization of a cDNA coding for human protein C.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984).
 RN [5]
 RP CARBOHYDRATE-LINKAGE SITE ASN-371.
 RX MEDLINE=90293094; PubMed=1694179;
 RA Miletich J.P., Broze G.J., Jr.;
 RT "Beta protein C is not glycosylated at asparagine 329. The rate of
 RT translation may influence the frequency of usage at asparagine-X-
 RT cysteine sites.";
 RL J. Biol. Chem. 265:11397-11404(1990).
 RN [6]
 RP HYDROXYLATION.
 RX MEDLINE=92184750; PubMed=1544894;
 RA Harris R.J., Ling V.T., Spellman M.W.;
 RT "O-linked fucose is present in the first epidermal growth factor
 RT domain of factor XII but not protein C.";
 RL J. Biol. Chem. 267:5102-5107(1992).
 RN [7]
 RP 3D-STRUCTURE MODELING OF 175-450.
 RX MEDLINE=94272342; PubMed=8003977;
 RA Fisher C.L., Greengard J.S., Griffin J.H.;
 RT "Models of the serine protease domain of the human antithrombotic
 RT plasma factor activated protein C and its zymogen.";
 RL Protein Sci. 3:588-599(1994).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 84-461.
 RX MEDLINE=97157472; PubMed=9003757;
 RA Mather T., Oganesyan V., Hof P., Huber R., Foundling S., Esmon C.,
 RA Bode W.;
 RT "The 2.8 A crystal structure of Gla-domainless activated protein C.";
 RL EMBO J. 15:6822-6831(1996).
 RN [9]
 RP REVIEW ON PROC VARIANTS.
 RX MEDLINE=93190290; PubMed=8446940;
 RA Reitsma P.H., Poort S.R., Bernardi F., Gandrille S., Long G.L.,
 RA Sala N., Cooper D.N.;
 RT "Protein C deficiency: a database of mutations. For the Protein C & S
 RT Subcommittee of the Scientific and Standardization Committee of the
 RT International Society on Thrombosis and Haemostasis.";
 RL Thromb. Haemost. 69:77-84(1993).
 RN [10]
 RP VARIANT CYS-444.
 RX MEDLINE=87204221; PubMed=2437584;
 RA Romeo G., Hassan H.J., Staempfili S., Roncuzzi L., Cianetti L.,
 RA Leonardi A., Vicente V., Mannucci P.M., Bertina R.M., Peschle C.,
 RA Cortese R.;
 RT "Hereditary thrombophilia: identification of nonsense and missense
 RT mutations in the protein C gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:2829-2832(1987).
 RN [11]
 RP VARIANT TRP-211 (LONDON-1).
 RX MEDLINE=90098906; PubMed=2602169;
 RA Grundy C.B., Chittolte A., Talbot S., Bevan D., Kakkar V.V.,
 RA Cooper D.N.;
 RT "Protein C London 1: recurrent mutation at Arg-169 (CGG->TGG) in
 RT the protein C gene causing thrombosis.";
 RL Nucleic Acids Res. 17:10513-10513(1989).
 RN [12]
 RP VARIANT CYS-272.
 RX MEDLINE=91329836; PubMed=1868249;
 RA Reitsma P.H., Poort S.R., Allart C.F., Briet E., Bertina R.M.;

RT "The spectrum of genetic defects in a panel of 40 Dutch families with
RT symptomatic protein C deficiency type I: heterogeneity and founder
RT effects.";
RL Blood 78:890-894(1991).
RN [13]
RP VARIANTS ALA-62 (VERMONT-1) AND MET-76.
RX MEDLINE=92190481; PubMed=1347706.
RA Bovill E.G., Tomczak J.A., Grant B., Bhushan F., Pillemer E.,
RA Rainville I.R., Long G.L.;
RT "Protein C venom: symptomatic type II protein C deficiency
RT associated with two GLA domain mutations.";
RL Blood 79:1456-1465(1992).
RN [14]
RP VARIANT ASP-418 (HONG KONG-2).
RX MEDLINE=92305321; PubMed=1611081;
RA Sugahara Y., Mura O., Yuen P., Aoki N.;
RT "Protein C deficiency Hong Kong 1 and 2: hereditary protein C
RT deficiency caused by two mutant alleles, a 5-nucleotide deletion and
RT a missense mutation.";
RL Blood 80:126-133(1992).
RN [15]
RP VARIANT LEU-289.
RX MEDLINE=92380660; PubMed=1511988;
RA Grundy C.B., Chisholm M., Kakkar V.V., Cooper D.N.;
RT "A novel homozygous missense mutation in the protein C (PROC) gene
RT causing recurrent venous thrombosis.";
RL Hum. Genet. 89:683-684(1992).
RN [16]
RP VARIANTS GLN-220 AND TRP-220.
RX MEDLINE=92380661; PubMed=1511989;
RA Grundy C.B., Schulman S., Tengborn L., Kakkar V.V., Cooper D.N.;
RT "Two different missense mutations at Arg 178 of the protein C (PROC)
RT gene causing recurrent venous thrombosis.";
RL Hum. Genet. 89:685-686(1992).
RN [17]
RP VARIANT GLN-220.
RX MEDLINE=93250852; PubMed=1301959;
RA Gaudrille S., Vidaud M., Alach M., Alhenc-Gelas M., Fischer A.M.,
RA Gonaud-Hellman M., Toulon P., Flessinger J.N., Goossens M.;
RT "Two novel mutations responsible for hereditary type I protein C
RT deficiency: characterization by denaturing gradient gel
RT electrophoresis.";
RL Hum. Mutat. 1:491-500(1992).
RN [18]
RP VARIANT SER-334.
RX MEDLINE=92276939; PubMed=1593215;
RA Yamamoto K., Matsushita T., Sugitani I., Takamatsu J., Itasaki E.,
RA Wada H., Deguchi K., Shirakawa S., Saito H.;
RT "Homozygous protein C deficiency: identification of a novel missense
RT mutation that causes impaired secretion of the mutant protein C.";
RL J. Lab. Clin. Med. 119:682-689(1992).
RN [19]
RP VARIANTS TRP-38; CYS-42; HIS-42; GLN-271 AND ASN-294.
RX MEDLINE=93313192; PubMed=8324221;
RA Gaudrille S., Alhenc-Gelas M., Gaussem P., Allaud M.-F., Dupuy E.,
RA Juhán-Vague I., Alach M.;
RT "Five novel mutations located in exons III and IX of the protein C
RT gene in patients presenting with defective protein C anticoagulant
RT activity.";
RL Blood 82:159-168(1993).
RN [20]
RP VARIANTS G-14; Q-211; Y-244; Q-253; L-321; C-328; I-385; T-388 AND
RP V-388.
RX MEDLINE=93271391; PubMed=8499565;
RA Poort S.R., Pabinger-Fasching I., Mannhalter C., Reitsma P.H.,
RA Bertina R.M.;
RT "Twelve novel and two recurrent mutations in 14 Austrian families
RT with hereditary protein C deficiency.";
RL Blood Coagul. Fibrinolysis 4:273-280(1993).
RN [21]
RP VARIANT TRP-57.
RX MEDLINE=93271396; PubMed=8499568;
RA Millar D.S., Grundy C.B., Bignell P., Moffat E.H., Martin R.,

RA Kakkar V.V., Cooper D.N.;
RT "A Gla domain mutation (Arg 15->Trp) in the protein C (PROC) gene
RT causing type 2 protein C deficiency and recurrent venous
RT thrombosis.";
RL Blood Coagul. Fibrinolysis 4:345-347(1993).
RN [22]
RP VARIANTS R-145; L-210; W-211; T-243; L-321; M-340 AND Y-426.
RX MEDLINE=94122329; PubMed=8292730;
RA Tsay W., Greengard J.S., Montgomery R.R., McPherson R.A., Fucci J.C.,
RA Koepfer M.A., Coughlin J., Griffin J.H.;
RT "Genetic mutations in ten unrelated American patients with
RT symptomatic type I protein C deficiency.";
RL Blood Coagul. Fibrinolysis 4:791-796(1993).
RN [23]
RP VARIANT SER-423.
RX MEDLINE=94001606; PubMed=8398832;
RA Marchetti G., Patrocchini P., Gemmati D., Castaman G., Rodeghiero F.,
RA Macey A., Cooper D.N., Tuddenham E.G., Bernardi F.;
RT "Symptomatic type II protein C deficiency caused by a missense
RT mutation (Gly 381->Ser) in the substrate-binding pocket.";
RL Br. J. Haematol. 84:285-289(1993).
RN [24]
RP SEQUENCE OF 43-64 FROM N.A. AND VARIANT GLY-57 (YONAGO).
RX MEDLINE=93237511; PubMed=8477066;
RA Minuro J., Muramatsu S., Kaneko M., Yoshitake S., Iijima K.,
RA Nakamura K., Sakata Y., Matsuda M.;
RT "An abnormal protein C (protein C Yonago) with an amino acid
RT substitution of Gly for Arg-15 caused by a single base mutation of C

Query Match 49.7%; Score 90; DB 1; Length 461;
Best Local Similarity 46.3%; Pred. No. 3.4e-09;
Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

Oy 1 ANGFLXLRXGSLKRCXKCSFXXAXIFRNXXRTQFV 41
Db 43 ANSFLELRHSSLERECIEICDFEAKETIQWDDTLAFW 83

RESULT 14
ID FA10_BOVIN STANDARD: PRT: 492 AA.
AC P00743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
GN F10.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE OF 1-487 FROM N.A.
RX MEDLINE=84247315; PubMed=6330671;
RA Fung M.R., Campbell R.M., McGillivray R.T.A.;
RT "Blood coagulation factor X mRNA encodes a single polypeptide chain
RT containing a prepro leader sequence.";
RL Nucleic Acids Res. 12:4481-4492(1984).
RN [2]
RP SEQUENCE OF 41-180.
RX MEDLINE=80130563; PubMed=6766735;
RA Enfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
RA Titani K.;
RT "Amino acid sequence of the light chain of bovine factor XI (Stuart
RT factor).";
RL Biochemistry 19:659-667(1980).
RN [3]
RP REVISION TO 103.
RX MEDLINE=83308813; PubMed=6688526;
RA McMillen B.A., Fujikawa K., Kisiel W.;
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
RT K-dependent blood coagulation zymogens.";

RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
 RN [4]
 RP SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
 RX MEDLINE=76053069; PubMed=1059093;
 RA Titani K., Fujikawa K., Entfield D.L., Ericsson L.H., Walsh K.A.,
 RT Neurath H.;
 RL "Bovine factor XI (Stuart factor): amino-acid sequence of heavy
 chain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).
 RN [5]
 RP SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=94062825; PubMed=8243461;
 RA Inoue K., Morita T.;
 RL "Identification of O-linked oligosaccharide chains in the activation
 of blood coagulation factor X. The role of the carbohydrate
 moieties in the activation of factor X.";
 RL Eur. J. Biochem. 218:153-163(1993).
 RN [6]
 RP ACTIVE SITE.
 RX MEDLINE=73053314; PubMed=4264286;
 RA Titani K., Hermodson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
 RT Neurath H., Davie E.W.;
 RL "Bovine factor X Ia (activated Stuart factor). Evidence of homology
 with mammalian serine proteases.";
 RL Biochemistry 11:4899-4903(1972).
 RN [7]
 RP PROCESSING.
 RX MEDLINE=76053121; PubMed=1059122;
 RA Fujikawa K., Titani K., Davie E.W.;
 RL "Activation of bovine factor X (Stuart factor): conversion of factor
 Xa-alpha to factor Xa-beta.";
 RL Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
 RN [8]
 RP CALCIUM-BINDING DATA.
 RX MEDLINE=84185716; PubMed=6546930;
 RA Sujo T., Bjork I., Holmgren A., Stenflo J.;
 RL "Calcium-binding properties of bovine factor X lacking the gamma-
 carboxyglutamic acid-containing region.";
 RL J. Biol. Chem. 259:5705-5710(1984).
 RN [9]
 RP SULFATION.
 RX MEDLINE=86140210; PubMed=3949800;
 RA Morita T., Jackson C.M.;
 RL "Localization of the structural difference between bovine blood
 coagulation factors XI and X2 to tyrosine 18 in the activation
 peptide.";
 RL J. Biol. Chem. 261:4008-4014(1986).
 RN [10]
 RP STRUCTURE BY NMR OF 85-126.
 RX MEDLINE=91084483; PubMed=2261466;
 RA Selander M., Persson E., Stenflo J., Drakenberg T.;
 RL "1H NMR assignment and secondary structure of the Ca2(+)-free form of
 the amino-terminal epidermal growth factor like domain in coagulation
 factor X.";
 RL Biochemistry 29:8111-8118(1990).
 RN [11]
 RP STRUCTURE BY NMR OF 85-126.
 RX MEDLINE=92329412; PubMed=1627540;
 RA Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,
 RL Teleman O.;
 RL "Three-dimensional structure of the apo form of the N-terminal
 EGF-like module of blood coagulation factor X as determined by NMR
 spectroscopy and simulated folding.";
 RL Biochemistry 31:5974-5983(1992).
 RN [12]
 RP STRUCTURE BY NMR OF 85-126.
 RX MEDLINE=92406922; PubMed=1527084;
 RA Selander-Sunnerhagen M., Ullner M., Persson E., Teleman O.,
 RL Stenflo J., Drakenberg T.;
 RL "How an epidermal growth factor (EGF)-like domain binds calcium. High
 resolution NMR structure of the calcium form of the NH2-terminal EGF-
 like domain in coagulation factor X.";
 RL J. Biol. Chem. 267:19642-19649(1992).

RN [13]
 RP STRUCTURE BY NMR OF 41-126.
 RX MEDLINE=96387194; PubMed=8794734;
 RA Sunnerhagen M., Olah G.A., Stenflo J., Forsen S., Drakenberg T.,
 RL Trewthella J.;
 RL "The relative orientation of Gla and EGF domains in coagulation
 factor X is altered by Ca2+ binding to the first EGF domain. A
 combined NMR-small angle X-ray scattering study.";
 RL Biochemistry 35:11547-11559(1996).
 RN [14]
 RP FUNCTION: FACTOR XA IS A VITAMIN K-DEPENDENT GLYCOPROTEIN THAT
 CONVERTS PROTHROMBIN TO THROMBIN IN THE PRESENCE OF FACTOR VA,
 CA++ AND PHOSPHOLIPID DURING BLOOD CLOTTING.
 CC CATALYTIC ACTIVITY: Preferential cleavage: Arg-1-Thr and then
 CC Arg-1-Ile bonds in prothrombin to form thrombin.
 CC SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 CC MORE DISULFIDE BONDS.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC -1- PTM: N- AND O-GLYCOSYLATED.
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 CC -----
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 CC -----
 DR EMBL: X00673; CAZ5286.1; -
 DR PIR: A00925; EXBO.
 DR PDB: IAP0: 31-JAN-94.
 DR PDB: 1CCE: 31-MAY-94.
 DR PDB: 1WHE: 15-MAY-97.
 DR PDB: 1WHE: 15-MAY-97.
 DR MEROPS: S01.216; -;
 DR CarBank: CCSD:7747; -;
 DR CarBank: CCSD:7899; -;
 DR CarBank: CCSD:11506; -;
 DR CarBank: CCSD:11508; -;
 DR GlycoSuiteDB: P00743; -;
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000742; EGF-2.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Trypsin.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam: PF00008; EGF; 2.
 DR Pfam: PF00594; gla; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00179; EGF_CA; 1.
 DR SMART: SM00001; EGF_Like; 1.
 DR SMART: SM00069; gla; 1.
 DR SMART: SM00020; TRY_PSp; 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; 1.
 DR PROSITE: PS01186; EGF-2; 1.
 DR PROSITE: PS01187; EGF_CA; 1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.

DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
 KM Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 KW Signal; Zymogen; EGF-like domain; Repeat; Sulfation; 3D-structure.
 FT SIGNAL 1 23
 FT PROPEP 24 40
 FT CHAIN 41 180
 FT CHAIN 183 492
 FT PROPEP 183 492
 FT CHAIN 234 492
 FT PROPEP 476 492
 FT DOMAIN 86 122
 FT DOMAIN 125 165
 FT DOMAIN 234 492
 FT ACT_SITE 275 275
 FT ACT_SITE 321 321
 FT ACT_SITE 418 418
 FT MOD_RES 46 46
 FT MOD_RES 47 47
 FT MOD_RES 54 54
 Query Match 48.6%; Score 88; DB 1; Length 492;
 Best local similarity 36.4%; Pred. No. 8,5e-09;
 Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;
 QY 1 ANGFLXLRKGLKRCXKXKXLCSEFXKXIFRNXXRTQFWVS 44
 DB 41 ANSFLKEVKGKGNLEKLEECLEACSLSEAREVEFDEQJDEFWSKY 84
 RESULT 15
 FA9_BOVIN STANDARD; PRT; 416 AA.
 AC P00741;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Coagulation factor IX (EC 3.4.21.22) (Christmas factor).
 GN F9.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxId=9913;
 RN [1]
 RP MEDLINE=80056619; PubMed=291916;
 RA Katayama K., Ericsson L.H., Enfield D.L., Walsh K.A., Neurath H.,
 RT "Comparison of amino acid sequence of bovine coagulation Factor IX
 RT (Christmas factor) with that of other vitamin K-dependent plasma
 RT proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 76:4990-4994(1979).
 RN [2]
 RP REVISION TO 64.
 RX MEDLINE=83308813; PubMed=6688526;
 RA McMullen B.A., Fujikawa K., Kisiel W.;
 RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
 RT K-dependent blood coagulation zymogens.";
 RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
 RN [3]
 RP SEQUENCE OF 51-111 FROM N.A.
 RX MEDLINE=82272386; PubMed=6287289;
 RA Choo K.H., Gould K.G., Rees D.J.G., Brownlee G.G.;
 RT "Molecular cloning of the gene for human anti-haemophilic factor IX.";
 RL Nature 299:178-180(1992).
 RN [4]
 RP STRUCTURE OF CARBOHYDRATE ON SER-53.
 RX MEDLINE=89213999; PubMed=3149637;
 RA Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T.,
 RA Miyata T., Iwanaga S., Takao T., Shimonishi Y., Ikenaka T.;
 RT "A new trisaccharide sugar chain linked to a serine residue in bovine

RT blood coagulation factors VII and IX.";
 RL J. Biochem. 104:867-868(1988).
 RN [5]
 RP STRUCTURE OF CARBOHYDRATE ON SER-53.
 RX MEDLINE=91344709; PubMed=2129367;
 RA Iwanaga S., Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T.;
 RT "A new trisaccharide sugar chain linked to a serine residue in the
 RT first EGF-like domain of clotting factors VII and IX and protein Z.";
 RL Adv. Exp. Med. Biol. 281:121-131(1990).
 RN [6]
 RP STRUCTURE OF CARBOHYDRATE ON SER-53.
 RX MEDLINE=90130422; PubMed=2105311;
 RA Hase S., Nishimura H., Kawabata S., Iwanaga S., Ikenaka T.;
 RT "The structure of (xylose)2glucose-O-serine 53 found in the first
 RT epidermal growth factor-like domain of bovine blood clotting factor
 RT IX.";
 RL J. Biol. Chem. 265:1858-1861(1990).
 CC -1- FUNCTION: FACTOR IX IS A VITAMIN K-DEPENDENT PLASMA PROTEIN THAT
 CC PARTICIPATES IN THE INTRINSIC PATHWAY OF BLOOD COAGULATION BY
 CC CONVERTING FACTOR X TO ITS ACTIVE FORM IN THE PRESENCE OF CA++
 CC IONS, PHOSPHOLIPIDS, AND FACTOR VIIIa.
 CC -1- CATALYTIC ACTIVITY: Hydrolyses one Arg-|-Ile bond in factor X to
 CC form factor Xa.
 CC -1- SUBUNIT: FACTOR IX IS ACTIVATED BY FACTOR XIa, WHICH EXCISES THE
 CC ACTIVATION PEPTIDE AND THUS PRODUCES A MOLECULE CONSISTING OF 2
 CC CHAINS HELD TOGETHER BY ONE OR MORE DISULFIDE BONDS.
 CC -1- MISCELLANEOUS: CALCIUM BINDS TO THE GAMMA-CARBOXYGLUTAMIC ACID
 CC (GLA) RESIDUES AND, WITH STRONGER AFFINITY, TO ANOTHER SITE,
 CC BEYOND THE GLA DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 CC -----
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 CC -----
 DR EMBL: J00007; AAA30520.1; -.
 DR PIR: A00923; KFBQ.
 DR HSSP: P00740; ICFH.
 DR MEROPS: S01.214; -.
 DR GLYCOSULEDB: P00741; -.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000742; EGF_2.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR001438; EGF_II.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Trypsin.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam: PF00008; EGF; 2.
 DR Pfam: PF00594; gla; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00010; EGFBLDOD.
 DR PRINTS: PR00001; GLABLOD.
 DR SMART: SM00179; EGF_Ca; 1.
 DR SMART: SM00001; EGF-like; 1.
 DR SMART: SM00069; gla; 1.
 DR SMART: SM00020; TRYP_SPC; 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; 1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF_CA; 1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.

RT Ca2+-binding site that lacks gamma-carboxyglutamic acid.";
 RL J. Biol. Chem. 259:5698-5704(1984).
 RN [12]
 RP ERRATUM.
 RA Morita T., Isaacs B.S., Eason C.T., Johnson A.E.;
 RL J. Biol. Chem. 260:2583-2583(1985).
 RN [13]
 RP SIGNAL SEQUENCE CLEAVAGE SITE.
 RX MEDLINE=86189947; PubMed=3009023;
 RA Bentley A.K., Rees D.J.G., Rizza C., Brownlee G.G.;
 RT "Defective propeptide processing of blood clotting factor IX caused
 by mutation of arginine to glutamine at position -4.";
 RL Cell 45:343-348(1986).
 RN [14]
 RP STRUCTURE OF CARBOHYDRATE ON SER-99.
 RX MEDLINE=90662160; PubMed=2511201;
 RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T., Takao T.,
 RA Shimonishi Y., Iwanaga S.;
 RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
 (Xyl2-Glc) O-glycosidically linked to a serine residue in the first
 epidermal growth factor-like domain of human factors VII and IX and
 protein Z and bovine protein Z.";
 RL J. Biol. Chem. 264:20320-20325(1989).
 RN [15]
 RP STRUCTURE OF CARBOHYDRATE ON SER-99.
 RX MEDLINE=91344709; PubMed=2129367;
 RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;
 RT "A new trisaccharide sugar chain linked to a serine residue in the
 first EGF-like domain of clotting factors VII and IX and protein Z.";
 RL Adv. Exp. Med. Biol. 281:121-131(1990).
 RN [16]
 RP STRUCTURE OF CARBOHYDRATE ON SER-107.
 RX MEDLINE=92388094; PubMed=1517205;
 RA Nishimura H., Takao T., Hase S., Shimonishi Y., Iwanaga S.;
 RT "Human factor IX has a tetrasaccharide O-glycosidically linked to
 serine 61 through the fucose residue.";
 RL J. Biol. Chem. 267:17520-17525(1992).
 RN [17]
 RP PHOSPHORYLATION OF SER-114.
 RA Harris R.J., Papac D.I., Truong L., Smith K.J.;
 RT "Partial phosphorylation of serine-68 in EGF-1 of human factor IX.";
 RL (In) Abstracts of 11th International conference on methods in protein
 structure analysis, pp.50-50, Annecy (1996).
 RN [18]
 RP POST-TRANSLATIONAL MODIFICATIONS.
 RX MEDLINE=20575397; PubMed=11133752;
 RA Arruda V.R., Hagstrom J.N., Delich J., Helman-Patterson T.,
 RA Camire R.M., Chu K., Fields P.A., Herzog R.W., Couto L.B.,
 RA Larson P.J., High K.A.;
 RT "Posttranslational modifications of recombinant myotube-synthesized
 human factor IX.";
 RL Blood 97:130-138(2001).
 RN [19]
 RP STRUCTURE BY NMR OF 47-93.
 RX MEDLINE=95229607; PubMed=7713897;
 RA Freedman S.J., Furie B.C., Furie B., Baleja J.D.;
 RT "Structure of the metal-free gamma-carboxyglutamic acid-rich membrane
 binding region of factor IX by two-dimensional NMR spectroscopy.";
 RL J. Biol. Chem. 270:7980-7987(1995).
 RN [20]
 RP STRUCTURE BY NMR OF 47-93.
 RX MEDLINE=96032604; PubMed=7547952;
 RA Freedman S.J., Furie B.C., Furie B., Baleja J.D.;
 RT "Structure of the calcium ion-bound gamma-carboxyglutamic acid-rich
 domain of factor IX.";
 RL Biochemistry 34:12126-12137(1995).
 RN [21]
 RP STRUCTURE BY NMR OF 47-93.
 RX MEDLINE=96279169; PubMed=8663165;
 RA Freedman S.J., Blostein M.D., Baleja J.D., Jacobs M., Furie B.C.,
 RA Furie B.;
 RT "Identification of the phospholipid binding site in the vitamin K-
 dependent blood coagulation protein factor IX.";

RL J. Biol. Chem. 271:16227-16236(1996).
 RN [22]
 RP STRUCTURE BY NMR OF 47-93.
 RX MEDLINE=97199336; PubMed=9047312;
 RA Li L., Darden T.A., Freedman S.J., Furie B.C., Furie B., Baleja J.D.,
 RA Smith H., Hisey R.G., Pedersen L.G.;
 RT "Refinement of the NMR solution structure of the
 gamma-carboxyglutamic acid domain of coagulation factor IX using
 molecular dynamics simulation with initial Ca2+ positions determined
 by a genetic algorithm.";
 RL Biochemistry 36:2132-2138(1997).
 RN [23]
 RP STRUCTURE BY NMR OF 91-133.
 RX MEDLINE=91308127; PubMed=1854745;
 RA Huang L.H., Cheng H., Pardi A., Tam J.P., Sweeney M.V.;
 RT "Sequence-specific 1H NMR assignments, secondary structure, and
 location of the calcium binding site in the first epidermal growth
 factor like domain of blood coagulation factor IX.";
 RL Biochemistry 30:7402-7409(1991).
 RN [24]
 RP STRUCTURE BY NMR OF 92-130.
 RX MEDLINE=93284090; PubMed=1304885;
 RA Baron M., Norman D.G., Harvey T.S., Handford P.A., Mayhew M.,
 RA Tse A.G.D., Brownlee G.G., Campbell I.D.C.;
 RT "The three-dimensional structure of the first EGF-like module of
 human factor IX: comparison with EGF and TGF-alpha.";
 RL Protein Sci. 1:81-90(1992).
 RN [25]
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 92-130.
 RX MEDLINE=95330802; PubMed=7606779;
 RA Rao Z., Handford P., Mayhew M., Knott V., Brownlee G.G., Stuart D.;
 RT "The structure of a Ca(2+)-binding epidermal growth factor-like
 domain: its role in protein-protein interactions.";
 RL Cell 82:131-141(1995).
 RN [26]
 RP MOLECULAR PATHOLOGY OF HEMOPHILIA B.
 RP Query Match 47.5%; Score 86; DB 1; Length 461;
 Best Local Similarity 39.5%; Pred. No. 1.9e-08;
 Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;
 Oy 2 NGFLXLLRGSLLRXCRXXLCSFFXAXXIFRNXXRTRFWFSY 44
 Db 49 SGKLEEFYQNLRECRMEKCSFEAREVFERTETFEWFOY 91
 RESULT 17
 PRTC_RABIT STANDARD: PRT: 458 AA.
 ID PRTC_RABIT AC Q28661;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
 DE (Autoproteolymph IIa) (Anticoagulant protein C) (Blood coagulation
 factor XIV) (Fragment).
 GN PROC.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OC NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP TISSUE: Liver;
 RC Shen L., He X., Dahlback B.;
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
 CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
 CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
 CC and VIIIA.
 CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
 CC INFO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE

CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
 CC TETRAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
 CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
 CC STRONGLY PROMOTED BY THROMBOMODULIN.
 CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
 CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
 CC THROMBIN-THROMBOMODULIN COMPLEX.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 CC -----
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 CC DR EMBL; U49333; AAA92956.1; -.
 CC DR HSSP; P04070; 1PCU.
 CC DR MEROPS; S01.218; -.
 CC DR InterPro; IPR000152; Asx_hydroxyl.
 CC DR InterPro; IPR000561; EGF-like.
 CC DR InterPro; IPR001881; EGF-Ca.
 CC DR InterPro; IPR001254; Trypsin.
 CC DR InterPro; IPR000294; VitK_dep_GLA.
 CC Pfam; PF00006; EGF; 2.
 CC Pfam; PF00594; gla; 1.
 CC Pfam; PF00089; trypsin; 1.
 CC SMART; SM00181; EGF; 2.
 CC SMART; SM00069; GLA; 1.
 CC SMART; SM00020; Tryp_Spc; 1.
 CC PROSITE; PS00010; ASX_HYDROXYL; 1.
 CC PROSITE; PS00022; EGF_1; 1.
 CC PROSITE; PS01186; EGF_2; 2.
 CC PROSITE; PS01187; EGF-Ca; 1.
 CC PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 CC PROSITE; PS02040; TRYPsin DOM; 1.
 CC PROSITE; PS00134; TRYPsin HIS; 1.
 CC PROSITE; PS00135; TRYPsin SER; 1.
 CC Blood coagulation; Glycoprotein; Serine protease;
 CC Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 CC EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
 CC KM EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
 CC FT NON_TER 1 1
 CC FT SIGNAL 1 27
 CC FT PROPEP 28 36 BY SIMILARITY.
 CC FT CHAIN 37 458 VITAMIN K-DEPENDENT PROTEIN C.
 CC FT CHAIN 37 192 PROTEIN C LIGHT CHAIN (BY SIMILARITY).
 CC FT CHAIN 195 458 PROTEIN C HEAVY CHAIN (BY SIMILARITY).
 CC FT PEPTIDE 195 209 ACTIVATION PEPTIDE (BY SIMILARITY).
 CC FT SITE 209 210 CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
 CC FT DOMAIN 91 126 EGF-LIKE 1.
 CC FT DOMAIN 130 170 EGF-LIKE 2.
 CC FT DOMAIN 210 458 SERINE PROTEASE.
 CC FT MOD_RES 42 42 GAMMA-CARBOXYGLUTAMIC ACID
 CC (BY SIMILARITY).
 CC FT MOD_RES 43 43 GAMMA-CARBOXYGLUTAMIC ACID
 CC (BY SIMILARITY).
 CC FT MOD_RES 50 50 GAMMA-CARBOXYGLUTAMIC ACID
 CC (BY SIMILARITY).
 CC FT MOD_RES 52 52 GAMMA-CARBOXYGLUTAMIC ACID
 CC (BY SIMILARITY).
 CC FT MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID
 CC (BY SIMILARITY).
 CC FT MOD_RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID
 CC (BY SIMILARITY).
 CC FT MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID
 CC (BY SIMILARITY).

FT MOD_RES 62 62 GAMMA-CARBOXYGLUTAMIC ACID
 FT (BY SIMILARITY).
 FT MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID
 FT (BY SIMILARITY).
 FT MOD_RES 107 107 HYDROXYLATION (BY SIMILARITY).
 FT ACT_SITE 250 250 CHARGE RELAY SYSTEM.
 FT ACT_SITE 296 296 CHARGE RELAY SYSTEM.
 FT ACT_SITE 399 399 CHARGE RELAY SYSTEM.
 FT DISULFID 53 58 BY SIMILARITY.
 FT DISULFID 86 105 BY SIMILARITY.
 FT DISULFID 95 100 BY SIMILARITY.
 FT DISULFID 99 114 BY SIMILARITY.
 FT DISULFID 116 125 BY SIMILARITY.
 FT DISULFID 134 145 BY SIMILARITY.
 FT DISULFID 141 154 BY SIMILARITY.
 FT DISULFID 156 169 BY SIMILARITY.
 FT DISULFID 177 316 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 235 251 BY SIMILARITY.
 FT DISULFID 370 384 BY SIMILARITY.
 FT DISULFID 395 423 BY SIMILARITY.
 FT CARBOHD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 458 AA; 51087 MW; D75A5F90C8F29D7 CRC64;
 Query Match 45.9%; Score 83; DB 1; Length 458;
 Best Local Similarity 40.9%; Pred. No. 6; 9e-08;
 Matches 18; Conservative 3; Mismatches 23; Indels 0; Gaps 0;
 Oy 1 ANGFLXLRKSGSLXRCXRLCSFXKXKIFNNXXRTQFWWSY 44
 Db 37 ANSFLELRPSSLERCBVECDLEBAKEIFOSVDDTLAFWKY 80
 RESULT 18
 FA9_CANFA STANDARD; PRT; 452 AA.
 AC P19540;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 GN Coagulation factor IX precursor (EC 3.4.21.22) (Christmas factor).
 DE
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxId=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=90311364; PubMed=2367529;
 RA Axelrod J.H., Read M.S., Brinkhous K.M., Verma I.M.;
 RT "Phenotypic correction of factor IX deficiency in skin fibroblasts of
 RT hemophilic dogs.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:5173-5177(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=89323338; PubMed=2752110;
 RA Evans J.P., Watzke H.H., Ware J.L., Stafford D.W., High K.A.;
 RT "Molecular cloning of a cDNA encoding canine factor IX.";
 RL Blood 74:207-212(1989).
 RN [3]
 RP VARIANT HEMOPHILIA B GLU-418.
 RX MEDLINE=9009303; PubMed=2481310;
 RA Evans J.P., Brinkhous K.M., Brayer G.D., Reissner H.M., High K.A.;
 RT "Canine hemophilia B resulting from a point mutation with unusual
 RT consequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:10095-10099(1989).
 CC -1- FUNCTION: FACTOR IX IS A VITAMIN K-DEPENDENT PLASMA PROTEIN THAT
 CC PARTICIPATES IN THE INTRINSIC PATHWAY OF BLOOD COAGULATION BY
 CC CONVERTING FACTOR X TO ITS ACTIVE FORM IN THE PRESENCE OF CA++

Query Match	Best Local Similarity	Score 81:	DB 1:	Length 459:
Matches 16:	Conservative 5:	Mismatches 22:	Indels 0:	Gaps 0:
FT	MOD_RES	61	61	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	64	64	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	67	67	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	70	70	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	74	74	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	98	98	HYDROXYLATION (BY SIMILARITY).
FT	ACT_SITE	265	265	CHANGE RELAY SYSTEM.
FT	ACT_SITE	313	313	CHANGE RELAY SYSTEM.
FT	ACT_SITE	409	409	CHANGE RELAY SYSTEM.
FT	DISULFID	52	57	BY SIMILARITY.
FT	DISULFID	85	96	BY SIMILARITY.
FT	DISULFID	90	105	BY SIMILARITY.
FT	DISULFID	107	116	BY SIMILARITY.
FT	DISULFID	122	133	BY SIMILARITY.
FT	DISULFID	129	143	BY SIMILARITY.
FT	DISULFID	145	158	BY SIMILARITY.
FT	CARBOHYD	192	192	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	211	211	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	304	304	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	363	363	H -> Q (IN REF. 2).
FT	CONFLICT	388	388	T -> I (IN REF. 2).
SO	SEQUENCE	459 AA:	51635 MW:	EF439C840DCBC1A CRC64:
Oy	2	NGFLKXLRKSGSLKRCRXXLCFXXAXXIFRNXXRTROFWY 44		
Db	37	SGKLEFVGRGNLERECIERCSFEAREVFENFTEKTFEWMQY 79		
RESULT 20				
FA10_CHICK	STANDARD:	PRT:	475 AA.	
AC	FA10_CHICK			
AC	P25155:			
DT	01-MAY-1992 (Rel. 22, Created)			
DT	01-MAY-1992 (Rel. 22, Last sequence update)			
DT	01-FEB-1996 (Rel. 33, Last annotation update)			
DE	Coagulation factor X precursor (BC 3.4.21.6) (Stuart factor)			
GN	(Virus activating protease) (VAP).			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.			
OX	NCBI_TaxID=9031:			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Chorioallantoic membrane;			
RX	MEDLINE=91257322; PubMed=2044767;			
RA	Suzuki H., Harada A., Hayashi Y., Wada K., Asaka J.-I., Gotoh B.,			
RA	Ogasawara T., Nagai Y.;			
RT	"Primary structure of the virus activating protease from chick			
RT	embryo. Its identity with the blood clotting factor Xa.";			
RL	FEMS Lett. 283:281-285(1991).			
RN	[2]			
RP	SEQUENCE OF 41-55 AND 241-261.			
RC	TISSUE=Allantoic fluid;			
RX	MEDLINE=91065352; PubMed=2174359;			
RA	Gotoh B., Ogasawara T., Toyoda T., Innocencio N.M., Hamaguchi M.,			
RA	Nagai Y.;			
RT	"An endoprotease homologous to the blood clotting factor X as a			
RT	determinant of viral tropism in chick embryo.";			
RL	EMBO J. 9:4189-4193(1990).			
CC	-1- FUNCTION: FACTOR XA IS A VITAMIN K-DEPENDENT GLYCOPROTEIN THAT			
CC	CONVERTS PROTHROMBIN TO THROMBIN IN THE PRESENCE OF FACTOR VA.			

CC CA++ AND PHOSPHOLIPID DURING BLOOD CLOTTING.

CC -1- FUNCTION: VAP CLEAVES THE FUSION PROTEINS OF SENDAI VIRUS, NDV,

CC AND INFLUENZA VIRUS A AT A SPECIFIC SINGLE ARGININE-CONTAINING

CC SITE, AND PLAYS A KEY ROLE IN THE VIRAL SPREADING IN THE ALLANTOIC

CC SAC.

CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-1-Thr and then

CC Arg-1-Ile bonds in prothrombin to form thrombin.

CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR

CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR

CC MORE DISULFIDE BONDS.

CC -1- TISSUE SPECIFICITY: LIVER AND CHORIOALLANTOIC MEMBRANE.

CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME

CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND

CC CALCIUM.

CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE

CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).

CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE

CC TRYPSIN FAMILY.

CC -----

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL: D00844; BAA00724.1; -.

CC PIR: S15838; S15838.

CC HSSP: P00742; 1HCG.

CC MEROPS: S01.216; -.

CC Interpro: IPR000152; Asx_hydroxyl.

CC Interpro: IPR001314; Chymotrypsin.

CC Interpro: IPR000561; EGF_1-like.

CC Interpro: IPR000742; EGF_2.

CC Interpro: IPR001881; EGF_Ca.

CC Interpro: IPR001438; EGF_IT.

CC Interpro: IPR002383; GLA_blood.

CC Interpro: IPR001254; Trypsin.

CC Interpro: IPR000294; Vitk_dep_GLA.

CC Pfam: PF00008; EGF_2.

CC Pfam: PF00594; gla_1.

CC Pfam: PF0089; trypsin_1.

CC PRINTS: PRO0722; CHYMOTRYPSIN.

CC PRINTS: PRO0010; EGF_BLOOD.

CC PRINTS: PRO0001; GLABLOOD.

CC SMART: SM00179; EGF_CA_1.

CC SMART: SM00069; GLA_1.

CC SMART: SM00020; TYP_Spc_1.

CC PROSITE: PS00010; ASX_HYDROXYL_1.

CC PROSITE: PS00022; EGF_1; 1.

CC PROSITE: PS01186; EGF_2; 2.

CC PROSITE: PS01187; EGF_CA_1.

CC PROSITE: PS00011; GLU_CARBOXYLATION_1.

CC PROSITE: PS0240; TRYPSIN_DOM_1.

CC PROSITE: PS00134; TRYPSIN_HIS_1.

CC PROSITE: PS00135; TRYPSIN_SER_1.

CC Glycoprotein: Hydroxylase: Serine protease: Plasma: Blood coagulation;

CC Gamma-carboxyglutamic acid; Hydroxylation: Calcium-binding; Vitamin K;

CC Signal; Zymogen: EGF-like domain; Repeat.

CC Signal; Zymogen: EGF-like domain; Repeat.

CC FT STGNL 1 20 OR 30, OR 31 (POTENTIAL).

CC FT PROPEP 21 40

CC FT CHAIN 41 180 FACTOR X LIGHT CHAIN.

CC FT CHAIN 186 475 FACTOR X HEAVY CHAIN.

CC FT PROPEP 186 241 ACTIVATION PEPTIDE.

CC FT CHAIN 242 475 ACTIVATED FACTOR XA, HEAVY CHAIN.

CC FT DOMAIN 86 122 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).

CC FT DOMAIN 125 168 EGF-LIKE 2.

CC FT DOMAIN 241 475 SERINE PROTEASE.

CC FT MOD_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID

CC FT MOD_RES 47 47 (BY SIMILARITY).

CC FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID

FT MOD_RES 54 54 (BY SIMILARITY).

FT MOD_RES 56 56 (BY SIMILARITY).

FT MOD_RES 59 59 (BY SIMILARITY).

FT MOD_RES 60 60 (BY SIMILARITY).

FT MOD_RES 65 65 (BY SIMILARITY).

FT MOD_RES 66 66 (BY SIMILARITY).

FT MOD_RES 69 69 (BY SIMILARITY).

FT MOD_RES 72 72 (BY SIMILARITY).

FT MOD_RES 79 79 (BY SIMILARITY).

FT MOD_RES 103 103 (BY SIMILARITY).

FT ACT_SITE 282 282 (BY SIMILARITY).

FT ACT_SITE 328 328 (BY SIMILARITY).

FT ACT_SITE 425 425 (BY SIMILARITY).

FT DISULFID 90 101 (BY SIMILARITY).

FT DISULFID 95 110 (BY SIMILARITY).

FT DISULFID 112 121 (BY SIMILARITY).

FT DISULFID 129 140 (BY SIMILARITY).

FT DISULFID 136 152 (BY SIMILARITY).

FT DISULFID 154 167 (BY SIMILARITY).

FT DISULFID 175 348 (BY SIMILARITY).

FT DISULFID 247 252 (BY SIMILARITY).

FT DISULFID 267 283 (BY SIMILARITY).

FT DISULFID 396 410 (BY SIMILARITY).

FT DISULFID 421 449 (BY SIMILARITY).

FT CARBOHYD 196 196 (BY SIMILARITY).

FT CARBOHYD 207 207 (BY SIMILARITY).

FT CARBOHYD 228 228 (BY SIMILARITY).

FT CARBOHYD 285 285 (BY SIMILARITY).

SO SOURCE 475 AA; 53142 MM; 570BF84956C5C74D CR664;

Query Match 44.2%; Score 80; DB 1; Length 475;

Best Local Similarity 34.1%; Pred. No. 2,6e-07;

Matches 15; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

Qy 1 ANGFLXLRKXSLRXCRRXKLCSPFXAXXIFRNXXRTROPVAY 44

Db 41 ANSTLEEMKOGNIFRECNERCSEKFEAREAFEDNEKEEEMNYY 84

RESULT 21

THRB_HUMAN STANDARD; PRT; 622 AA.

ID THRB_HUMAN

AC P00734;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Prothrombin precursor (EC 3.4.21.5) (coagulation factor II).

GN F2.

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_Taxid=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=88077877; PubMed=2825773;

RT Degen S.J.F., Davie E.W.;

RL Biochemistry 26:6165-6177(1987).

RN [2]

RP SEQUENCE OF 8-622 FROM N.A.

RA MEDLINE=83231469; PubMed=6305407;

RX Degen S.J.F., McGallivray R.T.A., Davie E.W.;

RT "Characterization of the complementary deoxyribonucleic acid and gene
RT coding for human prothrombin.";
RL Biochemistry 22:2087-2097(1983).
RN [3]
RP SEQUENCE OF 44-314.
RX MEDLINE-77193964; PubMed-266717;
RA Walz D.A., Hewett-Ellmet D., Seegers W.H.;
RT "Amino acid sequence of human prothrombin fragments 1 and 2.";
RL Proc. Natl. Acad. Sci. U.S.A. 74:1969-1972(1977).
RN [4]
RP SEQUENCE OF 315-622.
RX MEDLINE-77207112; PubMed-873923;
RA Butkowski R.J., Elion J., Downing M.R., Mann K.G.;
RT "Primary structure of human prothrombin 2 and alpha-thrombin.";
RL J. Biol. Chem. 252:4942-4957(1977).
RN [5]
RP PROCESSING.
RX MEDLINE-87008532; PubMed-3759598;
RA Rabiet M.J., Blashill A., Furie B., Furie B.C.;
RT "Prothrombin fragment 1 X 2 X 3, a major product of prothrombin
RT activation in human plasma.";
RL J. Biol. Chem. 261:13210-13215(1986).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE-90059942; PubMed-2583108;
RA Bode W., Mayr I., Baumann U., Huber R., Stone S.R., Hofsteege J.;
RT "The refined 1.9 A crystal structure of human alpha-thrombin:
RT interaction with D-Phe-Pro-Arg chloromethylketone and significance
RT of the Tyr-Pro-Pro-Tyr insertion segment.";
RL EMBO J. 8:3467-3475(1989).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX MEDLINE-90327074; PubMed-2374926;
RA Rydel T.J., Ravichandran K.G., Tulinsky A., Bode W., Huber R.,
RA Roltsch C., Fenton J.W. II;
RT "The structure of a complex of recombinant hirudin and human alpha-
RT thrombin.";
RL Science 249:277-280(1990).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE-94350942; PubMed-8071320;
RA Rydel T.J., Yin M., Padmanabhan K.P., Blankenship D.T., Cardin A.D.,
RA Correa P.E., Fenton J.W. II, Tulinsky A.;
RT "Crystallographic structure of human gamma-thrombin.";
RL J. Biol. Chem. 269:22000-22006(1994).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX MEDLINE-97357286; PubMed-9214615;
RA van de Loch A., Bode W., Huber R., Le Bonniec B.F., Stone S.R.,
RA Esmen C.T., Stubbs M.T.;
RT "The thrombin E192Q-BPTI complex reveals gross structural
RT rearrangements: implications for the interaction with antithrombin
RT and thrombomodulin.";
RL EMBO J. 16:2977-2984(1997).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 328-601.
RX MEDLINE-99162521; PubMed-10051558;
RA Guinto E.R., Caccia S., Rose T., Fuetterer K., Waksman G., di Cera E.;
RT "Unexpected crucial role of residue 225 in serine proteases.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:1852-1857(1999).
RN [11]
RP VARIANT BARCELONA.
RX MEDLINE-87033739; PubMed-3771562;
RA Rabiet M.-J., Furie B.C., Furie B.;
RT "Molecular defect of prothrombin Barcelona. Substitution of cysteine
RT for arginine at residue 273.";
RL J. Biol. Chem. 261:15045-15048(1986).
RN [12]
RP VARIANT FRANKFURT.
RX MEDLINE-95313001; PubMed-7792730;
RA Degen S.J.F., McDowell S.A., Sparks L.M., Scharrer I.;
RT "Prothrombin Frankfurt: a dysfunctional prothrombin characterized by
RT substitution of Glu-466 by Ala.";
RL Thromb. Haemost. 73:203-209(1995).
RN [13]
RP VARIANTS HIMI-1 AND HIMI-2.
RX MEDLINE-93043342; PubMed-1421398;
RA Morishita E., Saito M., Kumabashiri I., Asakura H., Matsuda T.,
RA Yamaguchi K.;
RT "Prothrombin Himi: a compound heterozygote for two dysfunctional
RT prothrombin molecules (Met-337-->Thr and Arg-388-->His)."
RL Blood 80:2275-2280(1992).
RN [14]
RP VARIANT PADUA-1.
RX MEDLINE-95169898; PubMed-7865694;
RA James H.L., Kim D.J., Zheng D.-O., Girolami A.;
RT "Prothrombin Padua I: incomplete activation due to an amino acid
RT substitution at a factor Xa cleavage site.";
RL Blood Coagul. Fibrinolysis 5:841-844(1994).
RN [15]
RP VARIANT QUICK-1.
RX MEDLINE-89207504; PubMed-3242619;
RA Henriksen R.A., Mann K.G.;
RT "Identification of the primary structural defect in the dysthrombin
RT thrombin Quick I: substitution of cysteine for arginine-382.";
RL Biochemistry 27:9160-9165(1988).
RN [16]
RP VARIANT QUICK-2.
RX MEDLINE-89247398; PubMed-2719946;
RA Henriksen R.A., Mann K.G.;
RT "Substitution of valine for glycine-558 in the congenital dysthrombin
RT thrombin Quick II alters primary substrate specificity.";
RL Biochemistry 28:2078-2082(1989).
RN [17]
RP VARIANT SALAKTA.
RX MEDLINE-92378975; PubMed-1354985;
RA Miyata T., Aruga R., Uneyama H., Bezeaud A., Guillin M.-C.,
RA Iwanaga S.;
RT "Prothrombin Salakta: substitution of glutamic acid-466 by alanine
RT reduces the fibrinogen clotting activity and the esterase activity.";
RL Biochemistry 31:7457-7462(1992).
RN [18]
RP VARIANT TOKUSHIMA.
RX MEDLINE-87185407; PubMed-3567158;
RA Miyata T., Morita T., Imomoto T., Kawauchi S., Shirakami A.,
RA Iwanaga S.;
RT "Prothrombin Tokushima, a replacement of arginine-418 by tryptophan
RT that impairs the fibrinogen clotting activity of derived thrombin
RT Tokushima.";
RL Biochemistry 26:1117-1122(1987).
RN [19]
RP VARIANT TOKUSHIMA.
RX MEDLINE-87101511; PubMed-3801671;
RA Imomoto T., Shirakami A., Kawauchi S., Shigekiyo T., Saito S.,
RA Miyoshi K., Morita T., Iwanaga S.;
RT "Prothrombin Tokushima: characterization of dysfunctional thrombin
RT derived from a variant of human prothrombin.";
RL Blood 69:565-569(1987).
RN [20]
RP VARIANT TOKUSHIMA.
RX MEDLINE-92256895; PubMed-1349838;
RA Iwanaga H., Yoshimoto K., Shigekiyo T., Shirakami A., Saito S.,
RA Itakura M.;
RT "Detection of a single base substitution of the gene for prothrombin
RT Tokushima. The application of PCR-SSCP for the genetic and molecular
RT analysis of dysprothrombinemia.";
RL Int. J. Hematol. 55:93-100(1992).
RN [21]
RP VARIANT TYPE-3.
RX MEDLINE-83204687; PubMed-6405779;
RA Board P.G., Shaw D.C.;
RT "Determination of the amino acid substitution in human prothrombin
RT type 3 (157 Glu leads to Lys) and the localization of a third
RT thrombin cleavage site.";
RL Br. J. Haematol. 54:245-254(1983).
CC -!- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS

FT ACT_SITE 402 402 CHANGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 458 458 CHANGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 564 564 CHANGE RELAY SYSTEM (BY SIMILARITY).
FT MOD_RES 50 50 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 51 51 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 58 58 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 63 63 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 64 64 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 73 73 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 76 76 GAMMA-CARBOXYGLUTAMIC ACID.
FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 412 412 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 552 552 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 61 66 BY SIMILARITY.
FT DISULFID 91 104 BY SIMILARITY.
FT DISULFID 109 187 BY SIMILARITY.
FT DISULFID 130 170 BY SIMILARITY.
FT DISULFID 158 182 BY SIMILARITY.
FT DISULFID 215 292 BY SIMILARITY.
FT DISULFID 236 276 BY SIMILARITY.
FT DISULFID 264 287 BY SIMILARITY.
FT DISULFID 332 478 INTERCHAIN (BY SIMILARITY).
FT DISULFID 387 403 BY SIMILARITY.
FT DISULFID 532 546 BY SIMILARITY.
FT DISULFID 560 590 BY SIMILARITY.
SQ SEQUENCE 617 AA; 70411 MW; AD27D1B71445DB1D CRC64;

Query Match 41.4%; Score 75; DB 1; Length 617;
Best Local Similarity 37.2%; Pred. No. 3e-06;
Matches 16; Conservative 4; Mismatches 23; Indels 0; Gaps 0;

QY 2 NGFLXLRKGSIXRXXRXXLCSEFXAXXIFRXXRTRQFWVSX 44
Db 46 SGFLELRKGNLRCEVEGCSYEAFALESPQDTDFVFMKX 88

RESULT 23
ID THRB_MOUSE STANDARD; PRT; 618 AA.
AC P19221;
DP 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DB Prothrombin precursor (EC 3.4.21.5).
GN F2 OR CF2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Liver;
RX MEDLINE=91025551; PubMed=2222810;
RA Friesner Degen S.J.; Schaffer L.A.; Jamison C.S.; Grant S.G.;
RA Fitzgibbon J.J.; Pal J.-A.; Chapman V.M.; Elliott R.W.;
RT "Characterization of the cDNA coding for mouse prothrombin and
RT localization of the gene on mouse chromosome 2.";
RL DNA Cell Biol. 9:487-498(1990).
RN [2]
RP SEQUENCE OF 384-618 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92212913; PubMed=1557383;
RA Banfield D.K.; Macgillivray R.T.;
RT "Partial characterization of vertebrate prothrombin cDNAs:
RT amplification and sequence analysis of the B chain of thrombin from
RT nine different species.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
CC -1- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS

CC FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,
CC AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.
CC -1- PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
CC RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOEAL
CC ENZYME. THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES
CC ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY
CC CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
CC OF PROTHROMBIN TO THROMBIN.
CC -1- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A
CC PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &
CC FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES
CC THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &
CC HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR
CC V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
CC THROMBIN.
CC -1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL
CC FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
CC BY FACTOR XA.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X52308; CAA6548.1; -;
CC EMBL: M81394; AAR40435.1; -;
CC PIR: A35827; A35827.
CC HSSP: P00734; 1B7X.
CC MEROPS: S01.217; -;
CC MGD: MGI:88380; F2.
CC InterPro: IPR001314; Chymotrypsin.
CC InterPro: IPR002383; GLA_blood.
CC InterPro: IPR000001; Kringleg.
CC InterPro: IPR003966; Prothrombin.
CC InterPro: IPR001254; Trypsin.
CC InterPro: IPR000294; Vltk_dep_GLA.
CC Pfam: PF00594; gla; 1.
CC Pfam: PF00051; kringleg; 2.
CC Pfam: PF00089; trypsin; 1.
CC PRINTS: PR00722; CHYMOTRYPSIN.
CC PRINTS: PR00001; GLABLOOD.
CC PRINTS: PR00018; KRINGLE.
CC PRINTS: PR01505; PROTHROMBIN.
CC SMART: SM00069; GLA; 1.
CC SMART: SM00130; KR; 2.
CC SMART: SM00020; TRYP_Spc; 1.
CC PROSITE: PS00011; GLU_CARBOXYLATION; 1.
CC PROSITE: PS00021; KRINGLE_1; 2.
CC PROSITE: PS50070; KRINGLE_2; 2.
CC PROSITE: PS50240; TRYPSIN_DOM; 1.
CC PROSITE: PS00134; TRYPSIN_HIS; 1.
CC PROSITE: PS00135; TRYPSIN_SER; 1.
CC Blood coagulation; Plasma; Calcium-binding; Glycoprotein; Repeat;
CC Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver;
CC Hydrolyase; Serine protease; Kringleg; Signal.
CC SIGNAL 1 24
CC PROPEP 25 43
CC CHAIN 44 618
CC PEPTIDE 44 200
CC PEPTIDE 201 324
CC CHAIN 325 360
CC CHAIN 361 618
CC DOMAIN 109 187
CC DOMAIN 215 292
CC DOMAIN 361 618
CC SITE 200 201
CC SITE 324 325
CC PROTHROMBIN.
CC ACTIVATION PEPTIDE (FRAGMENT 1).
CC ACTIVATION PEPTIDE (FRAGMENT 2).
CC THROMBIN LIGHT CHAIN (A).
CC THROMBIN HEAVY CHAIN (B).
CC KRINGLE 1.
CC KRINGLE 2.
CC SERINE PROTEASE.
CC CLEAVAGE (BY THROMBIN).
CC CLEAVAGE (BY FACTOR XA).

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FT SITE 360 361 CLEAVAGE (BY FACTOR XA).
FT ACT_SITE 403 403 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 459 459 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 565 565 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT MOD_RES 50 50 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 51 51 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 56 58 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 63 63 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 64 64 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 73 73 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 76 76 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 76 76 GAMMA-CARBOXYGLUTAMIC ACID.
FT DISULFID 61 66 BY SIMILARITY.
FT DISULFID 91 104 BY SIMILARITY.
FT DISULFID 109 187 BY SIMILARITY.
FT DISULFID 130 170 BY SIMILARITY.
FT DISULFID 156 182 BY SIMILARITY.
FT DISULFID 215 293 BY SIMILARITY.
FT DISULFID 236 276 BY SIMILARITY.
FT DISULFID 264 288 BY SIMILARITY.
FT DISULFID 333 479 INTERCHAIN (BY SIMILARITY).
FT DISULFID 388 404 BY SIMILARITY.
FT DISULFID 533 547 BY SIMILARITY.
FT DISULFID 561 591 BY SIMILARITY.
FT CARBOHYD 122 122 N-LINKED (GLCNAC. .).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. .).
FT CARBOHYD 413 413 N-LINKED (GLCNAC. .).
FT CARBOHYD 553 553 N-LINKED (GLCNAC. .).
SQ SEQUENCE 618 AA; 70268 MW; B89F719AAMP601E0 CRC64;

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Query Match 41.4%; Score 75; DB 1; Length 618;
Best Local Similarity 37.2%; Pred. No. 3e-06;
Matches 16; Conservative 4; Mismatches 23; Indels 0; Gaps 0;

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QY 2 NGFLXLRKXSLRXCRXXLCSEFXAXXIFRNXXRTQRFVSVY 44

DB 46 SGFLLELRKGNLERCEVCEQSYEAFFEALESPODITDVFWAKY 88

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RESULT 24
TMG4_HUMAN STANDARD; PRT; 202 AA.
AC 014669;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Transmembrane gamma-carboxyglutamic acid protein 2 precursor (Proline-rich
  rich Glu protein 2) (Proline-rich gamma-carboxyglutamic acid protein
  2).
DE PRRG3 OR TMG2 OR PRGP2.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=97404347; PubMed=9256434;
RA Kulman J.D., Harris J.E., Haldeman B.A., Davie E.W.;
RT "Primary structure and tissue distribution of two novel proline-rich
  gamma-carboxyglutamic acid proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Highly expressed in the thyroid.
CC -1- PTM: Glu residues are produced after subsequent posttranslational
  modifications of glutamic acid by a vitamin K-dependent gamma-
  carboxylase.
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CC -----
DR EMBL: AF009243; AAB67071.1; -.
DR MIM: 604429; -.
DR HSSP: P00740; IGFH.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00594; gla: 1.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00069; GLA: 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1. Transmembrane; Signal.
KW Gamma-carboxyglutamic acid; Vitamin K; Transmembrane; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT PROPEP 24 49
FT CHAIN 50 202
FT DOMAIN 50 109 TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
FT TRANSMEM 110 132 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 133 202 POTENTIAL.
FT DOMAIN 54 91 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 161 173 GLA-RICH.
FT DOMAIN 191 194 POLY-PRO.
SQ SEQUENCE 202 AA; 22393 MW; BC79400C98492060 CRC64;

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Query Match 38.1%; Score 69; DB 1; Length 202;
Best Local Similarity 37.5%; Pred. No. 1.3e-05;
Matches 15; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

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QY 5 LXXLRKXSLRXCRXXLCSEFXAXXIFRNXXRTQRFVSVY 44

DB 55 LEILTPGNLERCEVCEQSYEAFFEALESPODITDVFWAKY 94

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RESULT 25
TMG4_HUMAN STANDARD; PRT; 226 AA.
AC 09B2D6;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Transmembrane gamma-carboxyglutamic acid protein 4 precursor.
GN TMG4.
OS Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=21117044; PubMed=11171957;
RA Kulman J.D., Harris J.E., Xie L., Davie E.W.;
RT "Identification of two novel transmembrane gamma-carboxyglutamic acid
  proteins expressed broadly in fetal and adult tissues.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:1370-1375(2001).
RN (2)
RP SEQUENCE FROM N.A.
RX TISSUE=Placenta;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in lung, liver, kidney, pancreas and
  placenta.
CC -1- PTM: Glu residues are produced after subsequent posttranslational
  modifications of glutamic acid by a vitamin K-dependent gamma-
  carboxylase.
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CC or send an email to license@isb-slb.ch).
CC -----
DR EMBL, AF326351; AAK00956.1; -;
DR EMBL, BC010052; AAH10052.1; -;
DR HSSP; P00740; ICFH.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR000294; VLEK_dep_GLA.
DR PRINTS: PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
KM Gamma-carboxyglutamic acid; Vitamin K; Transmembrane; Signal.
FT SIGNAL 1 17
FT PROPEP 18 49 POTENTIAL.
FT CHAIN 50 226 TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
FT DOMAIN 50 113 PROTEIN 4.
FT TRANSMEM 114 134 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 135 226 POTENTIAL.
FT DOMAIN 56 93 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 203 208 GLA-RICH.
FT DOMAIN POLY-PRO.
SQ SEQUENCE 226 AA; 25403 MW; 45C783E3825797EE CRC64;

Query Match 38.1%; Score 69; DB 1; Length 226;
Best Local Similarity 38.2%; Pred. No. 14e-05;
Matches 13; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

OY 11 GSLRXRCRXLLCSFYXAXXIFRNXXKTRQFWVS 44
| : | | | : | | : | | | |
DB 63 GNLRRCNEELCNYPEAREIFVDEKTIAMQMEY 96

RESULT 26
THRB_BOVIN STANDARD; PRT; 625 AA.
AC P00735;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Prothrombin precursor (EC 3.4.21.5).
GN F2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88245190; PubMed=3379642;
RA Irwin D.M., Robertson K.A., McGillivray R.T.A.;
RT "Structure and evolution of the bovine prothrombin gene.";
RL J. Mol. Biol. 200;31:45(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=84203525; PubMed=6326805;
RA McGillivray R.T.A., Davie E.W.;
RT "Characterization of bovine prothrombin mRNA and its translation
RT product.";
RL Biochemistry 23:1626-1634(1984).
RN [3]
RP SEQUENCE OF 44-625, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RA Magnusson S., Soltrop-Jensen L., Petersen T.E., Claess H.;
RL (in) Hemker H.C., Veltkamp J.J. (eds.);
RL Biochemie symposium on prothrombin and related coagulation factors,
RL pp.25-46, Leiden University Press, Leiden (1975).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF ACTIVATION PEPTIDE 1.
RX MEDLINE=86296631; PubMed=3741841;
RA Park C.H., Tulinsky A.;
RT "Three-dimensional structure of the kringle sequence: structure of
RT prothrombin fragment 1.";

RL Biochemistry 25:3977-3982(1986).
RN [5]
RX X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF ACTIVATION PEPTIDE 1.
RX MEDLINE=91311686; PubMed=1856869;
RA Seshadri T.-P., Tulinsky A., Skrzypczak-Jankun E., Park C.H.;
RT "Structure of bovine prothrombin fragment 1 refined at 2.25-A
RT resolution.";
RL J. Mol. Biol. 220:481-494(1991).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF ACTIVATION PEPTIDE 1.
RX MEDLINE=92190185; PubMed=1547238;
RA Soriano-Garcia M., Padmanabhan K., de Vos A.M., Tulinsky A.;
RT "The Ca2+ ion and membrane binding structure of the Gla domain of Ca-
RL prothrombin fragment 1.";
RL Biochemistry 31:2554-2566(1992).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX MEDLINE=92218459; PubMed=1560020;
RA Martin P.D., Robertson W., Turk D., Huber R., Bode W., Edwards B.F.P.;
RT "The structure of residues 7-16 of the A alpha-chain of human
RT fibrinogen bound to bovine thrombin at 2.3-A resolution.";
RL J. Biol. Chem. 267:7911-7920(1992).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX MEDLINE=92389319; PubMed=1518046;
RA Brandstetter H., Turk D., Hoeffken H.W., Grosse D., Stuerzebecher J.,
RA Martin P.D., Edwards B.F.P., Bode W.;
RT "Refined 2.3 A X-ray crystal structure of bovine thrombin complexes
RT formed with the benzamide and arginine-based thrombin inhibitors
RT NAPAP, 4-TAPAP and MQPA. A starting point for improving
RT antithrombotics.";
RL J. Mol. Biol. 226:1085-1089(1992).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF COMPLEX WITH ORNITHODORIN.
RX MEDLINE=97102783; PubMed=8947023;
RA van de Locht A., Stubbs M.T., Bode W., Friedrich T., Bollschweiler C.,
RA Hoeffken W., Huber R.;
RT "The ornithodorin-thrombin crystal structure, a key to the TAP
RT enigma?";
RL EMBO J. 15:6011-6017(1996).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF COMPLEX WITH TRIABIN.
RX MEDLINE=98004486; PubMed=9342325;
RA Fuentes-Prior P., Noeske-Jungblut C., Donner P., Schleuning W.D.,
RA Huber R., Bode W.;
RT "Structure of the thrombin complex with triabin, a lipocalin-like
RT exosite-binding inhibitor derived from a tiratomin bug.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:11845-11850(1997).
RN [11]
RP GENE STRUCTURE.
RX MEDLINE=86077733; PubMed=3000440;
RA Irwin D.M., Ahern K.G., Pearson G.D., McGillivray R.T.A.;
RT "Characterization of the bovine prothrombin gene.";
RL Biochemistry 24:6854-6861(1985).
RN [12]
RP FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS
RP FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,
RP AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.
RP SUBCELLULAR LOCATION: Extracellular.
RP TISSUE SPECIFICITY: SYNTHESIZED IN THE LIVER; FOUND IN PLASMA.
RP -!- THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
RP RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL
RP ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES
RP ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY
RP CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
RP OF PROTHROMBIN TO THROMBIN.
RP MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A
RP PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &
RP FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES
RP THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &
RP HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR
RP V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
RP THROMBIN.
RP -!- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL

CC FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
 CC BY FACTOR XA.
 CC -1- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 CC -1- DATABASE: NAME-Prozyme technical fact sheet;
 CC WWW="http://www.prozyme.com/technical/thrombindata.html".
 CC -----
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 CC -----
 CC EMBL: V00135; CAA23451.1; -;
 CC EMBL: J00041; AAA30781.1; -;
 CC PIR: A00915; TBBO.
 CC PIR: S02537; S02537.
 CC PDB: 1B8K; 31-JAN-94.
 CC PDB: 1ETR; 31-JAN-94.
 CC PDB: 1ETS; 31-JAN-94.
 CC PDB: 1ERT; 31-JAN-94.
 CC PDB: 1HRT; 31-JAN-94.
 CC PDB: 2PE1; 31-JAN-94.
 CC PDB: 2PE2; 31-JAN-94.
 CC PDB: 2SPT; 31-MAY-94.
 CC PDB: 1MKW; 07-JUL-97.
 CC PDB: 1MXX; 07-JUL-97.
 CC PDB: 1TBO; 14-OCT-96.
 CC PDB: 1TBR; 14-OCT-96.
 CC PDB: 1TCC; 23-JUL-97.
 CC PDB: 1VIT; 21-APR-97.
 CC PDB: 1YCP; 06-MAY-98.
 CC PDB: 1A0H; 17-JUN-98.
 CC PDB: 1AVG; 16-FEB-99.
 CC MEROPS: S01.217; -;
 CC InterPro: IPR001314; Chymotrypsin.
 CC InterPro: IPR002383; GLA_blood.
 CC InterPro: IPR000001; Kringle.
 CC InterPro: IPR003966; Prothrombin.
 CC InterPro: IPR001254; Trypsin.
 CC InterPro: IPR000294; VitK_dep_GLA.
 CC Pfam: PF00594; gla; 1.
 CC Pfam: PF00051; kringle; 2.
 CC Pfam: PF00089; trypsin; 1.
 CC PRINTS: PR00722; CHYMOTRYPSIN.
 CC PRINTS: PR00001; GLABLOOD.
 CC PRINTS: PR00018; KRINGLE.
 CC PRINTS: PR01505; PROTHROMBIN.
 CC SMART: SM00069; GLA; 1.
 CC SMART: SM00130; KR; 2.
 CC SMART: SM00020; TRYP-Spc; 1.
 CC PROSITE: PS00011; GLU_CARBOXYLATION; 1.
 CC PROSITE: PS00021; KRINGLE_1; 2.
 CC PROSITE: PS00070; KRINGLE_2; 2.
 CC PROSITE: PS00240; TRYPSIN_DOM; 1.
 CC PROSITE: PS00134; TRYPSIN_HIS; 1.
 CC PROSITE: PS00135; TRYPSIN_SER; 1.
 CC Blood coagulation; Plasma; Calcium-binding; Glycoprotein; Repeat;
 CC Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver;
 CC Hydrolyase; Serine protease; Kringle; Signal; 3D-structure.
 CC FT SIGNAL 1 24
 CC FT PROPEP 25 43
 CC FT CHAIN 44 625
 CC FT PEPTIDE 44 199
 CC FT PEPTIDE 200 317
 CC FT CHAIN 318 366
 CC FT CHAIN 367 625
 CC FT DOMAIN 109 187
 CC FT DOMAIN 214 292
 CC FT DOMAIN 367 625
 CC
 CC PROTHROMBIN.
 CC ACTIVATION PEPTIDE (FRAGMENT 1).
 CC ACTIVATION PEPTIDE (FRAGMENT 2).
 CC THROMBIN LIGHT CHAIN (A).
 CC THROMBIN HEAVY CHAIN (B).
 CC KRINGLE 1.
 CC KRINGLE 2.
 CC SERINE PROTEASE.

FT SITE 199 200 CLEAVAGE (BY THROMBIN).
 FT SITE 317 318 CLEAVAGE (BY FACTOR XA).
 FT SITE 366 367 CLEAVAGE (BY FACTOR XA).
 FT ACT_SITE 409 409 CHARGE RELAY SYSTEM.
 FT ACT_SITE 465 465 CHARGE RELAY SYSTEM.
 FT ACT_SITE 571 571 CHARGE RELAY SYSTEM.
 FT MOD_RES 50 50 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 51 51 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 58 58 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 63 63 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 64 64 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 73 73 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 76 76 GAMMA-CARBOXYGLUTAMIC ACID.
 FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .).
 FT
 Query Match 38.1%; Score 69; DB 1; Length 625;
 Best Local Similarity 35.7%; Pred. No. 4e-05;
 Matches 15; Conservative 3; Mismatches 24; Indels 0; Gaps 0;
 QY 3 GELXXLRGSLRXRCRXXLCSEFXAXXIFRMXXTRQFWSY 44
 DB 47 GFLEVRKGNLERECLEPCSRBEAFALSLSATDFWAKY 88
 ID PRTS_BOVIN STANDARD; PRT; 675 AA.
 AC P07224;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Vitamin K-dependent protein S precursor.
 GN PROS1 OR PROS.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=66233400; PubMed=2940598;
 RA Dahlback B., Lundwall A., Stenflo J.;
 RT "Primary structure of bovine vitamin K-dependent protein S.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:4199-4203(1986).
 RN RN
 RP SEQUENCE FROM N.A.
 RA Wydro R., Cohen E., Deckowski W., Stenflo J., Lundwall A.,
 RA Dahlback B.;
 RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
 RN RN
 RP SEQUENCE OF 42-141.
 RX MEDLINE=66168236; PubMed=2937785;
 RA Dahlback B., Lundwall A., Stenflo J.;
 RT "Localization of thrombin cleavage sites in the amino-terminal region
 of bovine protein S.";
 RL J. Biol. Chem. 261:5111-5115(1986).
 CC -1- FUNCTION: ANTICOAGULANT PLASMA PROTEIN; IT IS A COFACTOR TO
 CC ACTIVATED PROTEIN C IN THE DEGRADATION OF COAGULATION FACTORS VA
 CC AND VIIIA. IT HELP TO PREVENT COAGULATION AND STIMULATING
 CC FIBRINOLYSIS.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- SIMILARITY: CONTAINS 2 LAMININ G-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 4 EGF-LIKE DOMAINS.
 CC -----
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CC -----

DR EMBL; M1304; AAA30757.1; -

DR EMBL; X12891; CAA31382.1; -

DR PIR; A24759; A24759.

DR HSSP; P00740; ICFH.

DR InterPro: IPR000152; Asx_hydroxyl.

DR InterPro: IPR000561; EGF-like.

DR InterPro: IPR001881; EGF_Ca.

DR InterPro: IPR002383; GLA_blood.

DR InterPro: IPR001791; Laminin_G.

DR InterPro: IPR000294; VitK_dep_GLA.

DR Pfam; PF00008; EGF; 4.

DR Pfam; PF00594; gla; 1.

DR Pfam; PF00054; laminin_G; 1.

DR PRINTS; PR00001; GLABLOOD.

DR SMART; SM00179; EGF_CA; 3.

DR SMART; SM00069; GLA; 1.

DR SMART; SM00282; Lamg; 2.

DR PROSITE; PS00010; ASX_HYDROXYL; 4.

DR PROSITE; PS00022; EGF_1; 1.

DR PROSITE; PS01186; EGF_2; 3.

DR PROSITE; PS01187; EGF_CA; 3.

DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.

DR PROSITE; PS00025; LAM_G_DOMAIN; 2.

KW Plasma; Gamma-carboxyglutamic acid; Calcium; Vitamin K; Zymogen;

KW Blood coagulation; Hydroxylation; Glycoprotein; Signal; Repeat;

KW EGF-like domain.

FT SIGNAL 1 24

FT PROPEP 25 41

FT CHAIN 42 675

FT DOMAIN 42 86

FT DOMAIN 87 116

FT DOMAIN 117 155

FT DOMAIN 157 200

FT DOMAIN 201 242

FT DOMAIN 243 283

FT DOMAIN 289 425

FT DOMAIN 484 665

FT MOD_RES 47 47

FT MOD_RES 48 48

FT MOD_RES 55 55

FT MOD_RES 57 57

FT MOD_RES 60 60

FT MOD_RES 61 61

FT MOD_RES 66 66

FT MOD_RES 67 67

FT MOD_RES 70 70

FT MOD_RES 73 73

FT MOD_RES 77 77

FT MOD_RES 136 136

FT DISULFID 121 134

FT DISULFID 126 143

FT DISULFID 145 154

FT DISULFID 161 175

FT DISULFID 171 184

FT DISULFID 186 197

FT DISULFID 205 217

FT DISULFID 212 226

FT DISULFID 228 241

FT DISULFID 247 256

FT DISULFID 252 265

FT DISULFID 267 282

FT CAROHD 499 499

FT CAROHD 509 509

SEQUENCE 675 AA; 75132 MW; CF7EC5B0C318DEE CRC64;

Query Match 38.1%; Score 69; DB 1; Length 675;

Best Local Similarity 36.4%; Pred. No. 4.3e-05;

Matches 16; Conservative 4; Mismatches 24; Indels 0; Gaps 0;

Qy 1 ANGFLXILRXGSLXRCRXILCSFXXXXIFRNXXTRQFWVS 44

Db 42 ANTLLEETKKGNLDERCIEELCNKEARIEFENPETEFYKY 85

RESULT 28

ID PRTS_RABIT STANDARD; PRT; 646 AA.

AC P98118.

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Vitamin K-dependent protein S precursor (Fragment).

GN PROS1 OR PROS.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxId=9986;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94039141; PubMed=8223642;

RA He X., Dahlbaeck B.;

RT "Molecular cloning, expression and functional characterization of rabbit anticoagulant vitamin K-dependent protein S.";

RL Eur. J. Biochem. 217:857-865(1993).

CC -!- FUNCTION: ANTICOAGULANT PLASMA PROTEIN: IT IS A COFACTOR TO ACTIVATED PROTEIN C IN THE DEGRADATION OF COAGULATION FACTORS VA AND VIIIA. IT HELP TO PREVENT COAGULATION AND STIMULATING FIBRINOLYSIS.

CC -!- FUNCTION: PROTEIN S INTERACTS WITH C4B-BINDING PROTEIN, A REGULATOR OF THE COMPLEX SYSTEM. IN RABBIT PLASMA HOWEVER, PROTEIN S APPEARS TO BE PRESENT ONLY IN FREE FORM.

CC -!- SUBCELLULAR LOCATION: Extracellular.

CC -!- TISSUE SPECIFICITY: PLASMA.

CC -!- SIMILARITY: CONTAINS 2 LAMININ G-LIKE DOMAINS.

CC -!- SIMILARITY: CONTAINS 4 EGF-LIKE DOMAINS.

CC -----

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CC -----

DR EMBL; Z26485; CAA81259.1; -

DR HSSP; P00740; ICFH.

DR InterPro: IPR000152; Asx_hydroxyl.

DR InterPro: IPR000561; EGF-like.

DR InterPro: IPR001881; EGF_Ca.

DR InterPro: IPR001791; Laminin_G.

DR InterPro: IPR000294; VitK_dep_GLA.

DR Pfam; PF00008; EGF; 4.

DR Pfam; PF00594; gla; 1.

DR Pfam; PF00054; laminin_G; 1.

DR SMART; SM00179; EGF_CA; 3.

DR SMART; SM00069; GLA; 1.

DR SMART; SM00282; Lamg; 2.

DR PROSITE; PS00010; ASX_HYDROXYL; 4.

DR PROSITE; PS00022; EGF_1; 1.

DR PROSITE; PS01186; EGF_2; 3.

DR PROSITE; PS01187; EGF_CA; 3.

DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.

DR PROSITE; PS00025; LAM_G_DOMAIN; 2.

KW Plasma; Gamma-carboxyglutamic acid; Calcium; Vitamin K; Zymogen;

KW Blood coagulation; Hydroxylation; Glycoprotein; Repeat;

KW EGF-like domain.

FT NON_TER 1 1

FT PROPEP <1 12

FT CHAIN 13 646

FT DOMAIN 13 57

FT DOMAIN 58 87

FT DOMAIN 88 126

POTENTIAL.

VITAMIN K-DEPENDENT PROTEIN S.

GLA.

THROMBIN-SENSITIVE.

EGF-LIKE 1.


```

FT MOD_RES 50 50 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 109 109 SIMILARITY).
FT DISULFID 94 107 HYDROXYLATION (BY SIMILARITY).
FT DISULFID 99 107 BY SIMILARITY.
FT DISULFID 118 127 BY SIMILARITY.
FT DISULFID 134 148 BY SIMILARITY.
FT DISULFID 144 157 BY SIMILARITY.
FT DISULFID 159 172 BY SIMILARITY.
FT DISULFID 178 190 BY SIMILARITY.
FT DISULFID 185 199 BY SIMILARITY.
FT DISULFID 201 214 BY SIMILARITY.
FT DISULFID 220 229 BY SIMILARITY.
FT DISULFID 225 238 BY SIMILARITY.
FT DISULFID 240 255 BY SIMILARITY.
FT CARBOHYD 472 472 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 482 482 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 503 503 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 649 AA; 72402 MW; 5C7C13D31CD7EB6B CRC64;

Query Match 37.6%; Score 68; DB 1; Length 649;
Best Local Similarity 34.1%; Pred. No. 6.4e-05;
Matches 15; Conservative 5; Mismatches 24; Indels 0; Gaps 0;

Oy 1 ANGFLXLRXGSLRXRCRXLCXFXKXAXXIFRNXXRTQFWYSY 44
Db 15 ANSMLEETKQGNLRECEIEELCNKEAREVFENDEPTDYFYKY 58

RESULT 30
PRTS_HUMAN
ID PRTS_HUMAN STANDARD; PRT; 676 AA.
AC P07225; Q15518;
DC 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Vitamin K-dependent protein S precursor.
GN PROS1 OR PROS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=91084445; PubMed=2148110;
RT Schmidel D.K., Tatro A.V., Phelps L.G., Tomczak J.A., Long G.L.;
RL "Organization of the human protein S genes.";
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE=Liver;
RC Ploos van Amstel H.K.;
RL Submitted (AUG-1987) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE OF 27-676 FROM N.A.
RA MEDLINE=91084445; PubMed=2148111;
RT "Ploos van Amstel H.K., Reitsma P.H., der Logt C.P., Bertina R.M.;
RT "Intron-exon organization of the active human protein S gene PS alpha
RT and its pseudogene PS beta: duplication and silencing during primate
RT evolution.";
RN [4]
RP Biochemistry 29:7853-7861(1990).
RN [5]
RP SEQUENCE OF 1-42 FROM N.A.
RA MEDLINE=88005138; PubMed=2820795;
RT Ploos van Amstel H.K., van der Zanden A.L., Reitsma P.H.,
RA Bertina R.M.;
RT "Human protein S cDNA encodes Phe-16 and Tyr 222 in consensus
RT sequences for the post-translational processing.";
RN [5]
RP PEBB Lett. 222:186-190(1987).
RN [5]
RP SEQUENCE FROM N.A.
RA MEDLINE=87092407; PubMed=3467362;

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RA Hoskins J., Norman D.K., Beckmann R.J., Long G.L.;
RT "Cloning and characterization of human liver cDNA encoding a protein
RT S precursor.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:349-353(1987).
RN [6]
RP SEQUENCE OF 27-676 FROM N.A.
RA MEDLINE=86313649; PubMed=2944113;
RT Lundwall A., Dackowski W., Cohen E., Shaffer M., Mahr A., Dahlback B.,
RA Stenflo J., Wydro R.;
RT "Isolation and sequence of the cDNA for human protein S, a regulator
RT of blood coagulation.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:6716-6720(1986).
RN [7]
RP VARIANT HEERLEN.
RA MEDLINE=90335440; PubMed=2143091;
RA Bertina R.M., Ploos van Amstel H.K., van Wijngaarden A.,
RA Coenen J., Leemhuis M.P., Deutz-Perlow P.P., van der Linden I.K.,
RA Reitsma P.H.;
RT "Heerlen polymorphism of protein S, an immunologic polymorphism due
RT to dimorphism of residue 460.";
RL Blood 76:538-548(1990).
RN [8]
RP VARIANT SER-258.
RA Cooper D.N.;
RL Unpublished observations (SEP-1993).
RN [9]
RP VARIANT TOKUSHIMA.
RA MEDLINE=94129009; PubMed=8298131;
RA Hayashi T., Nishiohara J., Shigekiyo T., Saito S., Suzuki K.;
RT "Protein S Tokushima: abnormal molecule with a substitution of Glu
RT for Lys-155 in the second epidermal growth factor-like domain of
RT protein S.";
RL Blood 83:683-690(1994).
RN [10]
RP FUNCTION: ANTICOAGULANT PLASMA PROTEIN. IT IS A COFACTOR TO
RN ACTIVATED PROTEIN C IN THE DEGRADATION OF COAGULATION FACTORS VA
RN AND VIIIA. IT HELPS TO PREVENT COAGULATION AND STIMULATING
RN FIBRINOLYSIS.
RN [11]
RP SUBCELLULAR LOCATION: Extracellular.
RN [12]
RP TISSUE SPECIFICITY: PLASMA.
RN [13]
RP DISEASE: DEFECTS IN PROS1 ARE ASSOCIATED WITH AN INCREASED RISK TO
RN DEVELOP THROMBOTIC DISEASE (THROMBOPHILIA).
RN [14]
RP SIMILARITY: CONTAINS 2 LAMININ G-LIKE DOMAINS.
RN [15]
RP SIMILARITY: CONTAINS 4 EGF-LIKE DOMAINS.
RN [16]
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RN or send an email to license@isb-sib.ch).
RN [17]
RP EMBL, M57853; AAA60357.1; JOINED.
RN EMBL, M57840; AAA60357.1; JOINED.
RN EMBL, M57841; AAA60357.1; JOINED.
RN EMBL, M57842; AAA60357.1; JOINED.
RN EMBL, M57843; AAA60357.1; JOINED.
RN EMBL, M57844; AAA60357.1; JOINED.
RN EMBL, M57845; AAA60357.1; JOINED.
RN EMBL, M57846; AAA60357.1; JOINED.
RN EMBL, M57847; AAA60357.1; JOINED.
RN EMBL, M57848; AAA60357.1; JOINED.
RN EMBL, M57849; AAA60357.1; JOINED.
RN EMBL, M57850; AAA60357.1; JOINED.
RN EMBL, M57851; AAA60357.1; JOINED.
RN EMBL, M57852; AAA60357.1; JOINED.
RN EMBL, M36564; AAA60180.1; JOINED.
RN EMBL, M36551; AAA60180.1; JOINED.
RN EMBL, M36552; AAA60180.1; JOINED.
RN EMBL, M36553; AAA60180.1; JOINED.
RN EMBL, M36554; AAA60180.1; JOINED.
RN EMBL, M36555; AAA60180.1; JOINED.
RN EMBL, M36556; AAA60180.1; JOINED.
RN EMBL, M36557; AAA60180.1; JOINED.

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DR	EMBL	M36558	AAA60180.1	JOINED.
DR	EMBL	M36559	AAA60180.1	JOINED.
DR	EMBL	M36560	AAA60180.1	JOINED.
DR	EMBL	M36561	AAA60180.1	JOINED.
DR	EMBL	M36563	AAA60180.1	JOINED.
DR	EMBL	Y00692	CAA68687.1	JOINED.
DR	EMBL	Y00692	CAA68688.1	ALT_SEQ.
DR	EMBL	M15036	AAA36479.1	--
DR	PIR	A35610	A35610.	
DR	PIR	A26157	A26157.	
DR	PIR	A25891	A25891.	
DR	PIR	S02424	S02424.	
DR	PIR	S09519	S09519.	
DR	HSSP	P07204	LEGT.	
DR	MIM	176880	--	
DR	InterPro	IPR000152	Asx_hydroxyl.	
DR	InterPro	IPR000561	EGF-like.	
DR	InterPro	IPR001881	EGF_Ca.	
DR	InterPro	JPR002383	GLA_D100d.	
DR	InterPro	IPR001791	Laminin_G.	
DR	InterPro	IPR000294	Vltk_dep_GLA.	
DR	Pfam	PF00008	EGF_4.	
DR	Pfam	PF00594	qla_1.	
DR	Pfam	PF00054	Laminin_G_1.	
DR	PRINTS	PR00001	GLABLOOD.	
DR	SMART	SM00179	EGF_CA_3.	
DR	SMART	SM00069	GLA_1.	
DR	SMART	SM00282	Lamg_2.	
DR	PROSITE	PS00010	ASX_HYDROXYL_4.	
DR	PROSITE	PS00022	EGF_1; 1.	
DR	PROSITE	PS01186	EGF_2; 3.	
DR	PROSITE	PS01187	EGF_CA_3.	
DR	PROSITE	PS00011	GLU_CARBOXYLATION_1.	
DR	PROSITE	PS50025	LAM_G_DOMAIN_2.	
KM	Plasma	Gamma-carboxyglutamic acid	Calcium; Vitamin K; Zymogen;	
KM	Blood coagulation	Hydroxylation	Glycoprotein; Signal; Repeat;	
KM	EGF-like domain	Polymorphism	Disease mutation; Thrombophilia.	
FT	SIGNAL	1	24	
FT	PROPEP	25	41	
FT	CHAIN	42	676	VITAMIN K-DEPENDENT PROTEIN S.
FT	DOMAIN	42	86	GLA.
FT	DOMAIN	87	116	THROMBIN-SENSITIVE.
FT	DOMAIN	117	155	EGF-LIKE 1.
FT	DOMAIN	157	200	EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	201	242	EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	243	283	EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	299	475	LAMININ G-LIKE 1.
FT	DOMAIN	484	666	LAMININ G-LIKE 2.
FT	MOD_RES	47	47	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	48	48	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	55	55	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	57	57	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	60	60	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	61	61	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	66	66	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	67	67	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	70	70	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	73	73	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	77	77	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	136	136	HYDROXYLATION (BY SIMILARITY).
FT	MOD_RES	121	134	BY SIMILARITY.
FT	DISULFD	126	143	BY SIMILARITY.
FT	DISULFD	145	154	BY SIMILARITY.
FT	DISULFD	161	175	BY SIMILARITY.
FT	DISULFD	171	184	BY SIMILARITY.
FT	DISULFD	186	199	BY SIMILARITY.
FT	DISULFD	205	217	BY SIMILARITY.
FT	DISULFD	212	226	BY SIMILARITY.
FT	DISULFD	228	241	BY SIMILARITY.
FT	DISULFD	247	256	BY SIMILARITY.
FT	DISULFD	252	265	BY SIMILARITY.
FT	DISULFD	267	282	BY SIMILARITY.
FT	CARBOHYD	499	499	N-LINKED (GLCNAC. .); EXCEPT IN VARIANT

FT	CARBOHYD	509	509	HEERLEN.
FT	CARBOHYD	530	530	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARIANT	196	196	K -> E (IN TOKUSHIMA; PROS DEFICIENCY).
FT	VARIANT	258	258	/FTID=VAR_0005566.
FT	VARIANT	501	501	N -> S (IN PROS DEFICIENCY).
FT	VARIANT	501	501	/FTID=VAR_0005567.
FT	CONFLICT	11	11	S -> P (IN HEERLEN).
FT	CONFLICT	26	26	/FTID=VAR_0005568.
FT	SEQUENCE	676 AA:	75122 MW;	L -> P (IN REF. 5).
				F -> L (IN REF. 5).
				2B88A04F65403F25 CRC64;
Query Match 37.6%; Score 68; DB 1; Length 676;				
Best Local Similarity 34.1%; Pred. No. 6.7e-05;				
Matches 15; Conservative 5; Mismatches 24; Indels 0; Gaps 0				
OY	1	ANGFLXXLRXGSLKRXCRXXLCSEFXAXXIPIFNXXKRTROFWMSV	44	
DB	42	ANSLLEETQGNLRECIHELCKNEAREVFENDEDTDYFPKY	85	
RESULT	31			
FA10_TROCA		STANDARD;	PRT;	376 AA.
ID	FA10_TROCA			
AC	P81428;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Coagulation factor X (EC 3.4.21.6) (Trophic prothrombin activator).			
OS	Tropidochelis carlinatus (Australian rough-scaled snake).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
CC	Leptodactylidae; Squamata; Scleroglossa; Serpentes; Colubroidae;			
CC	Elapidae; Tropidochelis.			
OX	NCBI_TaxId=100989;			
RN	[1]			
RP	SEQUENCE, AND CHARACTERIZATION.			
RC	TISSUE-Venom;			
RX	MEDLINE:99326314; PubMed:10397729;			
RA	Joseph J.S., Chung M.C.M., Jayaseelan K., Kini R.M.;			
RT	"Amino acid sequence of tiroctarin, a prothrombin activator from			
RT	Tropidochelis carlinatus venom: Its structural similarity to coagulation			
RT	factor Xa."			
RL	Blood 94:621-631(1999).			
CC	-I- FUNCTION: FACTOR XA IS A VITAMIN K-DEPENDENT GLYCOPROTEIN THAT			
CC	CONVERTS PROTHROMBIN TO THROMBIN IN THE PRESENCE OF FACTOR VA,			
CC	CALCIUM, AND PHOSPHOLIPID DURING BLOOD CLOTTING. ACTS AS A TOXIN			
CC	IN VENOM.			
CC	-I- CATALYTIC ACTIVITY: Preferential cleavage: Arg-I-Thr and then			
CC	Arg-I-Ile bonds in prothrombin to form thrombin.			
CC	-I- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR			
CC	AND ARE HELD TOGETHER BY 1 OR MORE DISULFIDE BONDS.			
CC	-I- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME			
CC	GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND			
CC	CALCIUM.			
CC	-I- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE			
CC	INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).			
CC	-I- SIMILARITY: CONTRAINS 2 EGF-LIKE DOMAINS.			
CC	-I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE			
CC	TRYPSIN FAMILY.			
DR	HSPS: P00742; IHCG.			
DR	MEROPS: S01.216; "			
DR	InterPro: IPR000152; Asx_hydroxyl.			
DR	InterPro: IPR001314; Chymotrypsin.			
DR	InterPro: IPR000561; EGF-like.			
DR	InterPro: IPR000742; EGF_2.			
DR	InterPro: IPR01881; EGF_Ca.			
DR	InterPro: IPR001438; EGF_IT.			
DR	InterPro: IPR002383; GLA_blood.			
DR	InterPro: IPR001254; Trypsin.			
DR	InterPro: IPR000294; Vitk_dep_GLA.			
DR	PRINTS: PR00722; CHYMOTRYPSIN.			

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DR PRINTS; PR00010; EGFBL00D.
DR PRINTS; PR00001; GLABLO0D.
DR SMART; SM00179; EGF_CA: 1.
DR SMART; SM00001; EGF_Like: 1.
DR SMART; SM00059; GLA: 1.
DR SMART; SM00020; Tryp-Spec: 1.
DR PROSITE; PS00010; ASX_HYDROXYL: 1.
DR PROSITE; PS00022; EGF_1: 1.
DR PROSITE; PS01187; EGF_CA: 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM: 1.
DR PROSITE; PS00134; TRYPSIN_HIS: 1.
DR PROSITE; PS00135; TRYPSIN_SER: 1.
KW Glycoprotein; Hydrolyase; Serine protease; Plasma; Blood coagulation;
KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
KW Zymogen; EGF-like domain; Repeat.
KW CHAIN 1 141 FACTOR X LIGHT CHAIN.
FT NON_CONS 141 142 FACTOR X HEAVY CHAIN.
FT CHAIN 142 376 ACTIVATED FACTOR XA, HEAVY CHAIN.
FT CHAIN 142 376 EGF-LIKE 1, CALCIUM-BINDING.
FT DOMAIN 50 81 EGF-Like 2.
FT DOMAIN 142 376 SERINE PROTEASE.
FT MOD_RES 7 7 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 14 14 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 16 16 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 19 19 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 20 20 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 25 25 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 26 26 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 29 29 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 32 32 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 35 35 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 63 63 HYDROXYLATION (BY SIMILARITY).
FT ACT_SITE 183 183 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 229 229 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 326 326 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 17 22 BY SIMILARITY.
FT DISULFID 50 61 BY SIMILARITY.
FT DISULFID 55 70 BY SIMILARITY.
FT DISULFID 72 81 BY SIMILARITY.
FT DISULFID 89 100 BY SIMILARITY.
FT DISULFID 96 109 BY SIMILARITY.
FT DISULFID 111 124 BY SIMILARITY.
FT DISULFID 132 249 INTERCHAIN (BY SIMILARITY).
FT DISULFID 148 153 BY SIMILARITY.
FT DISULFID 168 184 BY SIMILARITY.
FT DISULFID 297 311 BY SIMILARITY.
FT DISULFID 322 350 BY SIMILARITY.
FT CARBOHD 52 52 O-LINKED.
FT CARBOHD 186 186 N-LINKED (GLCNAC. .).
SO SEQUENCE 376 AA; 42455 MW; F5A5C7EB9BA561C1 CRC64;

Query Match 37.0%; Score 67; DB 1; Length 376;
Best Local Similarity 29.5%; Pred. No. 5.7e-05;
Matches 13; Conservative 7; Mismatches 24; Indels 0; Gaps 0;

QY 1 ANGFLXLRKSLKRXLCFFXXAXIFRNXXRTROFWY 44
DB 1 SLSLFEIRPGNIIEKCEIEKSKSEARVFEDEKTEIFWY 44

RESULT 32
PRTS_RAT
ID PRTS_RAT STANDARD; PRT: 675 AA.
AC P53813:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Vitamin K-dependent protein S precursor.
GN PROS1 OR PROS.

OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=95332263; PubMed=7608128;
RA Yasuda F., Hayashi T., Tanitame K., Nishioke J., Suzuki K.;
RT "Molecular cloning and functional characterization of rat plasma
RT protein S.";
RL J. Biochem. 117:374-383(1995).
CC -I- FUNCTION: ANTICOAGULANT PLASMA PROTEIN: IT IS A COFACTOR TO
CC ACTIVATED PROTEIN C IN THE DEGRADATION OF COAGULATION FACTORS VA
CC AND VIIIA. IT HELP TO PREVENT COAGULATION AND STIMULATING
CC FIBRINOLYSIS.
CC -I- SUBCELLULAR LOCATION: Extracellular.
CC -I- TISSUE SPECIFICITY: PLASMA.
CC -I- SIMILARITY: CONTAINS 2 LAMININ G-LIKE DOMAINS.
CC -I- SIMILARITY: CONTAINS 4 EGF-LIKE DOMAINS.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: S78744; AAC60704.1; -.
DR HSRP; P00740; ICFH.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF_Like.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001791; laminin.G.
DR InterPro; IPR000294; Vitk_dep_GLA.
DR Pfam; PF00008; EGF; 4.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00054; laminin_G; 1.
DR PRINTS; PR00001; GLABLO0D.
DR SMART; SM00179; EGF_CA: 3.
DR SMART; SM00001; EGF_Like: 1.
DR SMART; SM00059; GLA: 1.
DR SMART; SM00282; LamG; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 4.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS01187; EGF_CA: 3.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50025; LAM_G_DOMAIN; 1.
KW Plasma; Gamma-carboxyglutamic acid; Calcium; Vitamin K; Zymogen;
KW Blood coagulation; Hydroxylation; Glycoprotein; Signal; Repeat;
KW EGF-like domain.
FT SIGNAL 1 24 BY SIMILARITY.
FT PROPEP 25 41 BY SIMILARITY.
FT CHAIN 42 675 VITAMIN K-DEPENDENT PROTEIN S.
FT DOMAIN 42 86 GLA.
FT DOMAIN 87 116 THROMBIN-SENSITIVE.
FT DOMAIN 117 155 EGF-Like 1.
FT DOMAIN 157 200 EGF-Like 2, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 201 242 EGF-Like 3, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 243 283 EGF-Like 4, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 299 475 LAMININ G-Like 1.
FT DOMAIN 484 665 LAMININ G-Like 2.
FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 48 48 (BY SIMILARITY).
FT MOD_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 55 55 (BY SIMILARITY).
FT MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 57 57 (BY SIMILARITY).
FT MOD_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID

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FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID
FT (BY SIMILARITY).
FT MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID
FT (BY SIMILARITY).
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID
FT (BY SIMILARITY).
FT MOD_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID
FT (BY SIMILARITY).
FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID
FT (BY SIMILARITY).
FT MOD_RES 73 73 GAMMA-CARBOXYGLUTAMIC ACID
FT (BY SIMILARITY).
FT MOD_RES 77 77 GAMMA-CARBOXYGLUTAMIC ACID
FT (BY SIMILARITY).
FT MOD_RES 136 136 HYDROXYLATION (BY SIMILARITY).
FT DISULFID 121 134 BY SIMILARITY.
FT DISULFID 126 143 BY SIMILARITY.
FT DISULFID 145 154 BY SIMILARITY.
FT DISULFID 161 175 BY SIMILARITY.
FT DISULFID 171 184 BY SIMILARITY.
FT DISULFID 186 199 BY SIMILARITY.
FT DISULFID 205 217 BY SIMILARITY.
FT DISULFID 212 226 BY SIMILARITY.
FT DISULFID 228 241 BY SIMILARITY.
FT DISULFID 247 256 BY SIMILARITY.
FT DISULFID 252 265 BY SIMILARITY.
FT DISULFID 267 282 BY SIMILARITY.
FT CARBOHYD 499 499 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 509 509 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 675 AA; 74626 MW; B4338F756BA86075 CRC64;

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Query Match 36.5%; Score 66; DB 1; Length 675;
Best Local Similarity 34.1%; Pred. No. 0.00016;
Matches 15; Conservative 5; Mismatches 24; Indels 0; Gaps 0;

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Qy 1 ANGLAXLRKGSIXKRCRXIXCSYXXAXIFRNXXRTORVSV 44
Db 42 ANLLEETKKGKNERCEIEELCNKEAREVEFENNPEIDYFPKY 85

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RESULT 33
PRTZ_HUMAN STANDARD; PRT; 400 AA.
AC P22891; Q15213;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Vitamin K-dependent protein Z precursor.
GN PROZ.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=91058548; Pubmed=2244898;
RA "Ishino A., Takeya H., Espling E., Iwanaga S., Kistiel W., Davie E.W.;
RT "Amino acid sequence of human protein Z, a vitamin K-dependent plasma
RT glycoprotein."
RL Biochem. Biophys. Res. Commun. 172:1139-1144(1990).
RN [2]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=98244864; Pubmed=9578570;
RA Fujimaki K., Yamazaki T., Tanikawa M., Ichinose A.;
RT "The gene for human protein Z is localized to chromosome 13 at band
RT g44 and is coded by eight regular exons and one alternative exon."
RL Biochemistry 37:6838-6846(1998).
RN [3]
RP SEQUENCE OF 81-400 FROM N.A., AND PARTIAL SEQUENCE OF 63-103.
RX MEDLINE=90386637; Pubmed=2403355;
RA Setlina H., Hayashi T., Deyashiki Y., Nishioka J., Suzuki K.;

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RT "Primary structure of vitamin K-dependent human protein Z.";
RL Biochem. Biophys. Res. Commun. 171:661-668(1990).
RN [4]
RP STRUCTURE OF CARBOHYDRATE ON SER-93.
RX MEDLINE=90062160; Pubmed=2511201;
RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T., Takao T.,
RA Shimomishi Y., Iwanaga S.;
RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first
RT epidermal growth factor-like domain of human factors VII and IX and
RT protein Z and bovine protein Z."
RL J. Biol. Chem. 264:20320-20325(1989).
RN [5]
RP STRUCTURE OF CARBOHYDRATE ON SER-93.
RX MEDLINE=91344709; Pubmed=2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in the
RT first EGF-like domain of clotting factors VII and IX and protein Z."
RL Adv. Exp. Med. Biol. 281:121-131(1990).
CC -1- FUNCTION: APPEARS TO ASSIST HEMOSTASIS BY BINDING THROMBIN AND
CC PROMOTING ITS ASSOCIATION WITH PHOSPHOLIPID VESICLES.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- SIMILARITY: ALTHOUGH HOMOLOGOUS WITH THE VITAMIN K-DEPENDENT
CC CLOTTING FACTORS, IT HAS LOST TWO OF THE ESSENTIAL CATALYTIC
CC RESIDUES AND HAS NO ENZYMATIC ACTIVITY.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M55670; AAA36500.1; -
DR EMBL; M55671; AAA36501.1; -
DR EMBL; AB033749; BAA85763.1; -
DR EMBL; AB033749; BAA85764.1; -
DR EMBL; M55303; AAA36499.1; -
DR PIR; A36244; A36244.
DR HSSP; P00740; 1CFH.
DR MEROPS; S01.979; -.
DR GLYCONSULEDB; P22891; -.
DR MIM; 176895; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF-2.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Trypsin.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PSS0240; TRYPsin_DOM; 1.
KW Plasma; Glycoprotein; Gamma-carboxyglutamic acid; Hydroxylation;
KW Calcium; Serine protease homolog; Vitamin K; EGF-like domain; Signal;
KW Alternative splicing.
FT STGNAL 1 23
FT PROPER 24 40
FT CHAIN 41 400
FT DOMAIN 87 123

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VITAMIN K-DEPENDENT PROTEIN Z.
EGF-LIKE 1.

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FT DOMAIN 125 166 EGF-LIKE 2.
FT MOD_RES 175 400 SERINE PROTEASE.
FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 51 51 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 73 73 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 75 75 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 80 80 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 104 104 HYDROXYLATION (BY SIMILARITY).
FT DISULFID 91 102 BY SIMILARITY.
FT DISULFID 96 111 BY SIMILARITY.
FT DISULFID 113 122 BY SIMILARITY.
FT DISULFID 129 141 BY SIMILARITY.
FT DISULFID 137 150 BY SIMILARITY.
FT DISULFID 152 165 BY SIMILARITY.
FT CARBOHYD 93 93 O-LINKED (GLC. . .).
FT CARBOHYD 99 99 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (POTENTIAL).
FT CARBOHYD 225 225 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 233 233 O-LINKED (POTENTIAL).
FT CARBOHYD 236 236 O-LINKED (POTENTIAL).
FT CARBOHYD 306 306 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 315 315 O-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPIC 24 24 V -> ATSLKERHGLHSDSACTQGESL (IN ISOFORM
SQ SEQUENCE 400 AA; 44744 MW; 7EBD2DCC48860268 CRC64;

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Query Match 35.9%; Score 65; DB 1; Length 400;
 Best Local Similarity 32.5%; Pred. No. 0.00014;
 Matches 13; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

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QY 5 LXLRLGSLRXCRXXLCSFYXAXXIFRNXXRTQFWVS 44
DB 46 LEELEFEGNLEKECYEELICVYEAREFENEVYDEFWRRY 85

RESULT 34
PRTZ_BOVIN
ID PRTZ_BOVIN STANDARD; PRT; 396 AA.
AC P00744;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Vitamin K-dependent protein Z.
GN PROZ.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN RN
RP SEQUENCE.
RX MEDLINE=85204370; PubMed=3888670;
RA Hoejrup P., Jensen M.S., Petersen T.E.;
RT "Amino acid sequence of bovine protein Z: a vitamin K-dependent
RL FEBS Lett. 184:333-338(1985).
RN [2]
RN STRUCTURE OF CARBOHYDRATE ON SER-53.
RX MEDLINE=90062160; PubMed=2511201;
RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T., Takao T.,
RA Shimonishi Y., Iwanaga S.;
RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first

```

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RT epidermal growth factor-like domain of human factors VII and IX and
RT protein Z and bovine protein Z."
RT J. Biol. Chem. 264:20320-20325(1989).
RN [3]
RP STRUCTURE OF CARBOHYDRATE ON SER-53.
RX MEDLINE=91344709; PubMed=2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in the
RL first EGF-like domain of clotting factors VII and IX and protein Z."
RL Adv. Exp. Med. Biol. 281:121-131(1990).
CC -1- FUNCTION: APPEARS TO ASSIST HEMOSTASIS BY BINDING THROMBIN AND
CC PROMOTING ITS ASSOCIATION WITH PHOSPHOLIPID VESICLES.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- SIMILARITY: ALTHOUGH HOMOLOGOUS WITH THE VITAMIN K-DEPENDENT
CC CLOTTING FACTORS, IT HAS LOST TWO OF THE ESSENTIAL CATALYTIC
CC RESIDUES AND HAS NO ENZYMAIC ACTIVITY.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
DR PIR: A21711; KX802.
DR HSP; P00740; ICFH.
DR MEROPS; S01.979; -.
DR GlycoSiteDB; P00744; -.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Trypsin.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00083; trypsin; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00069; GLA; 2.
DR SMART; SM00020; TRYP_SPE; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
KW Plasma; Glycoprotein; Gamma-carboxyglutamic acid; Hydroxylation;
KW Calcium; Serine protease homolog; Vitamin K; EGF-like domain.
FT DOMAIN 47 83 EGF-LIKE 1.
FT MOD_RES 85 126 SERINE PROTEASE.
FT DOMAIN 135 357
FT MOD_RES 7 7
FT MOD_RES 8 8
FT MOD_RES 11 11 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 15 15 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 17 17 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 20 20 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 21 21 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 26 26 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 27 27 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 30 30 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 33 33 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 36 36 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 40 40 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 44 64 HYDROXYLATION.
FT MOD_RES 51 62 BY SIMILARITY.
FT DISULFID 56 71 BY SIMILARITY.
FT DISULFID 73 82 BY SIMILARITY.
FT DISULFID 89 101 BY SIMILARITY.
FT DISULFID 97 110 BY SIMILARITY.
FT DISULFID 112 125 BY SIMILARITY.
FT CARBOHYD 53 53 O-LINKED (GLC. . .).
FT CARBOHYD 59 59 /FTTG-CAR_000032.
FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .).
FT CARBOHYD 388 388 O-LINKED.
SQ SEQUENCE 396 AA; 43112 MW; 04C5D7A35849B116 CRC64;

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Qy	5	LXILRXGLXRRXCRRXXLCSFXXAXXIFRNXXRTXRFWSY	44
Db	6	LEELFEGLLEKECWEICVYEAREARVFEDEDTTDEFWRTY	45
Query Match			33.7%
Best Local Similarity			30.0%
Matches	12	Conservative	7
		Mismatches	21
		Indels	0
		Gaps	0

DR	PROSITE; PS00010; ASX_HYDROXYL; 4.
DR	PROSITE; PS00022; EGF_1; 1.
DR	PROSITE; PS01186; EGF_2; 3.
DR	PROSITE; PS01187; EGF_CA; 3.
DR	PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR	Prosite; P550025; LAM_G-DOMAIN; 2.
KV	Plasma; Gamma-carboxyglutamic acid; Calcium; Vitamin K; zymogen;
KW	Blood coagulation; Hydroxylation; Glycoprotein; signal; Repeat;
KW	EGF-like domain.
FT	SIGNAL 1 24 BY SIMILARITY.
FT	PROPEP 25 41 BY SIMILARITY.
FT	CHAIN 42 675 VITAMIN K-DEPENDENT PROTEIN S.
FT	DOMAIN 42 86 GLA.
FT	DOMAIN 87 116 THROMBIN-SENSITIVE.
FT	DOMAIN 117 155 EGF-LIKE 1.
FT	DOMAIN 157 200 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN 201 242 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN 243 283 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN 299 475 LAMININ G-LIKE 1.
FT	DOMAIN 484 665 LAMININ G-LIKE 2.
FT	MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID
FT	(BY SIMILARITY).
FT	MOD_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID
FT	(BY SIMILARITY).
FT	MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID
FT	(BY SIMILARITY).
FT	MOD_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID
FT	(BY SIMILARITY).
FT	MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID
FT	(BY SIMILARITY).
FT	MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID
FT	(BY SIMILARITY).
FT	MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID
FT	(BY SIMILARITY).
FT	MOD_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID
FT	(BY SIMILARITY).
FT	MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID
FT	(BY SIMILARITY).
FT	MOD_RES 73 73 GAMMA-CARBOXYGLUTAMIC ACID
FT	(BY SIMILARITY).
FT	MOD_RES 77 77 GAMMA-CARBOXYGLUTAMIC ACID
FT	(BY SIMILARITY).
FT	MOD_RES 136 136 HYDROXYLATION (BY SIMILARITY).
FT	DISULFID 121 134 BY SIMILARITY.
FT	DISULFID 126 143 BY SIMILARITY.
FT	DISULFID 145 154 BY SIMILARITY.
FT	DISULFID 161 175 BY SIMILARITY.
FT	DISULFID 171 184 BY SIMILARITY.
FT	DISULFID 186 199 BY SIMILARITY.
FT	DISULFID 205 217 BY SIMILARITY.
FT	DISULFID 212 226 BY SIMILARITY.
FT	DISULFID 228 241 BY SIMILARITY.
FT	DISULFID 247 256 BY SIMILARITY.
FT	DISULFID 252 265 BY SIMILARITY.
FT	DISULFID 267 282 BY SIMILARITY.
FT	CARBOHYD 499 499 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 509 509 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT 493 493 F->L (IN REF. 2).
SO	SEQUENCE 675 AA; 74934 MW; 79D51203EB5AF31F CRC64;
Query Match 32.6%; Score 59; DB 1; Length 675;	
Best Local Similarity 31.8%; Pred. No. 0.0033;	
Matches 14; Conservative 4; Mismatches 26; Indels 0; Gaps 0;	
OY	1 ANGFLXLRLXGSLRXRCRRXXLCSEFXAXXIIFNNXXRTROFWVS 44 : : : DB 42 ANTLFEETMKGNLRECEIELCNKEAREVPEENNDETQDYFYKY 85
RESULT 36	
ID VE1 BPV2 STANDARD: PR1 604 AA.	


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AC P11298;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Replication protein E1.
GN E1.
OS Bovine papillomavirus type 2.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10560;
RN NCBI_TaxID=10560;
RP [1]
RA SEQUENCE FROM N.A.
RA Groff D.E., Mitra R., Lancaster W.D.;
RL Submitted (MAY-1988) to the EMBL/Genbank/DDJ databases.
CC -1- FUNCTION: ATP-DEPENDENT DNA HELICASE REQUIRED FOR INITIATION OF
CC VIRAL DNA REPLICATION. IT FORMS A COMPLEX WITH THE VIRAL E2
CC PROTEIN. THE E1-E2 COMPLEX BINDS TO THE REPLICATION ORIGIN WHICH
CC CONTAINS BINDING SITES FOR BOTH PROTEINS.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M20219; AAA6833.1; -.
DR PIR; C31169; W1MLB2.
DR InterPro; IPR001177; Papillom_E1.
DR Pfam; PF00519; E1; 1.
DR Pfam; PF00524; E1_N; 1.
DR E1; Early protein; DNA replication; Helicase; ATP-binding; DNA-binding;
KW Nuclear protein.
FT NP_BIND 432 439 ATP (POTENTIAL).
FT SEQUENCE 604 AA; 68077 MW; D2D7036ADE88A9DD CRC64;
SQ

Query Match 29.8%; Score 54; DB 1; Length 604;
Best Local Similarity 45.5%; Pred. NO. 0.025;
Matches 10; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

Oy 21 LCSEFXAXXIFRNXXRTROFW 42
Db 171 LCSEFHDLTRFRKNDKXTNQOW 192

RESULT 37
VE1_BPV1 STANDARD: PRT; 605 AA.
AC P03116; Q9WMH1;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Replication protein E1.
GN E1.
OS Bovine papillomavirus type 1.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10559;
RN NCBI_TaxID=10559;
RP [1]
RA SEQUENCE FROM N.A.
RA MEDLINE=83012974; PubMed=6289124;
RA Chen E.Y., Howley P.M., Levinson A.D., Seeburg P.H.;
RT "The primary structure and genetic organization of the bovine
RT papillomavirus type 1 genome.";
RL Nature 299:529-534(1982).
RN
RN REQUIREMENT FOR REPLICATION.
RP MEDLINE=91122053; PubMed=1846806;
RA Ustav M., Stenlung A.;
RT "Transient replication of BPV-1 requires two viral polypeptides

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RT encoded by the E1 and E2 open reading frames.";
RL EMBL J. 10:449-457(1991).
RN
RN CHARACTERIZATION.
RP MEDLINE=93281701; PubMed=8389467;
RA Yang L., Mohr I., Fouts E., Lim D.A., Nohalle M., Botchan M.;
RT "The E1 protein of bovine papilloma virus 1 is an ATP-dependent DNA
RT helicase.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:5086-5090(1993).
CC -1- FUNCTION: ATP-DEPENDENT DNA HELICASE REQUIRED FOR INITIATION OF
CC VIRAL DNA REPLICATION. IT FORMS A COMPLEX WITH THE VIRAL E2
CC PROTEIN. THE E1-E2 COMPLEX BINDS TO THE REPLICATION ORIGIN WHICH
CC CONTAINS BINDING SITES FOR BOTH PROTEINS.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -----
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CC -----
DR EMBL; X02346; CAB46511.1; -.
DR PIR; A03663; W1WLEB.
DR InterPro; IPR001177; Papillom_E1.
DR Pfam; PF00519; E1; 1.
DR Pfam; PF00524; E1_N; 1.
DR E1; Early protein; DNA replication; Helicase; ATP-binding; DNA-binding;
KW Nuclear protein.
FT NP_BIND 433 440 ATP (POTENTIAL).
FT SEQUENCE 605 AA; 68190 MW; C8400B7B8F606E0B CRC64;
SQ

Query Match 29.8%; Score 54; DB 1; Length 605;
Best Local Similarity 45.5%; Pred. NO. 0.025;
Matches 10; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

Oy 21 LCSEFXAXXIFRNXXRTROFW 42
Db 172 LCSEFHDLTRFRKNDKXTNQOW 193

RESULT 38
NCAP_IHNV STANDARD: PRT; 413 AA.
AC P19691;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-MAY-1992 (Rel. 22, Last annotation update)
DE Nucleocapsid protein (Nucleoprotein).
GN N.
OS Infectious hematopoietic necrosis virus (strain Round Butte) (IHNV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; unclassified Rhabdoviridae.
OC NCBI_TaxID=11291;
RN NCBI_TaxID=11291;
RP [1]
RA SEQUENCE FROM N.A.
RA MEDLINE=89073771; PubMed=3201758;
RA Gilmore R.D., Jr., Leong J.C.;
RT "The nucleocapsid gene of infectious hematopoietic necrosis virus, a
RT fish rhabdovirus.";
RL Virology 167:644-648(1988).
CC -1- PTM: PHOSPHORYLATED.
CC -1- SIMILARITY: TO VHSV NUCLEOCAPSID PROTEIN.
CC -----
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CC -----
DR EMBL: J046321: AAA6240.1: -.
DR PIR: A31834: VHVNIH.
KW Nucleocapsid: Phosphorylation.
SQ SEQUENCE 413 AA: 45700 MW: 5E2AFFE659BBEE38 CRC64;

Query Match 27.6%; Score 50; DB 1; Length 413;
Best Local Similarity 32.3%; Pred. No. 0.098;
Matches 10; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

OY 11 GSLKRCXXKCSFXKXIFRNXXRTFRWF 41
   | | | | | | | | | | | | | | | |
DB 57 GEGTRRALGULCAFYIAETVHRCGRSPNFW 87

RESULT 39
GSHB_BUCAI STANDARD; PRT; 320 AA.
AC P57612;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Glutathione synthetase (EC 6.3.2.3) (Glutathione synthase) (GSH
DE synthetase) (GSH-S) (GSHase).
GN GSHB OR BU547.
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OS symbiotic bacterium).
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_TaxID=118099;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TOKIO 1998;
RX MEDLINE=20445173; PubMed=10993077;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
RT Buchnera sp. APS.";
RL Nature 407:81-86(2000).
CC -1- CATALYTIC ACTIVITY: ATP + gamma-L-glutamyl-L-cysteine + glycine -
CC ADP + phosphate + glutathione.
CC -1- PATHWAY: Glutathione biosynthesis; second step.
CC -1- SIMILARITY: BELONGS TO THE PROKARYOTIC GSH SYNTHASE FAMILY.
CC -----
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CC -----
DR EMBL: AF001119; BAB13239.1; -.
KW Glutathione biosynthesis; Ligase; ATP-binding; Complete proteome.
SQ SEQUENCE 320 AA: 37022 MW: F4FRLB99F3FDC4A3 CRC64;

Query Match 23.2%; Score 42; DB 1; Length 320;
Best Local Similarity 46.7%; Pred. No. 2.4;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 30 IFRNXXRTROFWYSY 44
   | | | | | | | | | | | | | | | |
DB 145 VTRNIFQIROFWERY 159

RESULT 40
RPRC_MYXXA STANDARD; PRT; 1275 AA.
AC Q50864;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE O-antigen biosynthesis protein rfbC.

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GN RPRC.
OS Myxococcus xanthus.
OC Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
OC Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus.
OX NCBI_TaxID=34;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DK6640;
RX MEDLINE=96198166; PubMed=8626291;
RA Guo D., Bowden M.G., Pershad R., Kaplan H.B.;
RT "The Myxococcus xanthus rfbABC operon encodes an ATP-binding cassette
RT transporter homolog required for O-antigen biosynthesis and
RT multicellular development.";
RL J. Bacteriol. 178:1631-1639(1996).
CC -1- FUNCTION: INVOLVED IN O-ANTIGEN BIOSYNTHESIS.
CC -----
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CC -----
DR EMBL: U36795; AAB05019.1; -.
DR Interpro: IPR001296; Glycos_transf_1.
DR Interpro: IPR001173; Glycos_transf_2.
DR Pfam: PF00534; Glycos_transf_1; 1.
DR Pfam: PF00535; Glycos_transf_2; 2.
KW Lipopolysaccharide biosynthesis.
SQ SEQUENCE 1275 AA: 139596 MW: 3AF9662A10A140F1 CRC64;

Query Match 23.2%; Score 42; DB 1; Length 1275;
Best Local Similarity 45.0%; Pred. No. 9.6;
Matches 9; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

OY 3 GFLXXLRXGSLKRCXXLC 22
   | | | | | | | | | | | | | | | |
DB 1144 GMLPAAERTGALYRCDVGLC 1163

RESULT 41
SLT2_YEAST STANDARD; PRT; 484 AA.
ID SLT2_YEAST
AC Q00772;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Mitogen-activated protein kinase SLT2/MPK1 (EC 2.7.1.1-) (MAP kinase
DE MPK1).
GN SLT2 OR MPK1 OR YHR030C.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AB320;
RX MEDLINE=92140049; PubMed=1779770;
RA Torres L., Martin H., Garcia-Saez M.I., Arroyo J., Molina M.,
RA Sanchez M., Nombela C.;
RT "A protein kinase gene complements the lytic phenotype of
RT Saccharomyces cerevisiae lyt2 mutants.";
RL Mol. Microbiol. 5:2845-2854(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=94378003; PubMed=8091229;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
RA Du Z., Favell A., Fulton L., Gattung S., Geisel C., Kirsten J.,
RA Krcaba T., Hillier L., Jier M., Johnston L., Langston Y.,
RA Latreille P., Louis E.J., Maerl C., Wardis E., Meneses S., Mouser L.,

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RA Nhan M., Rifkin L., Riles L., St Peter H., Trevasakis E., Vaughan K.,
RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
RA Vaudin M.: "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
RT VIII."
RT Science 265:2077-2082(1994).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE-94103336; PubMed-8276900;
RA Mazzoni C., Zarov P., Rambourg A., Mann C.:
RT "The SLT2 (MKI) MAP kinase homolog is involved in polarized cell
RT growth in Saccharomyces cerevisiae."
RL J. Cell Biol. 123:1821-1833(1993).
CC -1- FUNCTION: SERINE/THREONINE PROTEIN KINASE INVOLVED IN A SIGNAL
CC TRANSDUCTION PATHWAY THAT PLAY A ROLE IN YEAST CELL MORPHOGENESIS
CC AND CELL GROWTH. THIS PATHWAY SEEMS TO STARTS BY SMP; THEN
CC INVOLVE THE KINASE PKC1 THAT MAY ACT THE BACK KINASE THAT THEN
CC PHOSPHORYLATES MKK1 AND MKK2 WHICH THEMSELVES PHOSPHORYLATE THE
CC MKK1 KINASE WHICH ACTS ON A YET UNKNOWN SUBSTRATE.
CC -1- ENZYME REGULATION: ACTIVATED BY TYROSINE AND THREONINE
CC PHOSPHORYLATION BY MKK1 AND MKK2 (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE SUBFAMILY.
CC -----
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CC -----
DR EMBL; X59262; CAA41954.1; -
DR EMBL; 000062; AAB68912.1; -
DR PIR; S19051; S19051.
DR PIR; S46743; S46743.
DR HSSP; P27703; 1ERK.
DR SGD; S0001072; SLT2.
DR InterPro; IPR000719; Euk_Pkinase.
DR InterPro; IPR003527; MAP_kin.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR SMART; SMO0220; S_TKc; 1.
DR PROSITE; PS01351; MAPK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 23 318 PROTEIN KINASE.
FT NP_BIND 29 37 ATP (BY SIMILARITY).
FT BINDING 54 54 ATP (BY SIMILARITY).
FT ACT_SITE 153 153 BY SIMILARITY.
FT DOMAIN 370 391 POLY-GLN.
FT MOD_RES 190 190 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 192 192 PHOSPHORYLATION (BY SIMILARITY).
FT CONFLICT 56 56 V->L (IN REF. 1).
FT CONFLICT 467 467 T->S (IN REF. 1).
SQ SEQUENCE 484 AA; 55636 MW; 559A3B0D3EBDE5F9 CRC64;

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Query Match 22.7%; Score 41; DB 1; Length 484;
Best Local Similarity 28.2%; Pred. No. 5.6;
Matches 11; Conservative 4; Mismatches 22; Indels 2; Gaps 1;

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QY 8 LKXGSL--XRXCXXLXSGFXAXXIFRNXXRTQFWVSY 44
DB 154 LKPGULVWADQGLKICDGLARGYSENVENSOFLTER 192

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RESULT 42
ID ATPA_ODOSI STANDARD: PRT; 503 AA.

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AC 000820;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE ATP synthase alpha chain (EC 3.6.3.14).
GN ATPA.
OS Odontella sinensis.
OC Chloroplast.
OC Euxaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;
OC Biddulphiophycidae; Eupodiscatales; Eupodiscaceae; Odontella.
OX NCBI_Taxid=2839;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-92219274; PubMed-1532839;
RA Pantic P.G., Strothmann H., Kowallik K.V.:
RT "Chloroplast ATPase genes in the diatom Odontella sinensis reflect
RT cyanobacterial characters in structure and arrangement."
RL J. Mol. Biol. 224:529-536(1992).
RN [2]
RP SEQUENCE FROM N.A.
RA Kowallik K.V., Stoebe B., Schaffran I., Kroth-Pantic P., Freier U.:
RT "The chloroplast genome of a chlorophyll a+c-containing alga,
RT Odontella sinensis."
RL Plant Mol. Biol. Rep. 13:336-342(1995).
RN [3]
RP SEQUENCE OF 1-39 FROM N.A.
RX MEDLINE-91192176; PubMed-1826484;
RA Pantic P.G., Strothmann H., Kowallik K.V.:
RT "The delta subunit of the chloroplast ATPase is plastid-encoded in
RT the diatom Odontella sinensis."
RL FEBS Lett. 280:387-392(1991).
CC -1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
CC GRADIENT ACROSS THE MEMBRANE. THE ALPHA CHAIN IS A REGULATORY
CC SUBUNIT.
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(in) = ADP + phosphate +
CC H(+)(out).
CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
CC HAS THREE MAIN SUBUNITS: A, B AND C.
CC -1- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane.
CC -1- SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.
CC -----
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CC -----
DR EMBL; X60752; CAA43157.1; -
DR EMBL; 267753; CAA91694.1; -
DR EMBL; X57701; -; NOT_ANNOTATED_CDS.
DR PIR; S14445; S14445.
DR PIR; S23359; S23359.
DR HSSP; P09219; ISKY.
DR Mendel; 4268; ODOSI.atpa.1.
DR InterPro; IPR004100; ATP-synt_ab_N.
DR InterPro; IPR000793; ATPase_AB_C.
DR InterPro; IPR000790; ATPase_AB_C.
DR InterPro; IPR000194; ATPase_alpha_beta.
DR Pfam; PF00006; ATP-synt_ab; 1.
DR Pfam; PF00306; ATP-synt_ab_C; 1.
DR Pfam; PF02874; ATP-synt_ab_N; 1.
DR ProDom; PD001099; ATPase_A_C; 1.
DR PROSITE; PS00152; ATPASE_ALPHA_BETA; 1.
KW ATP synthetase; Chloroplast; Thylakoid; Membrane; CF(1);
KW ATP-binding; Hydrolase; Hydrogen ion transport.
FT NP_BIND 170 177 ATP (BY SIMILARITY).
FT ACT_SITE 363 363 BY SIMILARITY.
SQ SEQUENCE 503 AA; 54089 MW; 8636EA440225DB5 CRC64;

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Query Match 21.8%; Score 39.5; DB 1; Length 503;
Best Local Similarity 43.5%; Pred. No. 11;
Matches 10; Conservative 2; Mismatches 10; Indels 1; Gaps 1;
OY 2 NGFLXRLXGSLXRCXRLXCSF 24
| | | | | : : : : : | | | | |
Db 443 NGFLDELVASVKRYC-ASLISF 464

RESULT 43
ZAN_PIG STANDARD; PRT; 2476 AA.
AC 028983;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Zonadhesin precursor.
GN ZAN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 823-830; 859-872; 883-890;
RP 920-925; 960-967; 1235-1244; 1349-1354; 1518-1532; 1624-1656;
RP 1658-1667; 1777-1795 AND 1914-1921.
RC STRAIN=MEISHAN; TISSUE=Testis;
RX MEDLINE=96064658; PubMed=7592795;
RA Hardy D.M., Garbers D.L.;
RT "A sperm membrane protein that binds in a species-specific manner to
RT the egg extracellular matrix is homologous to von Willebrand
RT factor".
RL J. Biol. Chem. 270:26025-26028(1995).
CC -1- FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO THE ZONA PELLUCIDA
CC OF THE EGG. MAY BE INVOLVED IN GAMETE RECOGNITION AND/OR
CC SIGNALING.
CC -1- SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVELY ON THE
CC APICAL REGION OF THE SPERM HEAD (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: IN TESTIS, PRIMARILY IN HAPLOID SPERMATIDS.
CC NOT IN LUNG, LIVER, HEART, SPLEEN, BRAIN, KIDNEY, EPIDIDYMS.
CC -1- DOMAIN: THE MAM DOMAINS PROBABLY MEDIATE SPERM ADHESION TO THE
CC ZONA PELLUCIDA.
CC -1- DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS,
CC THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF
CC SPERMATOZOEA OR PROMOTING ADHESION TO THE OVIDUCTAL ISTHMUS.
CC -1- DOMAIN: THE VWED DOMAINS 2 AND 3 MAY MEDIATE COVALENT
CC OLIGOMERIZATION (BY SIMILARITY TO HUMAN INTESTINAL MUCIN MU2).
CC -1- PTM: THE MAM DOMAINS AND THE MUCIN-LIKE DOMAINS ARE MISSING
CC FROM THE ZONADHESIN THAT BINDS TO THE EGG EXTRACELLULAR MATRIX.
CC PROCESSING MIGHT OCCUR DURING SPERM MATURATION AND/OR
CC CAPACITATION.
CC -1- SIMILARITY: CONTAINS 2 MAM DOMAINS.
CC -1- SIMILARITY: CONTAINS 4.5 VWED DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

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DR EMBL: UA0024; AAC48486.1; -
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000998; MAM.
DR InterPro: IPR002919; TIL.
DR InterPro: IPR003328; TIL.
DR InterPro: IPR001007; VWFC.
DR InterPro: IPR001846; VWd.
DR Pfam: PF00629; MAM; 2.

DR Pfam: PF01826; TIL; 5.
DR Pfam: PF02345; TIL; 5.
DR Pfam: PF00094; VWd; 4.
DR SMART: SM00181; EGF; 1.
DR SMART: SM00137; MAM; 1.
DR SMART: SM00214; VNC; 2.
DR SMART: SM00216; VWd; 4.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 4.
DR PROSITE: PS00740; MAM_1; 1.
DR PROSITE: PS50060; MAM_2; 2.
KM Signal; Glycoprotein; Transmembrane; EGF-like domain; Cell adhesion;
KW Repeat.
FT SIGNAL 1 29
FT CHAIN 30 2476
FT DOMAIN 30 2418
FT TRANSMEM 2419 2439
FT DOMAIN 2440 2476
FT DOMAIN 31 144
FT DOMAIN 147 312
FT DOMAIN 319 687
FT DOMAIN 688 799
FT DOMAIN 800 1184
FT DOMAIN 1185 1573
FT DOMAIN 1574 1968
FT DOMAIN 1969 2370
FT DOMAIN 2366 2402
FT DISULFID 2370 2381
FT DISULFID 2375 2390
FT DISULFID 2392 2401
FT CARBOHYD 109 109
FT CARBOHYD 269 269
FT CARBOHYD 735 735
FT CARBOHYD 758 758
FT CARBOHYD 833 833
FT CARBOHYD 1154 1154
FT CARBOHYD 1329 1329
FT CARBOHYD 1448 1448
FT CARBOHYD 1544 1544
FT CARBOHYD 1596 1596
FT CARBOHYD 1654 1654
FT CARBOHYD 1843 1843
FT CARBOHYD 1965 1965
FT CARBOHYD 2122 2122
FT CARBOHYD 2165 2165
FT CARBOHYD 2178 2178
FT CARBOHYD 2329 2329
FT CARBOHYD 2359 2359
FT CONFLICT 823 823
FT CONFLICT 923 923
FT CONFLICT 965 965
FT CONFLICT 1241 1241
SQ SEQUENCE 2476 AA; 270364 MW; AL3B690375A654BC CMC64;

Query Match 21.5%; Score 39; DB 1; Length 2476;
Best Local Similarity 35.0%; Pred. No. 69;
Matches 7; Conservative 3; Mismatches 10; Indels 0; Gaps 0;
OY 5 LXXIRXGSLXRCXRLXCSF 24
| | | | | : : : : : | | | | |
Db 1013 LPHLRASSFFKSCFDMCNF 1032
RESULT 44
CDBL_HUMAN STANDARD; PRT; 818 AA.
AC 09Y5F3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Protocadherin beta 1 precursor (PCDH-beta1).

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GN PCDB1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99308636; PubMed=10380929;
RA Wu O., Maniatis T.;
RT "A striking organization of a large family of human neural cadherin-
RT like cell adhesion genes."
RL Cell 97:779-790(1999).
CC -1- FUNCTION: POTENTIAL CALCIUM-DEPENDENT CELL-ADHESION PROTEIN.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: CONTAINS 6 CADHERIN DOMAINS.
CC -----
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CC -----
CC EMBL: AF152488; AAD43749.1; -.
CC DR HSSP: P15116; INCI.
CC DR MIM: 606327; -.
CC DR MIM: 604967; -.
CC DR InterPro: IPR002126; Cadherin.
CC DR Pfam: PF00028; cadherin.5.
CC DR PRINTS: PR00205; CADHERIN.
CC DR SMART: SM00112; CA; 6.
CC DR PROSITE: PS00232; CADHERIN_1; 5.
CC DR PROSITE: PS00268; CADHERIN_2; 6.
CC DR Calcium-binding; Cell adhesion; Glycoprotein; Signal; Repeat;
CC Transmembrane; Multigene family.
CC KW SIGNAL.
CC FT SIGNAL 1 28 POTENTIAL.
CC FT CHAIN 29 691 EXTRACELLULAR (POTENTIAL).
CC FT DOMAIN 29 691 POTENTIAL.
CC FT TRANSMEM 692 712 POTENTIAL.
CC FT DOMAIN 713 818 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 35 133 POTENTIAL.
CC FT DOMAIN 138 242 CADHERIN 1.
CC FT DOMAIN 243 347 CADHERIN 2.
CC FT DOMAIN 348 452 CADHERIN 3.
CC FT DOMAIN 457 562 CADHERIN 4.
CC FT DOMAIN 577 672 CADHERIN 5.
CC FT CARBOHYD 169 169 CADHERIN 6.
CC FT CARBOHYD 209 209 N-LINKED (GLCNAc. . .) (POTENTIAL).
CC FT CARBOHYD 257 257 N-LINKED (GLCNAc. . .) (POTENTIAL).
CC FT CARBOHYD 419 419 N-LINKED (GLCNAc. . .) (POTENTIAL).
CC FT CARBOHYD 568 568 N-LINKED (GLCNAc. . .) (POTENTIAL).
CC SQ SEQUENCE 818 AA: 90456 MW: 48875E4EDBD604 CRC64.

Query Match 21.0%; Score 38; DB 1; Length 818;
Best Local Similarity 34.8%; Pred. No. 35;
Matches 8; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

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OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=JAPANESE WHITE; TISSUE=Brain;
RX MEDLINE=94206534; PubMed=7794412;
RA Yoshinara Y., Oka S., Nemoto Y., Watanabe Y., Nagata S.,
RA Kagamiyama H., Mori K.;
RT "An ICAM-related neuronal glycoprotein, telencephalin, with brain
RT segment-specific expression."
RL Neuron 12:541-553(1994).
CC -1- FUNCTION: ADHESION MOLECULE THAT BINDS TO LEUKOCYTE ADHESION
CC LFA-1 PROTEIN (INTEGRIN ALPHA-L/BETA-2).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed on neurons in the most rostral
CC segment of the mammalian brain, the telencephalon.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. ICAM
CC SUPERFAMILY.
CC -----
CC -1- SIMILARITY: CONTAINS 9 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L13199; AAA18478.1; -.
CC DR HSSP: P05362; IIC1.
CC DR InterPro: IPR003988; ICAM.
CC DR InterPro: IPR003987; ICAM_YCAM-1.
CC DR InterPro: IPR003006; IG_MHC.
CC DR InterPro: IPR003598; IG_C2.
CC DR InterPro: IPR003600; IG_Like.
CC DR Pfam: PF00047; Ig; 8.
CC DR PRINTS: PR01473; ICAM.
CC DR PRINTS: PR01472; ICAMVCAM1.
CC DR SMART: SM00410; IG_Like; 3.
CC DR SMART: SM00408; IGC2; 1.
CC KW Immunoglobulin domain; Cell adhesion; Glycoprotein; Transmembrane;
CC Repeat; Signal.
CC FT SIGNAL 1 29 POTENTIAL.
CC FT CHAIN 30 912 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 827 847 POTENTIAL.
CC FT DOMAIN 848 912 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 47 107 IG-LIKE C2-TYPE DOMAIN 1.
CC FT DOMAIN 132 202 IG-LIKE C2-TYPE DOMAIN 2.
CC FT DOMAIN 239 304 IG-LIKE C2-TYPE DOMAIN 3.
CC FT DOMAIN 332 385 IG-LIKE C2-TYPE DOMAIN 4.
CC FT DOMAIN 403 472 IG-LIKE C2-TYPE DOMAIN 5.
CC FT DOMAIN 486 552 IG-LIKE C2-TYPE DOMAIN 6.
CC FT DOMAIN 566 645 IG-LIKE C2-TYPE DOMAIN 7.
CC FT DOMAIN 659 724 IG-LIKE C2-TYPE DOMAIN 8.
CC FT DOMAIN 754 813 IG-LIKE C2-TYPE DOMAIN 9.
CC FT DISULFID 54 101 BY SIMILARITY.
CC FT DISULFID 139 195 BY SIMILARITY.
CC FT DISULFID 246 297 BY SIMILARITY.
CC FT DISULFID 339 378 BY SIMILARITY.
CC FT DISULFID 410 465 BY SIMILARITY.
CC FT DISULFID 493 546 BY SIMILARITY.
CC FT DISULFID 573 638 BY SIMILARITY.
CC FT DISULFID 666 717 BY SIMILARITY.
CC FT DISULFID 761 806 BY SIMILARITY.
CC FT CARBOHYD 53 53 N-LINKED (GLCNAc. . .) (POTENTIAL).
CC FT CARBOHYD 134 134 N-LINKED (GLCNAc. . .) (POTENTIAL).
CC FT CARBOHYD 192 192 N-LINKED (GLCNAc. . .) (POTENTIAL).
CC FT CARBOHYD 211 211 N-LINKED (GLCNAc. . .) (POTENTIAL).
CC FT CARBOHYD 311 311 N-LINKED (GLCNAc. . .) (POTENTIAL).
CC FT CARBOHYD 366 366 N-LINKED (GLCNAc. . .) (POTENTIAL).

```

Query Match
Best Local Similarity 21.0%; Score 38; DB 1; Length 912;
Matches 8; Conservativity 1; Mismatches 16; Indels 0; Gaps 0;

QY 17 CRXXLCSPXAXXIFRNXXRTQFW 41
DB 195 CRAELDLRPGQIALFENSSAPRLW 219

RESULT 46
GLSF_ANTSP STANDARD; PRT; 1536 AA.

AC 006434;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ferredoxin-dependent glutamate synthase (EC 1.4.7.1) (rd-GOGAT).
GN GLTB OR GLSF.
OS Antilhamion sp.
OC Chloroplast.
OC Eukaryote; Rhodophyta; Florideophyceae; Ceramiales; Ceramiales;
OC Antilhamion
OX NCBI_TaxID=2767;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9403329; Pubmed=8219058;
RA Valentin K.U., Kozirzawa M., Zetsche K.;
RT "Glutamate synthase is plastid-encoded in a red alga: implications
for the evolution of glutamate synthases.";
RL Plant Mol. Biol. 23:77-85(1993).
CC -1- CATALYTIC ACTIVITY: 2 L-glutamate + 2 oxidized ferredoxin = L-
glutamine + 2-oxoglutarate + 2 reduced ferredoxin.
CC -1- COFACTOR: BINDS A 3FE-4S CLUSTER: FAD AND FMN.
CC -1- PATHWAY: GLUTAMINE SYNTHETASE/GOGAT PATHWAY WHICH IS INVOLVED
IN THE ASSIMILATION OF AMMONIA.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Chloroplast stroma.
CC -1- SIMILARITY: TO OTHER GLUTAMATE SYNTHASES.
CC -----
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CC -----
DR EMBL; Z21705; CAY9809.1; -;
DR PIR; S31911; S31911.
DR PIR; S39510; S39510.
DR InterPro; IPR002489; DUF14.
DR InterPro; IPR003008; FMN_enzyme.
DR InterPro; IPR002932; Glu_synthase.
DR Pfam; PF01493; DUF14; 1.
DR Oxidoreductase; Iron-sulfur; 3Fe-4S; Flavoprotein; FAD; FMN;
KM Chloroplast; Glutamate biosynthesis
FT DOMAIN 27 380
FT METAL 1158 1158 IRON-SULFUR (3FE-4S) (BY SIMILARITY).
FT METAL 1164 1164 IRON-SULFUR (3FE-4S) (BY SIMILARITY).
FT METAL 1169 1169 IRON-SULFUR (3FE-4S) (BY SIMILARITY).
FT NE_BIND 1105 1162 FMN (BY SIMILARITY).
SQ SEQUENCE 1536 AA; 171111 MW; E803CED3004F921C CRC64;

Query Match
Best Local Similarity 20.7%; Score 37.5; DB 1; Length 1536;
Matches 7; Conservativity 6; Mismatches 10; Indels 1; Gaps 1;

QY 21 LCSFXAXXIFRNXXRTQFWVSY 44
DB 198 ICSPFSKRTYKGLRS-EFLVKY 220

RESULT 47
RRPL_SYNV STANDARD; PRT; 2116 AA.

AC P31332;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)
DE (L protein).
GN L.
OS Sonchus yellow net virus (SYNV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Nucleorhabdovirus.
OX NCBI_TaxID=11307;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC PV-263;
RX MEDLINE=92295567; Pubmed=1604816;
RA Choi T.-J., Kuwata S., Koonin E.V., Heaton L.A., Jackson A.O.;
RT "Structure of the L (polymerase) protein gene of sonchus yellow net
virus.";
RL Virology 189:31-39(1992).
CC -1- FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE
POLYMERASE. IT MAY FUNCTION IN RNA SYNTHESIS, CAPPING, AS WELL AS
METHYLATION OF CAPS, AND POLY(A) SYNTHESIS.
CC -1- SUBUNIT: THOUGHT TO FORM A TRANSCRIPTION COMPLEX WITH THE
NOCLEOCAPSID (N) PROTEIN.
CC -1- SIMILARITY: WITH THE L PROTEIN OF OTHER RHABDOVIRUSES AND
PARAMYXOVIRUSES.
CC -----
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CC -----
DR EMBL; L32603; AAA50385.1; -;
DR PIR; M87829; AAA47896.1; -;
DR PIR; A40230; ZIVNSY.
DR InterPro; IPR001016; Paramyx_RNA_pol.
DR Pfam; PF00946; Paramyx_RNA_pol; 1.
KM Transferase; RNA-directed RNA polymerase.
SQ SEQUENCE 2116 AA; 241536 MW; 74D186F3D4CF1D80 CRC64;

Query Match
Best Local Similarity 20.7%; Score 37.5; DB 1; Length 2116;
Matches 11; Conservativity 4; Mismatches 24; Indels 1; Gaps 1;

QY 3 GFLXXL-RXGSLRXRCRXXLCSPXAXXIFRNXXRTQFW 41
DB 666 GFRSLISRTSHIFKACYLYCSPGVVVISNQLTAQSPW 705

RESULT 48
Y152_HALHA STANDARD; PRT; 273 AA.

AC P04137;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

```

DE Hypothetical 31 kDa protein in transposable element ISH50.
OS Halobacterium halobium.
OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
CC Halobacterium.
OX NCBI_TaxID=2242;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83246542; PubMed=6306577;
RA Xu W.-L., Doolittle W.F.;
RT "Structure of the archaeobacterial transposable element ISH50.";
RL Nucleic Acids Res. 11:4195-4199(1983).
CC -----
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CC -----
DR EMBL; X01584; CAB37934.1; -
DR PIR; A05113; A05113.
RW Transposable element: Hypothetical protein.
SQ SEQUENCE 273 AA; 30985 MW; 3D171B6727DAD0BA CRC64;

Query Match 20.4%; Score 37; DB 1; Length 273;
Best Local Similarity 46.2%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 12 SLXRCRXKXLCF 24
   1: 11 11 1
Db 26 SIASCRALCDF 38

RESULT 49
URED_ECOLI
ID URED_ECOLI STANDARD: PRT: 278 AA.
AC Q03285;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Urease accessory protein ured.
GN URED.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
CC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93194816; PubMed=8449894;
RA D'Orazio S.E., Collins C.M.;
RT "Characterization of a plasmid-encoded urease gene cluster found in
RT members of the family Enterobacteriaceae.";
RL Bacteriol. 175:1860-1864(1993).
CC -1- FUNCTION: PROBABLY FACILITATES NICKEL INCORPORATION.
CC -1- SIMILARITY: BELONGS TO THE URED FAMILY.
CC -----
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CC -----
DR EMBL; L03307; AAA24744.1; -
DR PIR; A47090; A47090.
RW InterPro: IPR002669; Ured.
DR Pfam: PF01774; Ured; 1.
KW Nickel; Plasmid.
SQ SEQUENCE 278 AA; 31413 MW; C024E444E13611B9 CRC64;

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Query Match 20.4%; Score 37; DB 1; Length 278;
Best Local Similarity 62.5%; Pred. No. 18;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 37 TROFWVSY 44
   111:1:1
Db 261 TRQYWLGY 268

RESULT 50
BUD5_YEAST
ID BUD5_YEAST STANDARD: PRT: 538 AA.
AC P25300;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Bud site selection protein BUD5.
GN BUD5 OR YCR038C OR YCR38C OR YCR526.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92160397; PubMed=1789011;
RA Jaquet M., Buhler J.-M., Iborra F., Francinques-Galliard M.-C.,
RA Soustelle C.;
RT "The MAT locus revisited within a 9.8 kb fragment of chromosome III
RT containing BUD5 and two new open reading frames.";
RL Yeast 7:881-888(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SP1;
RX MEDLINE=91292524; PubMed=1905981;
RA Chant J., Corrado K., Pringle J.R., Herskowitz I.;
RT "Yeast BUD5, encoding a putative GDP-GTP exchange factor, is
RT necessary for bud site selection and interacts with bud formation
RT gene BEM1.";
RL Cell 65:1213-1224(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=91292525; PubMed=1905982;
RA Powers S., Gonzales E., Christensen T., Cubert J., Broek D.;
RT "Functional cloning of BUD5, a CDC25-related gene from S. cerevisiae
RT that can suppress a dominant-negative RAS2 mutant.";
RL Cell 65:1225-1231(1991).
RN [4]
RP SEQUENCE OF 181-538 FROM N.A.
RC STRAIN=S288C / FY1679;
RX MEDLINE=91181345; PubMed=1964349;
RA Thierry A., Fairhead C., Dujon B.;
RT "The complete sequence of the 8.2 kb segment left of MAT on
RT chromosome III reveals five ORFs, including a gene for a yeast
RT ribokinase.";
RL Yeast 6:521-534(1990).
CC -1- FUNCTION: PUTATIVE GDP-GTP EXCHANGE FACTOR. REQUIRED TO PRODUCE
CC BOTH THE AXIAL AND BIPOLAR PATTERNS OF BUD SITE SELECTION. IT
CC INTERACTS WITH BUD FORMATION GENE BEM1. BUD5 MIGHT ACT ON THE
CC RAS-LIKE PROTEINS, BUD1/RSR1 AND CDC42. IT APPEARS TO BIND TO
CC RAS PROTEINS BUT NOT TO ACTIVATE THE RAS PROTEINS.
CC -1- SIMILARITY: CONTAINS 1 RASGEF DOMAIN.
CC -----
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CC -----
DR EMBL; M63552; AAA34460.1; -

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DR EMBL: M68938; AAA34462.1; -;
DR EMBL: X59720; CAA42305.1; -;
DR EMBL: X56909; CAA40230.1; -;
DR PIR: S19450; BWBYD5.
DR SGD: S0000634; BUD5.
DR InterPro: IPR000651; RasGEFN.
DR InterPro: IPR001895; RasGEF_CDC25.
DR Pfam: PF00617; RasGEF; 1.
DR SMART: SM00147; RasGEF; 1.
DR SMART: SM00229; RasGEFN; 1.
DR PROSITE: PS00720; GDS.CDC25; 1.
KW Guanine-nucleotide releasing factor.
FT VARIANT 297 297 P -> L.
FT VARIANT 377 377 A -> S.
FT CONFLICT 6 6 R -> P (IN REF. 1).
FT CONFLICT 7 7 MISSING (IN REF. 3).
FT CONFLICT 121 121 V -> D (IN REF. 2).
SQ SEQUENCE 538 AA: 62917 MW: F700F81A78BB20DA CRC64;

Query Match

20.4%; Score 37; DB 1; Length 538;

Best Local Similarity 38.1%; Pred. No. 35;

Matches 8; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 24 FXXAXIFRNXXRTQFWVSY 44
| : | | | | : |
DB 224 FADIVOLFINKKRRRLKIHV 244

Search completed: September 3, 2002, 15:21:36
Job time: 359 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 3, 2002, 15:21:13 : Search time 41.95 seconds
(without alignments)
181.449 Million cell updates/sec

Title: US-09-302-239-4-COPY
Perfect score: 181

Sequence: 1 ANGFLXLRKXGSLKRCRXX.....XXAXIFRNXXRTQFWY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :

SPREMBL_19: *
1: sp.archaea: *
2: sp.bacteria: *
3: sp.fungi: *
4: sp.human: *
5: sp.invertebrate: *
6: sp.mammal: *
7: sp.mhc: *
8: sp.organelle: *
9: sp.phage: *
10: sp.plant: *
11: sp.potent: *
12: sp.virus: *
13: sp.vertebrate: *
14: sp.unclassified: *
15: sp.virus: *
16: sp.bacteriap: *
17: sp.archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	121	66.9	701	4	Q96PQ8
2	106	58.6	218	4	Q14668
3	105	58.0	460	11	Q91WN8
4	104	57.5	446	11	Q61109
5	99	54.7	231	4	Q9BZD7
6	99	54.7	456	6	Q9TRRO
7	99	54.7	460	11	Q99PC6
8	93	51.4	482	11	Q63207
9	90	49.7	481	11	Q88947
10	90	49.7	481	11	Q54740
11	90	49.7	481	11	Q99L32
12	86	47.5	49	6	Q95ME8
13	86	47.5	456	4	Q14316
14	86	47.5	461	6	Q95ND7
15	86	47.5	461	6	Q95ND6
16	86	47.5	469	6	Q9GMD9

17	80	44.2	138	6	Q28994	Q28994 sus scrofa
18	80	44.2	433	13	Q90YK1	Q90YK1 brachydanio
19	78	43.1	100	4	Q15253	Q15253 homo sapien
20	78	43.1	608	13	Q9PTW7	Q9PTW7 struthio ca
21	72	40.3	648	6	Q29094	Q29094 sus scrofa
22	72	39.8	399	11	Q9COW3	Q9COW3 mus musculu
23	69	38.1	202	4	Q14659	Q14659 homo sapien
24	69	38.1	226	4	Q9BZD6	Q9BZD6 homo sapien
25	68	37.6	650	4	Q9NSD0	Q9NSD0 homo sapien
26	68	37.6	650	4	Q16519	Q16519 homo sapien
27	66	36.5	607	13	Q91001	Q91001 gallus gall
28	57	31.5	678	4	Q14393	Q14393 homo sapien
29	56	30.9	25	11	Q9OYH6	Q9OYH6 rattus sp.
30	56	30.9	673	11	Q61592	Q61592 mus musculu
31	56	30.9	674	11	Q9AK57	Q9AK57 mus musculu
32	55	30.4	98	13	P82807	P82807 notechis sc
33	54	29.8	674	11	Q63772	Q63772 rattus sp.
34	49.5	27.3	575	10	Q94E17	Q94E17 oryza sativ
35	49.5	27.3	608	10	Q9XR36	Q9XR36 medicago sa
36	48.5	26.8	196	10	Q04284	Q04284 selaginella
37	48.5	26.8	594	10	Q9SU99	Q9SU99 arabidopsis
38	48.5	26.8	603	10	Q9LPG7	Q9LPG7 arabidopsis
39	48.5	26.8	606	10	Q945L8	Q945L8 arabidopsis
40	48	26.5	130	12	Q9DUB8	Q9DUB8 tt virus. o
41	47.5	26.2	431	10	Q94EX5	Q94EX5 arabidopsis
42	47.5	26.2	492	10	Q9SMJ7	Q9SMJ7 cicier ariet
43	47.5	26.2	543	10	Q9MB23	Q9MB23 arabidopsis
44	47.5	26.2	576	10	Q9C9U4	Q9C9U4 arabidopsis
45	47.5	26.2	589	10	Q9LMS2	Q9LMS2 arabidopsis
46	47.5	26.2	593	10	Q9LUC3	Q9LUC3 arabidopsis
47	47	26.0	472	13	Q98SU5	Q98SU5 gasterosten
48	47	26.0	613	13	Q98SU6	Q98SU6 gasterosten
49	47	26.0	910	13	Q98SU7	Q98SU7 gasterosten
50	45	24.9	687	2	P71196	P71196 enterobacte

ALIGNMENTS

RESULT 1
ID Q96PQ8 PRELIMINARY; PRT; 701 AA.
AC Q96PQ8:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE FACTOR VII ACTIVE SITE MUTANT IMMUNOCONJUGATE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21477448; PubMed=11593034;
RA Hu Z., Garen A.;
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
cells for immunotherapy in mouse models of prostatic cancer.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
DR EMBL; AF272774; AAK58686.1; -.
SQ SEQUENCE 701 AA; 77826 MW; 94ACGCEB42CC992F CRC64;

Query Match 66.9%; Score 121; DB 4; Length 701;
Best Local Similarity 52.3%; Pred. No. 1.76-14;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Oy 1 ANGFLXLRKXGSLKRCRXXIFRNXXRTQFWY 44
Db 61 ANAFLELRPGSLEREKCEOCSEAREIRKDAERTLFWISY 104
RESULT 2
Q14668

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ID 014668 PRELIMINARY; PRT; 218 AA.
AC 014668;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PROLINE-RICH GLA PROTEIN 1.
GN PRGPI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97404347; PubMed=9256434;
RA Kulman J.D., Harris J.E., Haldeman B.A., Davie E.W.;
RT "Primary structure and tissue distribution of two novel proline-rich
RT gamma-carboxyglutamic acid proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997).
DR EMBL: AF009242; AAB67070.1; -.
DR HSSP: P00740; ICFH.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR000294; VltK_dep_GLA.
DR Pfam: PF00594; gla; 1.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00069; GLA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
SQ SEQUENCE 218 AA; 24947 MW; 26538A61AB0AE98 CRC64;

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Query Match 58.6%; Score 106; DB 4; Length 218;
Best Local Similarity 38.6%; Pred. No. 3.8e-12;
Matches 17; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

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Qy 1 ANGFLXXLRKGSLSRXCRXXLCSEFXAXXIFRNXXRTQPFVSY 44
Db 21 ANGFEELRGNIERCKEEFCFEERAEFENNEKTKFWSY 64

RESULT 3
Q01WN8 PRELIMINARY; PRT; 460 AA.
AC 091WN8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE SIMILAR TO PROTEIN C.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC013896; AAH13896.1; -.
SQ SEQUENCE 460 AA; 51818 MW; 0117F26E68FC274 CRC64;

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Query Match 58.0%; Score 105; DB 11; Length 460;
Best Local Similarity 45.5%; Pred. No. 1.3e-11;
Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

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Qy 1 ANGFLXXLRKGSLSRXCRXXLCSEFXAXXIFRNXXRTQPFVSY 44
Db 42 ANGFLEEMRPGSLRECMCEICDFEEAQEIFQVVEDTLAFWIKY 85

RESULT 4
Q061109 PRELIMINARY; PRT; 446 AA.
AC 061109;
DT 01-NOV-1996 (TREMBLrel. 01, Created)

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DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE COAGULATION FACTOR VII.
GN F7 OR FVII.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=96276538; PubMed=8701412;
RA Idusogie F., Rosen E., Geng J.P., Carmeliet P., Collen D.,
RA Castellino F.J.;
RT "Characterization of a cDNA encoding murine coagulation factor VII.";
RL Thromb. Haemost. 75:481-487(1996).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPsin FAMILY.
DR EMBL: U44795; AAC52570.1; -.
DR HSSP: P08709; IFAR.
DR MGD: MGI:109325; F7.
DR InterPro: IPR002086; Aldehyde_dehydr.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR001064; Crystallin.
DR InterPro: IPR000561; EGF_Ca.
DR InterPro: IPR001881; EGF-like.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Trypsin.
DR Pfam: PF00008; EGF; 2.
DR Pfam: PF00594; gla; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00001; EGF_Like; 1.
DR SMART: SM00069; GLA; 1.
DR PROSITE: PS00020; TRYP_Spc; 1.
DR PROSITE: PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS02040; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ SEQUENCE 446 AA; 50318 MW; 482FD09BEFDA6870 CRC64;

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Query Match 57.5%; Score 104; DB 11; Length 446;
Best Local Similarity 47.7%; Pred. No. 1.9e-11;
Matches 21; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

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Qy 1 ANGFLXXLRKGSLSRXCRXXLCSEFXAXXIFRNXXRTQPFVSY 44
Db 42 ANSLLEELWPGSLRECMCEICDFEEARELFKSPERTKQFWIY 85

RESULT 5
Q09BZD7 PRELIMINARY; PRT; 231 AA.
AC 09BZD7;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID PROTEIN 3 TMG3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

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OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SPINAL CORD;
 RX MEDLINE=21117044; PubMed=11171957;
 RA Kulman J.D., Harris J.E., Xie L., Davie E.W.;
 RT "Identification of two novel transmembrane gamma-carboxyglutamic acid
 proteins expressed broadly in fetal and adult tissues.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:1370-1375(2001).
 DR EMBL: AF326350; AAK0955.1;
 DR HSSP: P00740; ICFH.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00069; GLA: 1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
 SQ SEQUENCE 231 AA; 25848 MW; 8A373E48490D81 CRC64;

Query Match 54.7%; Score 99; DB 4; Length 231;
 Best Local Similarity 38.6%; Pred. No. 8.7e-11;
 Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

OY 1 ANGFLXLRKGSGLKRXCRXXLCSEFXAXXIFRNXXRTQFWVSY 44
 Db 20 ANEFLELRQGTIERECMEICSEYEVKEFENKEKTEFMWKGY 63

RESULT 6
 Q9TTR0 PRELIMINARY; PRT; 456 AA.
 AC Q9TTR0;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PROTEIN C PRECURSOR.
 GN PROC.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_Taxid=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Leeb T., Kopp T., Deppe A., Breen M., Matlis U., Brunberg L.,
 RA Breenig B.;
 RT "Molecular characterization and chromosomal assignment of the canine
 protein C gene.";
 RL Mamm. Genome 10:135-139(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99371952; PubMed=10443005;
 RA Leeb T., Pfeiffer T., Kopp T., Deppe A., Breenig B.;
 RT "Analysis of canine protein C gene polymorphisms.";
 RL Anim. Genet. 30:237-238(1999).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 DR EMBL: AJ001979; CA05126.1; -.
 DR HSSP: P04070; lpcu.
 DR MEROPS: S01.218; -.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Trypsin.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam: PF00008; EGF; 1.
 DR Pfam: PF00594; gla; 2.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00181; EGF; 2.
 DR SMART: SM00069; GLA; 1.

DR SMART: SM00020; TRYP-Spc; 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; 1.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF_Ca; 1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE: PS0240; TRYP-SIN_DOM; 1.
 DR PROSITE: PS00134; TRYP-SIN_HIS; UNKNOWN_1.
 DR PROSITE: PS00135; TRYP-SIN_SER; 1.
 DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
 KM Hydroxylation; Repeat; Serine protease; Signal.
 FT SIGNAL 1 42
 FT CHAIN 43 192 PROTEIN C LIGHT CHAIN.
 FT CHAIN 193 194 PROTEIN C CONNECTING DIPEPTIDE.
 FT CHAIN 195 456 PROTEIN C HEAVY CHAIN.
 SQ SEQUENCE 456 AA; 50813 MW; 7AD3A8C1C34E59FF CRC64;

Query Match 54.7%; Score 99; DB 6; Length 456;
 Best Local Similarity 43.2%; Pred. No. 1.7e-10;
 Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

OY 1 ANGFLXLRKGSGLKRXCRXXLCSEFXAXXIFRNXXRTQFWVSY 44
 Db 43 ANSFLEIRAGSLERECMEICDFEAEKEIFQNVDDTLAWSKY 86

RESULT 7
 Q99PC6 PRELIMINARY; PRT; 460 AA.
 AC Q99PC6;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ANTICOAGULANT PROTEIN C.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL;
 RA Korf I.;
 RT "Complete sequence of UC72A01.";
 RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 DR EMBL: AF318182; AAK07918.1; -.
 DR HSSP: P04070; lpcu.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Trypsin.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00001; EGF-like; 2.
 DR SMART: SM00069; GLA; 1.
 DR SMART: SM00020; TRYP-Spc; 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; 1.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF_Ca; 1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE: PS0240; TRYP-SIN_DOM; 1.
 DR PROSITE: PS00134; TRYP-SIN_HIS; UNKNOWN_1.
 DR PROSITE: PS00135; TRYP-SIN_SER; 1.
 DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
 KW Hydroxylation; Repeat; Serine protease.

SEQUENCE 460 AA; 51784 MW; 0293HC25E9D3ED16 CRC64;

Query Match 54.7%; Score 99; DB 11; Length 460;
Best Local Similarity 43.2%; Pred. No. 1.8e-10;
Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

QY 1 ANGLAXLRKGSLLKRCRRXKICSYXXAXIFRNXXRTQFWVSY 44
DB 42 ANSFLEMRPGSLERECMEECIDLEAQLFQWVEDLAEWIKY 85

RESULT 8

ID 063207 PRELIMINARY; PRT; 482 AA.
AC 063207;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE FACTOR X.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA MEDLINE=96093366; PubMed=8578539;
RA Stanton C., Ross R.P., Hutson S., Wallin R.;
RT "Evidence for competition between vitamin K-dependent clotting factors
RT for intracellular processing by the vitamin K-dependent gamma-
RT carboxylase.";
RL Thromb. Res. 80:63-73(1995).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL: X79807; CA556202.1; -;
DR HSP: P00742; 1XKA.
DR MEROPS: S01.216; -;
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF-2.
DR InterPro: IPR001881; EGF-Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Trypsin.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; gla_1.
DR PRINTS: PR00089; trypsin_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA_1.
DR SMART: SM00001; EGF_like_1.
DR SMART: SM00069; GLA_1.
DR SMART: SM00020; TRYP_SPC_1.
DR PROSITE: PS00010; ASX_HYDROXYL_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA_1.
DR PROSITE: PS00011; GLU_CARBOXYLATION_1.
DR PROSITE: PS50240; TRYPsin_DOM_1.
DR PROSITE: PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KW Hydroxylation; Repeat; Serine protease.
SQ SEQUENCE 482 AA; 54265 MW; 0284678E3954A698 CRC64;

DB 41 ANSFEEIKGNLERECVEECISFEAREVEFEDNEKTEFWNKY 84

RESULT 9

ID 088947 PRELIMINARY; PRT; 481 AA.
AC 088947;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE COAGULATION FACTOR X PRECURSOR.
GN F10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL6 X CBA; TISSUE=LIVER;
RX MEDLINE=98347933; PubMed=9684791;
RA Liang Z., Cooper A., Deford M.E., Carmeliet P., Collen D.,
RA Castellino F.J., Rosen E.D.;
RT "Cloning and characterization of a cDNA encoding murine coagulation
RT factor X.";
RL Thromb. Haemost. 80:87-91(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129SJ.
RA Cooper A., Liang Z., Castellino F.J., Rosen E.D.;
RT "Cloning and Characterization of the Murine Factor X Gene.";
RL Thromb. Haemost. 0:0-0(2000).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL: AF087644; AAC36345.1; -;
DR EMBL: AF211347; AAC22980.1; -;
DR HSP: P00742; 1XKA.
DR MEROPS: S01.216; -;
DR MGD: MGI:103107; F10.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF-2.
DR InterPro: IPR001881; EGF-Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Trypsin.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; gla_1.
DR PRINTS: PR00089; trypsin_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA_1.
DR SMART: SM00001; EGF_like_1.
DR SMART: SM00069; GLA_1.
DR SMART: SM00020; TRYP_SPC_1.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA_1.
DR PROSITE: PS00011; GLU_CARBOXYLATION_1.
DR PROSITE: PS50240; TRYPsin_DOM_1.
DR PROSITE: PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease; Signal.
FT SIGNAL 1
FT CHAIN 41 481 POTENTIAL FACTOR X.
SQ SEQUENCE 481 AA; 54018 MW; 8AC09DE5EF9D271E CRC64;

Query Match 51.4%; Score 93; DB 11; Length 482;
Best Local Similarity 36.4%; Pred. No. 2.6e-09;
Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

Query Match 49.7%; Score 90; DB 11; Length 481;
Best Local Similarity 31.8%; Pred. No. 9.7e-09;

Matches 14; Conservative 9; Mismatches 21; Indels 0; Gaps 0;

OY 1 ANGFLXLRXGSLXRCXRLCSFXAXXIFRNXXRTROFWYSY 44
DB 41 ANSFEEFRKGNLRECEMEICSYEVRIFEDEKTKYWKY 84

RESULT 10

ID 054740 PRELIMINARY; PRT: 481 AA.

AC 054740.

DT 01-JUN-1998 (TREMBlrel. 06, Created)

DT 01-JUN-1998 (TREMBlrel. 06, last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)

DE COAGULATION FACTOR X PRECURSOR (EC 3.4.21.6).

GN F10.

OS Mus musculus (Mouse).

OC Plasmid pluscript.

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

CC NCBI_TaxID=10090.

CC NCBI_TaxID=10090.

CC NCBI_TaxID=10090.

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CC NCBI_TaxID=10090.

CC NCBI_TaxID=10090.

CC NCBI_TaxID=10090.

RESULT 11

ID 099132 PRELIMINARY; PRT: 481 AA.

AC 099132.

DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)

DE COAGULATION FACTOR X.

GN F10.

OS Mus musculus (Mouse).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

CC NCBI_TaxID=10090.

CC NCBI_TaxID=10090.

CC NCBI_TaxID=10090.

CC NCBI_TaxID=10090.

CC NCBI_TaxID=10090.

CC NCBI_TaxID=10090.

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CC NCBI_TaxID=10090.

RESULT 12

ID 095ME8 PRELIMINARY; PRT: 49 AA.

AC 095ME8.

DT 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)

DE COAGULATION FACTOR IX (FRAGMENT).

GN Bos taurus (Bovine).

OS Bos taurus (Bovine).

SEQUENCE 481 AA: 54004 MW: BD88E96CA80B7E7F CRC64;

Query Match 49.7%; Score 90; DB 11; Length 481;

Best Local Similarity 31.8%; Pred. No. 9.7e-09;

Matches 14; Conservative 9; Mismatches 21; Indels 0; Gaps 0;

OY 1 ANGFLXLRXGSLXRCXRLCSFXAXXIFRNXXRTROFWYSY 44
DB 41 ANSFEEFRKGNLRECEMEICSYEVRIFEDEKTKYWKY 84

RESULT 12

ID 095ME8 PRELIMINARY; PRT: 49 AA.

AC 095ME8.

DT 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)

DE COAGULATION FACTOR IX (FRAGMENT).

GN Bos taurus (Bovine).

OS Bos taurus (Bovine).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
ON NCBI_TaxID=9913;
RX [1]
RP SEQUENCE FROM N.A.
RA Mizlaria M.N., Amaral E.J.;
RT "Partial sequence of bovine F9 coding gene.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF394598; AAK7556.1; -.
FT NON_TER 1
FT NON_TER 49
SQ SEQUENCE 49 AA; 6023 MW; D15C6DE9CCBA4A14 CRC64;

Query Match 47.5%; Score 86; DB 6; Length 49;
Best Local Similarity 37.2%; Pred. No. 5.4e-09;
Matches 16; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

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QY 2 NGFLXLRXGSLXRCXRXLCSPFXAXXIFRNXXRTQFWVS 44
Db 6 SGKLEEFVQGNLERECMEKCSFEAREVFENTRTTEFWKQY 48

RESULT 13
ID Q14316 PRELIMINARY; PRT; 456 AA.
AC Q14316;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-AUG-1999 (TREMBlrel. 11, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE F9 (COAGULATION FACTOR IX (PLASMA THROMBOPLASTIC COMPONENT, CHRISTMAS DISEASE, HAEMOPHILIA B)) (FACTOR IX).
GN F9 OR FACTOR IX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bird C.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 3-19 FROM N.A.
RX MEDLINE=88327116; PubMed=3416069;
RA Reiltsma P.A., Bertina R.M., ploos van Amstel J.K., Riemeis A.,
RA Briet E.;
RT "The putative factor IX gene promoter in hemophilia B Leyden.";
RL Blood 72:1074-1076(1988)
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AL033403; CAA21954.1; -.
DR EMBL; X55008; CAB38245.2; -.
DR HSSP; P00740; 1CFH.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF-2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001438; EGF_II.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Trypsin.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF000594; gla; 2.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS; PRO0722; CHYMOTRPSIN.
DR PRINTS; PRO0010; EGFBLD.
DR PRINTS; PRO0001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS0010; ASX_HYDROXYL; UNKNOWN_1.

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DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ SEQUENCE 456 AA; 51149 MW; 54E20A1B3964E234 CRC64;

Query Match 47.5%; Score 86; DB 4; Length 456;
Best Local Similarity 39.5%; Pred. No. 5.3e-08;
Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

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QY 2 NGFLXLRXGSLXRCXRXLCSPFXAXXIFRNXXRTQFWVS 44
Db 44 SGKLEEFVQGNLERECMEKCSFEAREVFENTRTTEFWKQY 86

RESULT 14
ID Q95ND7 PRELIMINARY; PRT; 461 AA.
AC Q95ND7;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE COAGULATION FACTOR XI.
GN F9.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=504;
RA Saita Y.;
RT "Comparison of DNA and protein polymorphisms between humans and
RT chimpanzees.";
RL Genes Genet. Syst. 0:0-0(2001).
DR EMBL; AB062470; BAB58885.1; -.
DR EMBL; AB062458; BAB58885.1; JOINED.
DR EMBL; AB062460; BAB58885.1; JOINED.
DR EMBL; AB062462; BAB58885.1; JOINED.
DR EMBL; AB062464; BAB58885.1; JOINED.
DR EMBL; AB062466; BAB58885.1; JOINED.
DR EMBL; AB062468; BAB58885.1; JOINED.
SQ SEQUENCE 461 AA; 51764 MW; 30C2F857C0E77F45 CRC64;

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Query Match 47.5%; Score 86; DB 6; Length 461;
Best Local Similarity 39.5%; Pred. No. 5.4e-08;
Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

QY 2 NGFLXLRXGSLXRCXRXLCSPFXAXXIFRNXXRTQFWVS 44
Db 49 SGKLEEFVQGNLERECMEKCSFEAREVFENTRTTEFWKQY 91

RESULT 15
ID Q95ND6 PRELIMINARY; PRT; 461 AA.
AC Q95ND6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE COAGULATION FACTOR XI.
GN F9.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_TaxID=9598;

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[1]
RP SEQUENCE FROM N.A.
RC STRAIN-505;
RA Satia Y.;
RT "Comparison of DNA and protein polymorphisms between humans and chimpanzees.";
RL Genes Genet. Syst. 0:0-0(2001).
DR EMBL: AB062471; BAB58886.1; -.
DR EMBL: AB062459; BAB58886.1; JOINED.
DR EMBL: AB062461; BAB58886.1; JOINED.
DR EMBL: AB062463; BAB58886.1; JOINED.
DR EMBL: AB062465; BAB58886.1; JOINED.
DR EMBL: AB062467; BAB58886.1; JOINED.
DR EMBL: AB062469; BAB58886.1; JOINED.
SO SEQUENCE 461 AA; 51695 MW; 8F5A69A525DF65B5 CRC64;

Query Match 47.5%; Score 86; DB 6; Length 461;
Best Local Similarity 39.5%; Pred. No. 5.4e-08;
Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

OY 2 NGFLXXLRXGSLXRCXAXXIFRNXXRTQFWVS 44
Db 49 SGKLEEFVQGNLRECEMEKCSFEAREVFENTERTTFEMKQY 91

RESULT 16
Q9GMD9 PRELIMINARY; PRT; 469 AA.
AC Q9GMD9;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE COGULATION FACTOR X.
OS Ornithorhynchus anatinus (Duckbill platypus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.
OX NCBI_TaxID=9258;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21015017; PubMed=11132153;
RX Poorafshar M., Aveskog M., Munday B., Hellman L.;
RT "Identification and structural analysis of four serine proteases in a monotreme, the platypus, Ornithorhynchus anatinus.";
RL Immunogenetics 52:19-28(2000).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. ALSO KNOWN AS THE TRYPSIN FAMILY.
DR EMBL: AF275654; AAC00453.1; -.
DR HSSP: P00742; 1KKB.
DR MEROPS: S01.216; -.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Trypsin.
DR InterPro: IPR000294; VILK_dep_GLA.
DR Pfam: PF00089; trypsin.1.
DR PRINTS: PR00022; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00181; EGF_2.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00001; EGF_like; 2.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; TRY-spec; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
KW Hydrolase; Serine protease.
SO SEQUENCE 469 AA; 52196 MW; 4C66C230D0758F6A CRC64;

Query Match 47.5%; Score 86; DB 6; Length 469;

Best Local Similarity 34.1%; Pred. No. 5.5e-08;
Matches 15; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

OY 1 ANGFLXXLRXGSLXRCXAXXIFRNXXRTQFWVS 44
Db 41 ANSLFEELKGNLRECEMEKCSFEAREVFEDTDKTNEFWNLY 84

RESULT 17
Q28994 PRELIMINARY; PRT; 138 AA.
ID Q28994;
AC Q28994;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MATURE PORCINE FACTOR IX (FRAGMENT).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=96823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=96003866; PubMed=7568220;
RA Brandstetter H., Bauer M., Huber R., Lollar P., Bode W.;
RT "X-ray structure of clotting factor IXa: active site and module structure related to Xase activity and hemophilia B.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:9796-9800(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Lollar P.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U51135; AAA96318.1; -.
DR HSSP: P00740; 1EDM.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001438; EGF-II.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR000294; VILK_dep_GLA.
DR Pfam: PF00089; EGF_2.
DR Pfam: PF00594; gla; 1.
DR PRINTS: PR00010; EGFBLDOD.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00069; GLA; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
FT NON_TER 1 138
FT NON_TER 1 138
SO SEQUENCE 138 AA; 15515 MW; 793BABDE4D5FAFAD CRC64;

Query Match 44.2%; Score 80; DB 6; Length 138;
Best Local Similarity 41.2%; Pred. No. 2.2e-07;
Matches 14; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

OY 11 GSLXRCXAXXIFRNXXRTQFWVS 44
Db 4 GNLRECEMEKCSFEAREVFENTERTTFEMKQY 37

RESULT 18
Q90YK1 PRELIMINARY; PRT; 433 AA.
ID Q90YK1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DE 01-DEC-2001 (TReMBrel. 19, Last annotation update)
DE COAGULATION FACTOR VII.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Danio.
OX NCBI_TaxID=7955.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21353085; Pubmed=11459993;
RA Sheehan J., Tempier M., Gregory M., Hanumanthiah R., Troyer D.,
Phan T., Thankavel B., Jagadeeswaran P., Hanumanthiah R., Troyer D.,
RT "Demonstration of the extrinsic coagulation pathway in teleostei:
RT Identification of zebrafish coagulation factor VII."
RL Proc. Natl. Acad. Sci. U.S.A. 98:8768-8773(2001).
DR EMBL: AY040345; AAK74192.1; -.
SQ SEQUENCE 433 AA; 48680 MW; CD9D1B179601BAC CRC64;

Query Match 44.2%; Score 80; DB 13; Length 433;
Best Local Similarity 32.6%; Pred. No. 7.1e-07;
Matches 14; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

OY 2 NGFLXLRKSGSLKRCXKXLCSEFXAXXIFRNXXRTQFWWSY 44
DB 40 SGWFEELKTNLERECLEKCKSYEEAREVPEHTEATNEFWKXY 82

RESULT 19
O15253 PRELIMINARY; PRT; 100 AA.
AC O15253;
DT 01-NOV-1996 (TReMBrel. 01, Created)
DT 01-NOV-1996 (TReMBrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBrel. 19, Last annotation update)
DE THROMBIN PRECURSOR (FRAGMENT).
GN F2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87182874; Pubmed=3471151;
RA Macgillivray R.T., Irwin D.M., Guineto E.R., Stone J.C.;
RT "Recombinant genetic approaches to functional mapping of thrombin."
RL Ann. N. Y. Acad. Sci. 485:73-79(1986).
DR EMBL: M33031; AAA60220.1; -.
DR HSSP: P00735; 2PFI.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR000294; VltK_dep_GLA.
DR Pfam: PF00594; gla: 1.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00069; GLA: 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
KW SIGNAL.
FT SIGNAL 1 43
FT CHAIN 44 >100 POTENTIAL.
FT NON_TER 100 100
SQ SEQUENCE 100 AA; 11302 MW; FD0E5D0174E1F6FE CRC64;

Query Match 43.1%; Score 78; DB 4; Length 100;
Best Local Similarity 36.4%; Pred. No. 3.8e-07;
Matches 16; Conservative 4; Mismatches 24; Indels 0; Gaps 0;

OY 1 ANGFLXLRKSGSLKRCXKXLCSEFXAXXIFRNXXRTQFWWSY 44
DB 44 ANTFLEEVKGNLERECVECTCYEEAFEALESSTATDVPWAKY 87

RESULT 20
O9PTW7

ID O9PTW7 PRELIMINARY; PRT; 608 AA.
AC O9PTW7;
DT 01-MAY-2000 (TReMBrel. 13, Created)
DT 01-MAY-2000 (TReMBrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBrel. 19, Last annotation update)
DE PROTHROMBIN.
GN O9PT.
OS Struthio camelus (Ostrich).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Palaeognathae; Struthioniformes; Struthionidae;
OC Struthio.
OX NCBI_TaxID=8801;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20579470; Pubmed=11137455;
RC TISSUE=LIVER.
RA Frost C., Naude R., Oelofsen W., Muramoto K., Naganuma T., Ogawa T.,
RT "Purification and characterization of ostrich prothrombin."
RL Int. J. Biochem. Cell Biol. 32:1151-1159(2000).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL: AB028871; BAA89046.1; -.
DR HSSP: P00734; 1UVS.
DR MEROPS: S01.217; -.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR001254; Trypsin.
DR InterPro: IPR000294; VltK_dep_GLA.
DR Pfam: PF00594; gla: 1.
DR Pfam: PF00051; Kringle_2.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR PRINTS: PR00018; KRINGLE.
DR SMART: SM00069; GLA: 1.
DR SMART: SM00130; KR: 2.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00021; KRINGLE_1; 2.
DR PROSITE: PS00070; KRINGLE_2; 2.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease.
SQ SEQUENCE 608 AA; 69392 MW; 11B974B9AE54E2 CRC64;

Query Match 43.1%; Score 78; DB 13; Length 608;
Best Local Similarity 33.3%; Pred. No. 2.4e-06;
Matches 14; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

OY 3 GFLXLRKSGSLKRCXKXLCSEFXAXXIFRNXXRTQFWWSY 44
DB 47 GFLEELKGNLERECLEICIEYEEAFEALESSTATDEFWWSY 88

RESULT 21
O29094
ID O29094 PRELIMINARY; PRT; 648 AA.
AC O29094;
DT 01-NOV-1996 (TReMBrel. 01, Created)
DT 01-NOV-1996 (TReMBrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBrel. 19, Last annotation update)
DE PROTEIN S (FRAGMENT).
GN PROS.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;

Matches 15; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

Qy 5 LXXLRGSLXRCXXKXLCSEFXAXXIFRNXXRTQGFWSY 44
 Db 55 LELLTPGNLEECLEERCSEWEAREVEFNDTLTERFWSY 94

RESULT 24
 Q9BZD6 PRELIMINARY; PRT; 226 AA.

AC Q9BZD6; 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID PROTEIN 4 TMG4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21117044; PubMed=11171957;
 RA Kulman J.D., Harris J.E., Xie L., Davie E.W.;
 RT "Identification of two novel transmembrane gamma-carboxyglutamic acid
 RT proteins expressed broadly in fetal and adult tissues.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:1370-1375(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA, CHORIOCARCINOMA;
 RA Strausberg R.;
 RL Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF326351; AKK00956.1; -;
 DR EMBL; BC010052; AAH10052.1; -;
 DR HSSP; P00740; ICFH.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART; SM00069; GLA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 SQ SEQUENCE 226 AA; 25403 MW; 45C783E3825797EE CRC64;

Query Match 38.1%; Score 69; DB 4; Length 226;
 Best Local Similarity 38.2%; Pred. No. 4.6e-05;
 Matches 13; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 11 GSLXRCXXKXLCSEFXAXXIFRNXXRTQGFWSY 44
 Db 63 GNLERECNEELCNWEAREVEFNDTLTERFWSY 96

RESULT 25
 Q9NSDO PRELIMINARY; PRT; 650 AA.

AC Q9NSDO; 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PROTEIN S PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Wydro R., Cohen E., Dackowski W., Stenflo J., Lundwall A.,
 RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X12892; CAA31383.1; -;
 DR HSSP; P00740; ICFH.
 DR InterPro: IPR000152; ASX_hydroxyl.
 DR InterPro: IPR000561; EGF-like.

DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001791; Laminin_G.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam; PF00054; Laminin_G; 1.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 3.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00282; LamG; 2.
 DR PROSITE; PS00010; ASX_HYDROXYL; 3.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS01187; EGF_CA; 2.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat;
 FT SIGNAL 1 15 POTENTIAL.
 FT CHAIN 16 650 POTENTIAL.
 SQ SEQUENCE 650 AA; 72480 MW; C67345ECB645174 CRC64;

Query Match 37.6%; Score 68; DB 4; Length 650;
 Best Local Similarity 34.1%; Pred. No. 0.00021;
 Matches 15; Conservative 5; Mismatches 24; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRGSLXRCXXKXLCSEFXAXXIFRNXXRTQGFWSY 44
 Db 16 ANSLLEETKOGNLEECLEECNKEAREVEFNDPEFDYFPHY 59

RESULT 26
 Q16519 PRELIMINARY; PRT; 650 AA.

AC Q16519; 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PROTEIN S PRECURSOR (FRAGMENT).
 GN PROS1.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86313649; PubMed=2944113;
 RA Lundwall A., Dackowski W., Cohen E., Shaffer M., Mahr A., Dahlback B.,
 RA Stenflo J., Wydro R.;
 RT "Isolation and sequence of the cDNA for human protein S, a regulator
 RT of blood coagulation.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:6716-6720(1986).
 DR EMBL; M14338; AAB60181.1; -;
 DR HSSP; P00740; ICFH.
 DR InterPro: IPR000152; ASX_hydroxyl.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF_CA.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001791; Laminin_G.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 4.
 DR Pfam; PF00594; g1a; 1.
 DR Pfam; PF00054; Laminin_G; 1.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 3.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00282; LamG; 2.
 DR PROSITE; PS00010; ASX_HYDROXYL; 3.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS01187; EGF_CA; 2.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat;
 KW Signal.

FT NON_TER 1 1
 FT SIGNAL <1 15 POTENTIAL.
 FT CHAIN 16 650 PROTEIN S.
 SQ SEQUENCE 650 AA: 72462 MW: 9A8C044C503BF474 CRC64;

Query Match 37.6%; Score 68; DB 4; Length 650;
 Best Local Similarity 34.1%; Pred. No. 0.00021;
 Matches 15; Conservative 5; Mismatches 24; Indels 0; Gaps 0;

OY 1 ANGFLXLRXGSLRXCRRXXLCSPXXAXIFRNXXRTROFWVSY 44
 DB 16 ANSLEETKQCNLERECIEELCNKEAREVFENDEPETYFPKY 59

RESULT 27
 ID 091001 PRELIMINARY; PRT; 607 AA.

AC 091001;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE THROMBIN.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauaria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_TaxID=9031;

RN SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=92212913; PubMed=1557383;
 RA Banfield D.K., MacGillivray R.T.;
 RT "Partial characterization of vertebrate prothrombin cDNAs:
 RT amplification and sequence analysis of the B chain of thrombin from
 RT nine different species.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
 RN [2]

RN SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=94223694; PubMed=7513365;
 RA Banfield D.K., Irwin D.M., Walz D.A., MacGillivray R.T.;
 RT "Evolution of prothrombin: isolation and characterization of the cDNAs
 RT encoding chicken and hagfish prothrombin.";
 RL J. Mol. Evol. 38:177-187(1994).
 RN [3]

RN SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Banfield D.K.;
 RL Submitted (DEC-1991) to the EMBL/Genbank/DBJ databases.
 DR EMBL; M81391; AAA21619.1; -.

DR HSRP; P00734; IUVS.

DR MEROPS; S01.217; -.

DR InterPro; IPR001314; Chymotrypsin.

DR InterPro; IPR002383; GLA blood.

DR InterPro; IPR000001; Kringle.

DR InterPro; IPR003966; Prothrombin.

DR InterPro; IPR001254; Trypsin.

DR Pfam; PF00594; gla; 1.

DR Pfam; PF00051; kringle; 2.

DR SMART; SM00089; trypsin; 1.

DR PRINTS; PR00722; CHYMOTRYPSIN.

DR PRINTS; PR00001; GLABLOOD.

DR PRINTS; PR00018; KRINGLE.

DR PRINTS; PR01505; PROTHROMBIN.

DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR Hydrolase; Serine protease.
 SQ SEQUENCE 607 AA: 69110 MW: 002F3606EA36270F CRC64;

Query Match 36.5%; Score 66; DB 13; Length 607;
 Best Local Similarity 31.0%; Pred. No. 0.00047;
 Matches 13; Conservative 5; Mismatches 24; Indels 0; Gaps 0;

OY 3 GFLXLRXGSLRXCRRXXLCSPXXAXIFRNXXRTROFWVSY 44
 DB 47 GFLXLRXGSLRXCRRXXLCSPXXAXIFRNXXRTROFWVSY 88

RESULT 28
 ID 014393 PRELIMINARY; PRT; 678 AA.

AC 014393;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE GROWTH-ARREST-SPECIFIC PROTEIN.
 CN GAS6.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]

RN SEQUENCE FROM N.A.
 RX MEDLINE=93330291; PubMed=8336730;
 RA Manfioletti G., Brancolini C., Avanzi G., Schneider C.;
 RT "The protein encoded by a growth arrest-specific gene (gas6) is a new
 RT member of the vitamin K-dependent proteins related to protein S, a
 RT negative coregulator in the blood coagulation cascade.";
 RL Mol. Cell. Biol. 13:4976-4985(1993).
 DR EMBL; L13720; AAA58494.1; -.

DR HSRP; P00740; ICFH.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001881; EGF-Ca.
 DR InterPro; IPR002383; GLA blood.
 DR InterPro; IPR001791; Laminin G.
 DR InterPro; IPR000294; VitK_dep_GLA.

DR Pfam; PF00008; EGF; 4.
 DR Pfam; PF00594; gla; 1.
 DR Pfam; PF00054; laminin_G; 1.
 DR PRINTS; PR00001; GLABLOOD.

DR SMART; SM00179; EGF_CA; 3.

DR SMART; SM00001; EGF-like; 1.

DR SMART; SM00069; GLA; 1.

DR SMART; SM00282; LamG; 2.

DR PROSITE; PS00010; ASX_HYDROXYL; 4.

DR PROSITE; PS00022; EGF_1; UNKNOWN_1.

DR PROSITE; PS01186; EGF_2; 3.

DR PROSITE; PS01187; EGF_CA; 3.

DR PROSITE; PS00011; GLU-CARBOXYLATION; 1.

DR Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.

KW SEQUENCE 678 AA: 74925 MW: BB6D8AB0FC48EA9 CRC64;

Query Match 31.5%; Score 57; DB 4; Length 676;
 Best Local Similarity 36.1%; Pred. No. 0.028;
 Matches 13; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

OY 9 RKGSLRXCRRXXLCSPXXAXIFRNXXRTROFWVSY 44
 DB 57 KOGHLRECEVELCSREAREVFENDEPETYFPKY 92

RESULT 29
 ID 09QVH6 PRELIMINARY; PRT; 25 AA.

AC O9QVH6;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE FACTOR X LIGHT CHAIN.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=92041742; PubMed=1718949;
RA Enjyoji K., Miyazaki K., Kato H.;
RT "Characterization of rat factors X and Xa: demonstration of factor Xa
in rat plasma.";
RL J. Biochem. 109:890-898(1991).
DR HSSP: P00740; ICFH.
DR InterPro: IPR002383; GLA_blood.
DR PRINTS: PR00001; GLABLOOD.
SQ SEQUENCE 25 AA; 2932 MW; 657A6E9B57BEE56B CRC64;

Query Match 30.9%; Score 56; DB 11; Length 25;
Best Local Similarity 45.8%; Pred. No. 0 0015;
Matches 11; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 ANGFLXLRXGSLXRCXRLXCSF 24
Db 1 ANSFEEIKKGNLERECVXEICSF 24

RESULT 30
ID 061592 PRELIMINARY; PRT; 673 AA.
AC 061592;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE GAS6 PROTEIN.
GN GAS6 OR GAS6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Manfioletti G., Brancolini C., Bordo D., Philipson L., Schneider C.;
RT "Growth-arrest is associated with a negative control element in the
blood coagulation pathway";
RL MOL. Cell. Biol. 13:0-0(1993).
DR EMBL: X59846; CAA42507.1; -.
DR HSSP: P00740; ICFH.
DR MGD: MGI:95660; Gas6.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001791; Laminin_G.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF_4.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00054; Laminin_G; 2.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00001; EGF_CA; 3.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00282; LamG; 2.
DR PROSITE: PS00010; ASX_HYDROXYL; 4.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 3.
DR PROSITE: PS01187; EGF_CA; 3.
DR PROSITE: PS00011; GLU CARBOXYLATION; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.

SQ SEQUENCE 673 AA; 74512 MW; 6A49B3F004F92815 CRC64;

Query Match 30.9%; Score 56; DB 11; Length 673;
Best Local Similarity 33.3%; Pred. No. 0 043;
Matches 12; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

QY 9 RXGSLXRCXRLXCSFXXAXIFRNXXRTQFWVS 44
Db 54 KQGLHRECVCEVCSKEAREVFENDETEYFPR 89

RESULT 31
ID 099K57 PRELIMINARY; PRT; 674 AA.
AC 099K57;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE GROWTH ARREST SPECIFIC 6.
GN GAS6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC005444; AAH05444.1; -.
DR HSSP: P00740; ICFH.
DR MGD: MGI:95660; Gas6.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001791; Laminin_G.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF_4.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00054; Laminin_G; 2.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00181; EGF; 4.
DR SMART: SM00179; EGF_CA; 4.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00282; LamG; 2.
DR PROSITE: PS00010; ASX_HYDROXYL; 4.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 3.
DR PROSITE: PS01187; EGF_CA; 3.
DR PROSITE: PS00011; GLU CARBOXYLATION; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
SQ SEQUENCE 674 AA; 74609 MW; 7C41F7693903F401 CRC64;

Query Match 30.9%; Score 56; DB 11; Length 674;
Best Local Similarity 33.3%; Pred. No. 0 043;
Matches 12; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

QY 9 RXGSLXRCXRLXCSFXXAXIFRNXXRTQFWVS 44
Db 54 KQGLHRECVCEVCSKEAREVFENDETEYFPR 89

RESULT 32
ID P82807 PRELIMINARY; PRT; 98 AA.
AC P82807;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE COAGULATION FACTOR XA-LIKE PROTEIN (EC 3.4.21.6) (FRAGMENTS).
OS Notochis scutatus scutatus (Mainland tiger snake) (Common tiger

RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
 clone:P003E08."
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AP003222; BAB63546.1; -
 KW Kinase
 SQ SEQUENCE 575 AA; 65726 MW; 01701EFDf17321A4 CRC64;

Query Match 27.3%; Score 49.5; DB 10; Length 575;
 Best Local Similarity 35.7%; Pred. No. 0.64;
 Matches 10; Conservative 2; Mismatches 15; Indels 1; Gaps 1;

QY 17 CRXXLCSEFXAXXIFRNXXRTQFWVS 44
 Db 151 CKLKICDFGLARVAF-NDPTTFWTDY 177

RESULT 35
 Q9XF36 PRELIMINARY; PRT; 608 AA.

AC Q9XF36;
 DT 01-NOV-1999 (TReMBLrel. 12, Created)
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOGUE.
 GN TDY1.
 OS Medicago sativa (Alfalfa).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Fabales; Fabaceae; Papilionoideae; Trifoliales; Medicago.
 OX NCBI_TaxId=3879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94446225; PubMed=10517028;
 RA Schoenbeck M.A., Samac D.A., Fedorova M., Gregerson R.G., Gantt J.S.,
 RA Vance C.P.;
 RT "The alfalfa (Medicago sativa) TDY1 gene encodes a mitogen-activated
 RT protein kinase homolog."
 RL MOL. Plant Microbe Interact. 12:882-893(1999).
 DR EMBL: AF129087; AAD26617.1; -
 DR HSSP: P27703; 1ERK.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003527; MAP_kin.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS01351; MAPK; UNKNOWN_1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW ATP-binding; Kinase; Transferase.
 SQ SEQUENCE 608 AA; 68903 MW; E5FD33A74BD5A8E6 CRC64;

Query Match 27.3%; Score 49.5; DB 10; Length 608;
 Best Local Similarity 35.7%; Pred. No. 0.67;
 Matches 10; Conservative 2; Mismatches 15; Indels 1; Gaps 1;

QY 17 CRXXLCSEFXAXXIFRNXXRTQFWVS 44
 Db 163 CKLKVCDFGLARVAF-NDPTTFWTDY 189

RESULT 36
 O04284 PRELIMINARY; PRT; 196 AA.

AC O04284;
 DT 01-JUL-1997 (TReMBLrel. 04, Created)
 DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE MAP KINASE-LIKE PROTEIN (FRAGMENT).
 GN SDHN-6R.
 GN Selaginella lepidophylla.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Lycopodiophyta; Isoetopsida; Selaginellales; Selaginellaceae;
 OC Selaginella.
 OX NCBI_TaxId=59777;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Choi D.-W., Close T.J., Iturriaga G.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U96716; AAB57843.1; -
 DR HSSP: P27703; 1ERK.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003527; MAP_kin.
 DR Pfam: PF00069; pkinase; 1.
 DR PROSITE: PS01351; MAPK; UNKNOWN_1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW ATP-binding; Kinase; Transferase.
 FT NON_TER
 SQ SEQUENCE 196 AA; 22852 MW; 11417FA4E31CF72D CRC64;

Query Match 26.8%; Score 48.5; DB 10; Length 196;
 Best Local Similarity 35.7%; Pred. No. 0.33;
 Matches 10; Conservative 2; Mismatches 15; Indels 1; Gaps 1;

QY 17 CRXXLCSEFXAXXIFRNXXRTQFWVS 44
 Db 154 CKLKICDFGLARVAF-NDAPTAFWTDY 180

RESULT 37
 Q9SJG9 PRELIMINARY; PRT; 594 AA.

AC Q9SJG9;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE PUTATIVE MAP KINASE.
 GN ATG42880.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxId=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
 RA Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,
 RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
 RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
 RA Salzberg S.L., Fraser C.M., Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 RT thaliana."
 RL Nature 402:761-768(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Lin X.;

DR Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC006931; AAD21721.1; -
 DR HSSP: P24941; 1B38.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003527; MAP_kin.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS01351; MAPK; UNKNOWN_1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.

RT phylogenetic relatedness."
 RL Virology 277:368-378(2000).
 DR EMBL: AB041961; BAB19319.1; -
 SQ SEQUENCE 130 AA; 13841 MW; AF0ABD10BD5272EB CRC64;

Query Match 26.5%; Score 48; DB 12; Length 130;
 Best Local Similarity 36.0%; Pred. No. 0.27;
 Matches 9; Conservative 2; Mismatches 14; Indels 0; Gaps 0;

QY 17 CRXXLCSEFXAXXIFRNXXRTPQWVSY 41
 DB 27 CHOLFCCSSAMDLRNIILOTGWM 51

RESULT 41
 ID 094EY5 PRELIMINARY; PRT; 431 AA.

DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 GN PUTATIVE MAP KINASE.
 GN F25P22.9.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lam B., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
 RA Palm C.J., Bowser L., Jones T., Banh J., Carlincl P., Chen H.,
 RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamlya A., Kawat J.,
 RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
 RA Sekurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
 RA Ecker J., Theologis A., Davis R.W.
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF387019; AAK62464.1; -
 KW KINASE.
 SQ SEQUENCE 431 AA; 49425 MW; 471AAF18FD524C4 CRC64;

Query Match 26.2%; Score 47.5; DB 10; Length 431;
 Best Local Similarity 35.7%; Pred. No. 1.1;
 Matches 10; Conservative 2; Mismatches 15; Indels 1; Gaps 1;
 QY 17 CRXXLCSEFXAXXIFRNXXRTPQWVSY 44
 DB 228 CKLKICDFGLARVSF-NDAPTAIFWTDY 254

RESULT 42
 ID 09SMJ7 PRELIMINARY; PRT; 492 AA.
 AC 09SMJ7;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE MAP KINASE PROTEIN (FRAGMENT).
 OS Cicer arietinum (chickpea) (Garbanzo).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Ciceraceae; Cicer.
 OX NCBI_TaxID=3827;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. CASTELLANA. TISSUE-ETIOLATED EPICOTYLS;
 RA Duplico B., Esteban R., Labrador E.;
 RT "A MAP kinase is expressed in chickpea epicotyls."
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A2275316; CAB61750.1; -
 HSSP: Q165539; 1WFC.

DR InterPro: IPR000719; Euk_pkinase.
 DR Pfam: PF00069; pkinase.1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW ATP-binding; Kinase; Transferase.
 FT NON_TER 1
 SQ SEQUENCE 492 AA; 55638 MW; 8791EF36365A6811 CRC64;

Query Match 26.2%; Score 47.5; DB 10; Length 492;
 Best Local Similarity 35.7%; Pred. No. 1.3;
 Matches 10; Conservative 2; Mismatches 15; Indels 1; Gaps 1;

QY 17 CRXXLCSEFXAXXIFRNXXRTPQWVSY 44
 DB 51 CKLKVCDGFLARVAF-NDAPTSIFWTDY 77

RESULT 43
 ID 09MB23 PRELIMINARY; PRT; 543 AA.

AC 09MB23;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE AtMPK8.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA.
 RA Mizoguchi T., Ichimura K., Shinozaki K.;
 RT "Arabidopsis thaliana mRNA for MAP kinase."
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB036693; BAN9222.1; -
 DR HSSP: P24941; IHCL.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003527; MAP_kin.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase.1.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PS01351; MAPK; UNKNOWN_1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW ATP-binding; Transferase.
 SQ SEQUENCE 543 AA; 61513 MW; 60D508FDD40A94E9 CRC64;

Query Match 26.2%; Score 47.5; DB 10; Length 543;
 Best Local Similarity 35.7%; Pred. No. 1.4;
 Matches 10; Conservative 2; Mismatches 15; Indels 1; Gaps 1;

QY 17 CRXXLCSEFXAXXIFRNXXRTPQWVSY 44
 DB 242 CKLKICDFGLARVSF-NDAPTAIFWTDY 268

RESULT 44
 ID 09C904 PRELIMINARY; PRT; 576 AA.
 AC 09C904;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PUTATIVE MAP KINASE.
 GN F25P22.9.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;

[1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA:
 RX MEDLINE-21016719; PubMed-11130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buehler E., Chan A., Chao Q., Cheuk R.F., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
 RA Dunn P., Etgu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen H., Hughes B., Huizar L.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremetska I., Kurtz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Malti R., Maritali A.,
 RA Miltcher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 RA Sakano H., Salzer S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
 RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
 RT "Sequence and analysis of chromosome I of the plant Arabidopsis
 thaliana."
 RL Nature 408:816-820(2000).
 DR EMBL: AC012679; AAC52072.1; -
 DR HSSP: P24941; 1HCL.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00220; S_TKC; 1.
 DR SMART: SM00219; TyrKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR ATP-binding; Kinase; Transferase.
 KW SEQUENCE 576 AA; 65250 MW; F4P429EAF3CF4EE7 CRC64;
 SQ

Query Match 26.2%; Score 47.5; DB 10; Length 576;
 Best Local Similarity 35.7%; Pred. No. 1.5; Mismatches 10; Conservative 2; Indels 1; Gaps 1;
 Matches 10; Conservative 2; Mismatches 15; Indels 1; Gaps 1;
 QY 17 CRXXLCSEFXAXXIFRNXXRTROFWY 44
 DB 228 CLKIKICFGLARVSF-NDAPTAIFWTDY 254

RESULT 45
 O9LMS2 PRELIMINARY: PRT; 589 AA.
 ID O9LMS2: PRELIMINARY: PRT; 589 AA.
 AC O9LMS2:
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE T10F20.15 PROTEIN (PUTATIVE AMPK8 PROTEIN).
 GN T10F20.15.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_Taxid=3702;
 RT clones."
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA:
 RA Sakano H., Liu S.X., Etgu P., Lee J.M., Lenz C., Pham P., Toriumi M.,
 RA Yu G., Chan A., Chung M., Goldsmith A., Liu A., Smith A., Vaysberg M.,
 RA Altati H., Brooks S., Buehler E., Chao Q., Conn L., Conway A.B.,
 RA Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M.,
 RA Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W., Ecker J.R.,
 RA Federspiel N.A., Theologis A.,
 RT "The sequence of BAC T10F20 from Arabidopsis thaliana chromosome 1."
 RL Submitted (Aug-2000) to the EMBL/Genbank/DBJ databases.
 KW SEQUENCE FROM N.A.
 SQ

RA Yamada K., Liu S.X., Pham P.K., Banh J., Dale J.M., Goldsmith A.D.,
 RA Jiang P.X., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M.,
 RA Yamamura Y., Yu G., Yu S., Bowser L., Caninci P., Chen H., Cheuk R.,
 RA Hayashizaki Y., Ishida J., Jones T., Kamliya A., Katlin-Neumann G.,
 RA Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M.,
 RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
 RA Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W.,
 RA Ecker J.R., Theologis A., Tracy S.E., Shinozaki K., Davis R.W.,
 RT "Full Length cDNA of gene T10F20.15 (GI:9719729)."
 RL Submitted (Jul-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AC034107; AAF97831.1; -
 DR EMBL: AY045931; AAK76605.1; -
 DR HSSP: P24941; 1HCL.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003527; MAP_kin.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PS01351; MAPK; UNKNOWN_1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR ATP-binding; Kinase; Transferase.
 KW SEQUENCE 589 AA; 66231 MW; 96769BA5E16BD74 CRC64;
 SQ

Query Match 26.2%; Score 47.5; DB 10; Length 589;
 Best Local Similarity 35.7%; Pred. No. 1.6; Mismatches 10; Conservative 2; Indels 1; Gaps 1;
 Matches 10; Conservative 2; Mismatches 15; Indels 1; Gaps 1;
 QY 17 CRXXLCSEFXAXXIFRNXXRTROFWY 44
 DB 242 CLKIKICFGLARVSF-NDAPTAIFWTDY 268

RESULT 46
 O9LUC3 PRELIMINARY: PRT; 593 AA.
 ID O9LUC3: PRELIMINARY: PRT; 593 AA.
 AC O9LUC3:
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE MITOGEN-ACTIVATED PROTEIN KINASE.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_Taxid=3702;
 RT clones."
 RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA:
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.,
 RA Submitted (Feb-1999) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA:
 RX MEDLINE-20277480; PubMed-10819329;
 RA Nakamura Y.,
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
 features of the regions of 4,504,864 bp covered by sixty pl and YAC
 clones."
 RT DNA Res. 7:131-135(2000).
 RL EMBL: AB023038; BAB02403.1; -
 DR HSSP: P24941; 1HCL.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003527; MAP_kin.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PS01351; MAPK; UNKNOWN_1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR ATP-binding; Kinase; Transferase.
 KW SEQUENCE 593 AA; 66812 MW; 466BF08A131D23 CRC64;
 SQ

Query Match 26.2%; Score 47.5; DB 10; Length 593;
 Best Local Similarity 35.7%; Pred. No. 1.6;
 Matches 10; Conservative 2; Mismatches 15; Indels 1; Gaps 1;

OY 17 RXCRXXLCSEFXAXXIF-----RNXXRTQFW 44
 DB 158 CLKVKDFGLARVSF-NDPTTFWTDY 184

RESULT 47

O98SU5 PRELIMINARY; PRT; 472 AA.

AC O98SU5; 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DE SPICGIN GAMMA.

OS Gasterosteus aculeatus (three spined stickleback).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
 OC Gasterosteidae; Gasterosteus.
 OX NCBI_TaxID=69293;

RN SEQUENCE FROM N.A.
 RX MEDLINE-21264567; PubMed-11279178;

RA Jones I., Lindberg C., Jakobsson S., Hellqvist A., Hellman U.,
 Borg B., Olsson P.E.;
 RT "Molecular cloning and characterization of spiggin. An androgen-
 regulated extragenital adhesive with structural similarities to von
 Willebrand factor-related proteins.";
 RL J. Biol. Chem. 276:17857-17863(2001).

DR EMBL: AF323734; AAK15299.1; -;
 DR InterPro: IPR001846; Vwd.
 DR InterPro: IPR001007; VWFC.
 DR Pfam: PF00094; Vwd; 2.
 DR SMART: SM00214; VWC; 1.
 DR SMART: SM00216; VMD; 1.
 SQ SEQUENCE 472 AA; 54455 MW; BBE506FECAB3A394 CRC64;

Query Match 26.0%; Score 47; DB 13; Length 472;
 Best Local Similarity 27.0%; Pred. No. 1.6;
 Matches 10; Conservative 4; Mismatches 13; Indels 10; Gaps 1;

OY 15 RXCRXXLCSEFXAXXIF-----RNXXRTQFW 41
 DB 221 RLCKENICGFENSOSIFCPFEVVASQCNOSRINFW 257

RESULT 48

O98SU6 PRELIMINARY; PRT; 613 AA.

AC O98SU6; 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DE SPICGIN BETA.

OS Gasterosteus aculeatus (three spined stickleback).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
 OC Gasterosteidae; Gasterosteus.
 OX NCBI_TaxID=69293;

RN SEQUENCE FROM N.A.
 RX MEDLINE-21264567; PubMed-11279178;

RA Jones I., Lindberg C., Jakobsson S., Hellqvist A., Hellman U.,
 Borg B., Olsson P.E.;
 RT "Molecular cloning and characterization of spiggin. An androgen-
 regulated extragenital adhesive with structural similarities to von
 Willebrand factor-related proteins.";
 RL J. Biol. Chem. 276:17857-17863(2001).

RT Willebrand factor-related proteins.";
 RL J. Biol. Chem. 276:17857-17863(2001).
 DR EMBL: AF323733; AAK15298.1; -;
 DR InterPro: IPR001846; Vwd.
 DR InterPro: IPR001007; VWFC.
 DR Pfam: PF00094; Vwd; 2.
 DR SMART: SM00214; VWC; 1.
 DR SMART: SM00216; VMD; 2.
 SQ SEQUENCE 613 AA; 69621 MW; 5A8B5EDF82337DF3 CRC64;

OY 15 RXCRXXLCSEFXAXXIF-----RNXXRTQFW 41
 DB 221 RLCKENICGFENSOSIFCPFEVVASQCNOSRINFW 257

RESULT 49

O98SU7 PRELIMINARY; PRT; 910 AA.

AC O98SU7; 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DE SPICGIN ALPHA.

OS Gasterosteus aculeatus (three spined stickleback).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
 OC Gasterosteidae; Gasterosteus.
 OX NCBI_TaxID=69293;

RN SEQUENCE FROM N.A.
 RX MEDLINE-21264567; PubMed-11279178;

RA Jones I., Lindberg C., Jakobsson S., Hellqvist A., Hellman U.,
 Borg B., Olsson P.E.;
 RT "Molecular cloning and characterization of spiggin. An androgen-
 regulated extragenital adhesive with structural similarities to von
 Willebrand factor-related proteins.";
 RL J. Biol. Chem. 276:17857-17863(2001).

DR EMBL: AF323732; AAK15297.1; -;
 DR InterPro: IPR003571; Snake_toxin.
 DR InterPro: IPR001846; Vwd.
 DR InterPro: IPR001007; VWFC.
 DR Pfam: PF00094; Vwd; 3.
 DR SMART: SM00214; VWC; 1.
 DR SMART: SM00216; VMD; 2.
 DR PROSITE: PS00272; SNAKE_TOXIN; UNKNOWN_1.
 SQ SEQUENCE 910 AA; 102673 MW; 6B7P6E43ED3A5BD1 CRC64;

Query Match 26.0%; Score 47; DB 13; Length 910;
 Best Local Similarity 27.0%; Pred. No. 3.1;
 Matches 10; Conservative 4; Mismatches 13; Indels 10; Gaps 1;

OY 15 RXCRXXLCSEFXAXXIF-----RNXXRTQFW 41
 DB 221 RLCKENICGFENSOSIFCPFEVVASQCNOSRINFW 257

RESULT 50

O98SU6 PRELIMINARY; PRT; 687 AA.

AC O98SU6; 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DE TRAE.

OS Enterobacter aerogenes (Aerobacter aerogenes).
 OC Bacteria; Firmicutes; Bacilli; Enterobacteriaceae; Enterobacter.
 OX NCBI_TaxID=573;

RN SEQUENCE FROM N.A.
 RX MEDLINE-11279178; PubMed-11279178;

RA Jones I., Lindberg C., Jakobsson S., Hellqvist A., Hellman U.,
 Borg B., Olsson P.E.;
 RT "Molecular cloning and characterization of spiggin. An androgen-
 regulated extragenital adhesive with structural similarities to von
 Willebrand factor-related proteins.";
 RL J. Biol. Chem. 276:17857-17863(2001).

OC Plasmid R751.
 CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Enterobacter.
 OX NCBI_TaxID=548;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-98428622; PubMed-9753548;
 RA Thorsted P.B., Macartney D.P., Akhtar P., Haines A.S., Ali N.,
 RA Davidson P., Stafford T., Pocklington M.J., Pansegrau W.,
 RA Wilkins B.M., Lanka E., Thomas C.M.;
 RT "Complete sequence of the IncpBeta plasmid R751: implications for
 RT evolution and organisation of the IncP backbone.";
 RL J. Mol. Biol. 282:969-990(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Thomas C.M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Haines A.S., Thomas C.M.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U67194; AAC64472.1; -.
 DR HSP; P06612; 1ECL.
 DR InterPro: IPR003601; DNATopI_ATP_bind.
 DR InterPro: IPR003602; DNATopI_DNA_bind.
 DR InterPro: IPR003603; Pro_topoisomerase.
 DR InterPro: IPR002936; Toprim.
 DR Pfam: PF01131; Topoisom_bac; 1.
 DR Pfam: PF01751; Toprim; 1.
 DR Pfam: PF01396; zif-C4_Topoisom; 1.
 DR SMART: SM00437; TOP1Ac; 1.
 DR SMART: SM00436; TOP1Bc; 1.
 DR SMART: SM00493; TOPRIM; 1.
 KW plasmid.
 SQ SEQUENCE 687 AA; 75062 MW; E3FA0FE6DA3B5676 CRC64;

Query Match 24.9%; Score 45; DB 2; Length 687;
 Best Local Similarity 61.5%; Pred. No. 5.5;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 31 FRNXXRTROFVNS 43
 ||| 1:||||
 DB 125 FRNSKPVRRFVNS 137

Search completed: September 3, 2002, 15:21:14
 Job time: 347 sec

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